MICROBIAL DIVERSITY AND IMMUNOGENETICS OF WHIPTAIL LIZARDS (*ASPIDOSCELIS*)

by

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Chapter 1: Comparison of Cloacal Microbiomes in Whiptail Lizards (Aspidoscelis) Across Environments

Introduction

All multicellular organisms are inhabited by a variety of microorganisms which, along with their respective genomes, are collectively known as the host's microbiome. For vertebrates these microbiota can be found externally (e.g. skin, hair) and throughout many different systems internally (e.g. digestive, respiratory, reproductive) (Ley et al. 2008; Trevelline et al. 2018). The host-microbiome relationship is highly complex, with each affecting the other in significant ways (Ley et al. 2008). These communities, especially those in the gastrointestinal tract, play a significant role in host physiology (e.g. immune response, digestion, nutrient uptake; Bonder et al. 2016; Ley et al. 2006). The acquisition, development, and maintenance of these communities can be influenced by several factors such as the host's environment, diet, and genetics (Goodrich et al. 2014; Park et al. 2021; Spor, Koren, and Ley 2011; Wu et al. 2018).

Many environmental factors such as habitat, climate, and altitude have all been shown to play a role in the composition of these gut communities (Longo et al. 2017; Rothschild et al. 2018; Wu et al. 2018). In human studies, household sharing is seen to to affect microbiome composition more than relatedness of individuals, and studies in mice and lizards have found significant associations between gut communities and altitude shifts (Gorkiewicz et al. 2018; Rothschild et al. 2018; Suzuki, Martins, and Nachman 2019; Zhang et al. 2018). Research has also shown that diet may have the biggest affect on community composition and can significantly alter the presence and abundances of microbes, which can have downstream affects when it comes to food digestion and nutrient uptake (Kohl and Carey 2016; Kohl et al. 2017; Ley et al. 2018; Robertson et al. 2019; Spor, Koren, and Ley 2011). For example, an incredible shift in species richness and diversity is seen in human infants when solid foods are introduced to their diets, and similar shifts are seen in omnivorous lizards when they are transitioned to fully herbivorous diets (Kohl et al. 2016; Robertson et al. 2019).

Gut microbial communities can also be influenced by host genetics, though to what extent is still unknown (Bonder et al. 2016). Some studies have identified heritable bacterial taxa and have found associations between certain bacterial taxa and specific genes, while other studies have found that host genetics play a minor role at best (Bonder et al. 2016; Blekhman et al. 2015; Sanna et al. 2022). These conflicting results may arise for a number of reasons including sampling methods, study system, lab-reared vs wild organisms, and analytical methods (Goodrich et al. 2014; Kohl et al. 2017; Sanna et al. 2022). Evidence of this can be seen in studies finding significant correlations between host genetics and gut bacterial communities of lab-reared model organisms (e.g. mice) where environmental conditions are highly controlled, versus studies of wild organisms in which the host's affect on gut bacteria is less clear (Bahrndorff et al. 2016; Kohl et al. 2016, 2017).

It is also worth noting the disproportionate amount of vertebrate microbiome studies that use mammalian versus non-mammalian systems, leaving the latter poorly explored despite making up a large portion of vertebrates (Pascoe et al. 2017). Additionally, the overwhelming majority of these studies are done on lab-reared model systems or captive animals like livestock and pets (Pascoe et al. 2017). Neither of which give an accurate representation of the animal's natural microbiome, and leaves the microbiomes of wild vertebrates wildly understudied. Increasing the number of studies using natural populations will allow us to learn more about the relationship between the host and microbiome, as well as enhance our understanding of biodiversity and natural history of populations.

To address these concerns, we utilized wild populations of Whiptail lizards (genus *Aspidoscelis*) which are widespread throughout the southwestern United States and Mexico, and exhibit both sexual and asexual reproduction. The latter are all-female clonal lineages that arise via hybridization events between two sexual species and reproduce via parthenogenesis, requiring no reproductive or genetic input from males (Manning et al. 2005; Wright et al. 1993). True parthenogenesis is rare in nature, and in vertebrates is only seen in lizards and snakes (Avise 2008; Fujita et al. 2020). Thus, whiptails provide a unique opportunity to investigate the factors that influence microbiome composition in vertebrates as asexual species can serve as a control for genetic variation and live in sympatry with their sexually reproducing relatives. Comparisons between these sympatric sexual and asexual species allow an explicit test between the influences of host population genetics and the environment.

Here, we aim to identify differences in gut microbial community composition between reproductive modes within sympatric localities and across different localities. We expect there to be a shared "core" community between all species as their habitats and diets will be the same, but anticipate differences in the abundance of some bacterial taxa as a result of different reproductive mode. The asexual species presumably come into less physical contact with other individuals as they do not require a mate to reproduce, which would result in decreased sharing of communities. We expect to see the "core" communities across localities as well, but could again see differences in abundance as well as diversity due to varying environmental conditions. Ultimately by addressing these questions we will gain a deeper understanding of the host-microbiome relationship, and specifically how the host's genetics and environment may affect microbial community composition.

Methods

Sample collection

Sampling for this study took place across Texas (Presidio Co., Brewster Co., Webb Co., Jeff Davis Co., and Potter Co.), New Mexico (Otero Co. and Socorro Co.), Colorado (Otero Co.), and California (Orange Co.). We categorized regions by biome as follows the Commission for Environmental Cooperation (Mumme and Duncan 1997): Mediterranean California (MC), South Central Semiarid Prairies (SCSP), Tamaulipas-Texas Semiarid Plains (TTSP), and Warm North American Deserts (WNAD). For the asexuals, we targeted *Aspidoscelis exsanguis, A. laredoensis, A. neomexicanus, A.*

neotesselatus, A. sonorae, A.tesselatus, and *A. uniparens*. For the sexuals, we targeted *A. gularis, A. inornatus, A. marmoratus,* and *A. septemvittatus*. (Sample information is available in Appendix I)

Immediately following verification of euthanasia (ACUC protocol A13.010), lizards were prepared for bacterial sampling by cleaning the vent and surrounding area with an ethanol wipe. A sterile swab (Puritan 253316U Ultra Flocked Swab) was then inserted into the cloaca and rotated back and forth ~10 times, followed by collection of a second swab done in the same manner (Colston, Noonan, and Jackson 2015). Each swab was placed in a sterile cryovial and stored in liquid nitrogen until returned to the lab where they were transferred to a -80ºC freezer until further processing. In addition to cloacal swabs, various tissues (liver, heart, skeletal muscle, spleen, stomach and a portion of hind-gut containing fecal matter) were also collected when possible for use in additional studies and stored in either RNAlater or liquid nitrogen. All individuals were then prepared as museum specimens and deposited in the collections of the Amphibian and Reptile Diversity Research Center (ARDRC) at University of Texas at Arlington.

DNA Extraction, Amplification, and Sequencing

We extracted DNA from all cloacal swabs using the DNEasy PowerSoil Pro Kit (Qiagen) and also included one “blank” extraction from each kit used in order to correct for any potential contaminates from the extraction process. We then assessed DNA yield using the dsDNA High Sensitivity Assay Kit on a Qubit Fluorometer 2.0. The V3V4 region of the 16S rRNA gene was amplified via polymerase chain reaction using indexed primers. Each 25ul reaction contained: 5ul of Q5 reaction buffer (5x), 5ul of Q5 high GC enhancer (5x), 0.2ul of 25mM dNTP, 1ul of both primers (5uM), 0.2ul of Q5 Hot Start DNA polymerase (NEB), 1-10ng DNA and water to reach the final 25ul volume. Each reaction was done in triplicate and run under the following thermocycling conditions: 98ºC for 2 min (initial denaturation), followed by 32 cycles of 98ºC for 2 min (denaturation), 53.6ºC for 20s (annealing), 72ºC for 20s (extension), and final extension at 72ºC for 2 min. Once PCR products were verified on a 1% agarose gel, the triplicates were pooled for each individual sample and quantified again using the Qubit. Amplicons were then pooled at equal concentrations (2ng per sample) into a single library. Sequencing was done using an Illumina MiSeq v3 platform for 300 bp paired-end reads.

Data processing

Sequences were received demultiplexed. We used *cutadapt* to remove primers and then imported them to R for further processing. The DADA2 package was used for quality filtering and trimming of sequences, merging paired reads, constructing an Amplicon Sequence Variant (ASV) table, removing chimeras, and assigning taxonomy using the Silva 138 reference database (Callahan et al. 2016). Once taxonomy and ASV count tables were generated, potential contaminants were removed based on the sequences that were returned for the two negative controls (decontam). Sequences were aligned using the R package DECIPHER and an unrooted tree was inferred from the alignment using the neighbor-joining algorithm in the R package phangorn (Schliep 2011; Wright 2016). This tree served as the starting point for a maximum likelihood analysis using the function optim.pml() employing the GTR model with NNI branch swapping. Using the phyloseq package (McMurdie and Holmes 2013), the sample metadata, ASV count table, taxonomy table, sequences, and tree were all combined into a single object. Finally, all ASVs assigned to Chloroplast or Mitochondria were filtered out and the resulting object was used for all further analyses.

Statistical Analysis

Observed richness and Shannon diversity index (SDI) values were obtained using the *phyloseq* function estimate_richness(), and Faith's phylogenetic diversity values were calculated using the estimate_pd() function from the *btools* package. Normality testing was performed using the Shapiro-Wilk test. Subsequently, for the two biomes where both reproductive modes were sampled (TTSP and WNAD), the effect of reproductive mode on each alpha diversity metric was tested for significance using the Wilcoxon rank-sum test. The effect of biome on alpha diversity for each reproductive mode was also tested for significance using either the Wilcoxon rank-sum test or the Kruskal-Wallis rank sum test. Additionally, the mean, min, median, max, and standard deviation of the alpha diversity metrics were calculated for each reproductive mode in each biome. ASV counts were then transformed to relative abundances and ASVs were agglomerated separately at the phylum and family levels, resulting in two new phyloseq objects (Appendices II & III, respectively). The following steps were performed for each object at their respective taxonomic level: the mean ASV abundances were calculated separately for each reproductive mode in each biome, and these means were then used to identify the most abundant taxa across all samples. Any ASV not in the top 5 most abundant phyla or top 10 most abundant families were designated as “Other” for plotting purposes.

Comparison of beta diversity was done between sexuals and asexuals within the TTSP and WNAD biomes, as well as for each reproductive mode across all biomes. Bray-Curtis distances were calculated using the vegdist() function in the vegan package, and both weighted and unweighed UniFrac distances were obtained with phyloseq. Once again using vegan, the betadisper() function was used to calculate dispersion between groups and the adonis() function was used to perform a PERMANOVA for each distance metric. Differential abundance of bacterial phyla and families was tested using differentialTest() in the R package corncob.

Results

Sampling

Overall, we collected cloacal swabs, tissue, and specimens from 167 individuals across all collection sites under IACUC-approved protocols (A13.010; Fig 1). For the asexuals we collected a total of 60 individuals from *A. exsanguis* (n = 17), *A. laredoensis* (n = 3), *A. neomexicanus* (n = 9), *A. neotesselatus* (n = 1), *A. sonorae* (n = 21), *A.tesselatus* (n = 7), and *A. uniparens* (n = 2). For the sexuals we collected a total of 107 individuals from *A. gularis* (n = 16), *A. inornatus* (n = 33), *A. marmoratus* (n = 29), and *A. septemvittatus* (n = 29)(Fig. 1; all specimen locality data is available in Appendix I). DNA was extracted from the first swab for all samples, and the following results are based on those extractions.

Data Processing

Sequencing resulted in 22,788,874 paired-end 300-bp reads, 6,434,514 of which were not indexed, resulting in 16,354,360 indexed, 300-bp paired-end reads. Processing in DADA2 returned 10,290,732 reads after quality filtering and trimming, 4,810,110 merged paired-end reads, and 4,483,922 non-chimeric paired-end reads. Assigning taxonomy in DECIPHER resulted in 14,810 ASVs, which was reduced to 14,787 after removing likely contaminants with decontam. Filtering with phyloseq resulted in the removal of 26 Mitochondrial sequences, 28 Chloroplast sequences, and 112 sequences that were unassigned at class level. The resulting dataset contained 14,621 ASVs, which were further reduced to 14,582 after filtering those that did not appear at least once in any sample.

Statistical Analyses

Mediterranean California

The mean observed richness for asexuals (n= 21) in Mediterranean California was 56, the mean Shannon diversity index was 1.8, and the mean phylogenetic diversity was 17.7 (Table 1; Fig. 2-4). The top four most abundant phyla were *Firmicutes* (55.4% ± 5.9% (SE)), *Actinobacteriota* (24% ± 4.7%), *Proteobacteria* (14.5% ± 5.6%), and *Bacteroidota* (4.4% ± 0.68%) (Fig. 5). The most abundant bacterial family was *Lachnospiraceae* which accounted for 43.6% (± 5.0%) (Fig. 6). The next two most abundant families were *Diplorickettsiaceae* (10.3% ± 5.8%) and *Dietziaceae* (8.9% ± 2.1%), and eleven other families contributed between 1%-3% (Fig. 6).

South Central Semiarid Prairies

The single asexual individual from the South Central Semiarid Prairies had a richness of 100, Shannon diversity index of 2.3, and phylogenetic diversity of 17.4 (Table 1; Fig. 2-4). The top four most abundant phyla were *Actinobacteriota* (76%), *Firmicutes* (18.9%), *Proteobacteria* (2.68%), and *Campylobacterota* (1.1%) (Fig. 5). The most abundant family for this individual was *Micrococcacea* (37.6%), followed by *Dietziaceae* (14.7%), *Lachnospiraceae* (13.7%), *Brevibacteriaceae* (6.2%), *Dermabacteraceae* (6.2%), and several others accounting for 1% - 2% each (Fig. 6).

Tamaulipas-Texas Semiarid Plains

In the Tamaulipas-Texas Semiarid Plains, the mean observed richness for asexuals (n= 3) was 46, the mean Shannon diversity index was 1.5, and the mean phylogenetic diversity was 15 (Table 1; Fig. 2-4). The top four most abundant phyla for asexuals were *Actinobacteriota* (95.9% ± 0.78%), *Firmicutes* (2.1% ± 1.3%), *Proteobacteria* (1.6% ± 0.70%), and *Bacteroidota* (0.14% ± 0.08%) (Fig. 5). The most abundant families for the asexuals were *Micrococcaceae* (43.8% ± 20.6%) and *Intrasporangiaceae* (15.1% ± 8.7%), but had contributions of 2% - 9% from other families (*Nocardiaceae*, *Nocardioidaceae*, *Brevibacteriaceae*, and *Dietziaceae*) (Fig. 6). Sexuals (n= 8) in this biome had a mean observed richness of 39, a mean Shannon diversity index of 1.6, and mean phylogenetic diversity of 12.5 (Table 1; Fig. 2-4). The top four most abundant phyla for sexuals were *Actinobacteriota* (95% ± 2.3%), *Proteobacteria* (3.6% ± 1.9%), *Firmicutes* (0.73% ± 0.42%), and *Bacteroidota* (0.28% ± 0.16%) (Fig. 5). The most abundant family for the sexuals was *Dietziaceae* (40.4% ± 9.6%), with four other families contributing 10% - 15% (*Brevibacteriaceae*, *Dermabacteraceae*, *Corynebacteriaceae*, and *Micrococcaceae*) (Fig. 6). There were no significant differences for any of the alpha diversity metrics between sexuals and asexuals (Table 2; Fig. 2-4). However, when comparing beta diversity by Bray-Curtis distance, there was a significant difference (*p*= 0.011) in composition between sexuals and asexuals, though they were dispersed similarly (Table 3; Fig. 7). Clustering by both weighted and unweighted UniFrac distances did not show significant differences in community composition or community membership, and both groups showed similar dispersion (Table 3; Fig. 8-9). Differential abundance analyses did not show any significant differences between asexuals and sexuals for bacterial families or phyla.

Warm North American Deserts

In the Warm North American Deserts, the mean observed richness for asexuals (n=35) was 46, the mean Shannon diversity index was 1.4, and the mean phylogenetic diversity was 14.8 (Table 1; Fig. 2-4). The most abundant phyla for asexuals were *Actinobacteriota* (68.5% ± 5.6%), *Firmicutes* (19.4% ± 4.6%), *Proteobacteria* (7% ± 1.7%), and *Bacteroidota* (3.6% ± 1.1%) (Fig. 5). The most abundant families for asexuals were *Dietziaceae* (36% ± 7.4%), *Micrococcacea* (16.4% ± 5.3%), and *Lachnospiraceae* (10.3% ± 2.9%), with a dozen others each contributing 1%-3% (Fig. 6). Sexuals (n= 99) had a mean observed richness of 49, a mean Shannon diversity index of 1.8, and mean phylogenetic diversity of 15.8 (Table 1-2; Fig. 2-4). Sexuals had the same top three phyla of *Actinobacteriota* (56.1% ± 3.6%), *Firmicutes* (23.5% ± 3%), and *Proteobacteria* (8.1% ± 1.1%), but their fourth was *Campylobacterota* (5.4% ± 1.7%) (Fig. 5). The sexuals had the same three most abundant families as the asexuals, though with different abundances: *Dietziaceae* (18.9% ± 2.6%), *Lachnospiraceae* (14.7% ± 2.0%) and *Micrococcaceae* (13.8% ± 2.5%) (Fig. 6). When comparing alpha diversity, the only significant difference between groups was in Shannon diversity index (*p*=0.021; Table 2). When comparing beta diversity, there was a significant difference in Bray-Curtis distance (*p*= 0.015), but the groups were similarly dispersed (Table 3; Fig. 7). Clustering by weighted UniFrac showed a significant difference in both community composition (*p*=0.014) and dispersion (*p*= 0.029), but no significant differences in community membership or dispersion were observed when clustering by unweighed UniFrac (Table 3; Fig 8-9). Differential abundance analysis between reproductive modes showed that bacterial families *Nocardiaceae*, *Enterobacteriaceae*, and *Moraxellaceae* were significantly higher in asexuals (p < 0.005), while *Corynebacteriaceae*, *Monoglobaceae*, *Helicobacteraceae*, and *Brevibacteriaceae* were significantly higher in sexuals (p < 0.005; Table 4). Only one phylum (*Campylobacterota*) showed to be differentially abundant, and was significantly higher in sexuals (p < 0.001; Table 4).

Reproductive modes across biomes

Beta diversity of asexuals was compared across all four biomes (MC, SCSP, TTSP, and WNAD) and showed significant differences and different dispersions for all methods ("Asexual ~ Biome"; Table 3; Fig. 7-9). When measured by Bray-Curtis distance, *p*= 0.001 and dispersion *p*=0.0001 (Table 3). Clustering by weighted UniFrac, *p*= 0.001 and dispersion *p*< 0.001 (Table 3). Clustering by unweighted UniFrac, *p* = 0.001 and dispersion p< 0.001 (Table 3). Pairwise comparisons of beta-diversity of asexuals between biomes resulted in two significant comparisons in Bray-Curtis dissimilarity, unweighted UniFrac, and weighted UniFrac: comparisons between MC and the TTSP, and between MC and WNAD (Table 5) Differential abundance testing showed that asexuals in WNAD and TTSP had significantly higher abundances of bacterial phylum *Actinobacteriota* than those in MC, but significantly lower abundances of *Firmicutes*, *Bacteroidota*, and *Campylobacterota* (Table 6). Additionally, asexuals in WNAD also had significantly lower abundances of *Campylobacterota* than those in SCSP. A number of bacterial families were shown to be significantly differentially abundant, and can be seen in Table 6.

Comparisons were also made for sexuals across the two biomes in which they were sampled (TTSP and WNAD; Table 7). A significant difference was seen in beta-diversity when measured by Bray-Curtis ($p = 0.001$) and groups were dispersed differently ($p < 0.001$; Table 3; Fig. 7). Additionally, there were significant differences when clustering by weighted ($p = 0.002$) and unweighted ($p = 0.01$) UniFrac, though groups were only dispersed differently for weighted ($p < 0.001$) UniFrac ("Sexual ~ Biome"; Table 3; Fig. 8-9). There were no differentially abundant bacterial phyla between sexuals across biomes, though there were three families that were significantly higher in those from TTSP when compared to WNAD sexuals: *Intrasporangiaceae, Dermabacteraceae, Brevibacteriaceae* (Table 7). All diversity metrics per sample are detailed in Appendix IV.

Discussion

Given the crucial role the vertebrate gut microbiome plays in the health and overall success of its host, a common aim of microbiome studies is to gain a deeper understanding of the composition of these communities and how they are influenced by various factors (e.g. habitat, diet, host genetics; Blekhman et al. 2015; Knutie et al.

2017; Rothschild et al. 2018). While there has been a shift in recent years to investigate the microbiomes of wild non-model organisms, reptiles remain underutilized as study systems despite being one of the most diverse vertebrate groups (Kohl et al. 2016; Zhang et al. 2018). Our study contributes to the growing number of reptile microbiome studies while also seeking to identify how the composition of the microbiome differs in sympatric parthenogenetic and sexually reproducing lizards of the same genus across and within different biomes.

Comparison across environments

We characterized the cloacal microbiomes of sexual and asexual whiptail lizards across four biomes in the southwestern United States. When examining microbial communities of sexuals and asexuals within-biome, we found significant differences in alpha-diversity (Shannon Diversity Index - WNAD), beta-diversity (community dissimilarity - WNAD and TTSP; phylogenetic community composition - WNAD), and differentially abundant taxa (Phyla and Families - WNAD; Tables 2-4; Fig. 2-4). We also examined both reproductive modes between-biomes, and in sexuals found significant differences in beta-diversity (community dissimilarity and phylogenetic community composition) as well as differentially abundant bacterial families (Tables 3,7). In contrast, for asexuals between biomes there were significant differences in beta-diversity (community dissimilarity, phylogenetic community composition, and community membership) and many more differentially abundant phyla and families (Tables 3,5-6).

While we do see significant differences between reproductive modes, the results in their entirety tend to suggest that the environment (biome) had a larger influence on microbiome communities (Table 2; Fig. 5-6). However, it is worth noting that some of these comparisons could have been affected by uneven sampling, as we were only able to obtain samples from both reproductive modes in two (WNAD and TTSP) out of the four biomes we collected in, and one biome in particular was more heavily sampled than the others (WNAD).

Additionally, some of the biggest differences seen between biomes were observed among the samples within the Mediterranean California biome. The asexual lizards collected there (*Aspidoscelis sonorae*) are highly urbanized and considered to be invasive as they are native to the desert habitats of Arizona, New Mexico, and adjacent Mexico (Fisher, Fisher, and Pauly 2022). Similar to other microbiome studies on species from natural populations in disturbed versus undisturbed areas, we also see the impact of urbanization on microbiome community composition among closely-related species (Murray et al. 2020; Wu et al. 2018). Specifically, the asexual species from MC had a significantly higher abundance of the phylum *Firmicutes* than any other group in any other biome (Fig. 5). There is a well established link between high abundances of this phylum including increased adipose tissue, obesity , and decreased fitness (Turnbaugh et al. 2006; Abenavoli et al. 2019). Future analyses on more detailed and direct effects of urbanization on the microbiome would include a direct comparison of the MC *A. sonorae* samples with other *A. sonorae* from its native range. Though in this instance we are analyzing an invasive lizard population, this pattern still provides more evidence for the negative effects that urbanization and human disturbance could have on the health of wildlife (Bahrndorff et al. 2016; Wu et al. 2018).

Sexuals vs asexuals

We were able to collect individuals from both reproductive modes in two different biomes: the Warm North American Deserts (WNAD) and the Tamaulipas-Texas Semiarid Plains (TTSP). The top three most abundant phyla for both reproductive modes in both biomes were *Actinobacteriota*, *Firmicutes*, and *Proteobacteria* (Fig. 5). In TTSP, asexuals and sexuals also shared the same fourth most abundant phylum, *Bacteriodota*. In WNAD however, *Bacteriodota* was the fourth most abundant phylum for asexuals, while *Campylobacterota* was the fourth most abundant for sexuals (Fig. 5). While the difference in SDI between sexuals and asexuals was significant within the WNAD, we saw no significant difference between reproductive mode within the TTSP (Fig. 2). Within the WNAD, we did have somewhat uneven sampling (35 asexuals vs 99 sexuals), and in future analyses we would improve upon the sampling strategy to include sampling of more individuals, more even sampling within and between biomes, and collection of additional media, such as plants, water, or soil, for comparison.

Moreover, as previous studies have done, we would also compare the microbiome composition of the cloacal swabs used in this study to fecal samples collected from the hind-gut (Kohl et al. 2017; Videvall et al. 2018).

Conclusion

Overall our study utilized wild populations of a non-model system to investigate the drivers in microbiome diversity. Our results suggest that host environment (biome) plays a more significant role in influencing microbiome community than that of reproductive mode in whiptail lizards, which is consistent with findings of other studies investigating the various factors that influence microbiome composition. We also show that the composition of an urbanized group of whiptail lizards is distinctly different from groups in their natural population ranges. Specifically of note was the much higher abundance of the bacterial phylum *Firmicutes* in the urbanized lizards, as this phylum is very closely linked with obesity and could be an indication of the impacts urbanization and humans have on the overall health of wildlife. Further investigation into what potential effects host-genetics might have on the microbiome could help better define brad host-microbiome interactions in this useful lizard system.

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Tables

Table 1 Mean Alpha diversity metrics by Biome and reproductive mode. Rep=Reproduction mode; SDI=Shannon Diversity Index; SD=Standard Deviation; Obs=Observed richness; PD= Faith's Phylogenetic Diversity.

Biome	Rep	n	SDI Min	SDI Median	SDI Max	SDI Mean
Mediterranean California	asexual	21	0.4956	1.7929	3.3057	1.8482
Mediterranean California	sexual	1	NA	NA	NA	NA
South Central Semiarid Prairies	asexual	1	2.2626	2.2626	2.2626	2.2626
South Central Semiarid Prairies	sexual	1	NA	NA	NA	NA
Tamaulipas - Texas Semiarid Plains	asexual	3	1.3145	1.4288	1.7308	1.4914
Tamaulipas - Texas Semiarid Plains	sexual	8	0.5040	1.5710	2.5043	1.6267
Warm North American Deserts	asexual	35	0.0790	1.2994	3.2855	1.4040
Warm North American Deserts	sexual	99	0.1735	1.9063	3.3261	1.8370
Biome	**Rep**		**SDI SD**	**Obs Min**	**Obs Median**	**Obs Max**
Mediterranean California	asexual		0.7294	22.0000	58.0000	113.0000
Mediterranean California	sexual		NA	NA	NA	NA
South Central Semiarid Prairies	asexual		NA	58.0000	58.0000	58.0000
South Central Semiarid Prairies	sexual		NA	NA	NA	NA
Tamaulipas - Texas Semiarid Plains	asexual		0.2151	27.0000	36.0000	76.0000
Tamaulipas - Texas Semiarid Plains	sexual		0.6265	12.0000	33.5000	89.0000
Warm North American Deserts	asexual		1.0615	8.0000	42.0000	114.0000
Warm North American Deserts	sexual		0.8674	7.0000	43.0000	136.0000
Biome	**Rep**		**Obs Mean**	**Obs SD**	**PD Min**	**PD Median**
Mediterranean California	asexual		56.2381	22.0996	7.5845	18.0737
Mediterranean California	sexual		NA	NA	NA	NA
South Central Semiarid Prairies	asexual		58.0000	NA	17.3919	17.3919
South Central Semiarid Prairies	sexual		NA	NA	NA	NA
Tamaulipas - Texas Semiarid Plains	asexual		46.3333	26.0832	8.9776	9.9585
Tamaulipas - Texas Semiarid Plains	sexual		39.2500	25.2855	3.3959	10.6228
Warm North American Deserts	asexual		46.3143	23.5569	2.8871	13.2284

Warm North American Deserts	sexual		49.3737	26.2463	2.7933	14.2407
Biome	**Rep**		**PD Max**	**PD Mean**	**PD SD**	
Mediterranean California	asexual		33.3450	17.7185	6.2940	
Mediterranean California	sexual		NA	NA	NA	
South Central Semiarid Prairies	asexual		17.3919	17.3919	NA	
South Central Semiarid Prairies	sexual		NA	NA	NA	
Tamaulipas - Texas Semiarid Plains	asexual		26.2563	15.0641	9.7051	
Tamaulipas - Texas Semiarid Plains	sexual		29.0144	12.5161	8.6208	
Warm North American Deserts	asexual		36.3240	14.8286	7.5978	
Warm North American Deserts	sexual		43.4204	15.8160	8.2763	

Table 2 Significance testing of pairwise comparisons of alpha-diversity. Bolded p-value is significant.

	Species Richness			**Shannon Diversity Index**			**Faith's PD**		
	Wilcoxon								
Comparison	**W**	**p-value**		**W**	**p-value**		**W**	**p-value**	
WNAD ~ Reproduction	1637	0.6303		1287	***0.02148***		1607	0.5267	
TTSP ~ Reproduction	15	0.5394		9	0.6303		13	0.9212	
Sexual ~ Biome	274.5	0.1517		333	0.4591		265	0.1222	
	Kruskal-Wallis								
	χ^2	**df**	**p-value**	**χ^2**	**df**	**p-value**	**χ^2**	**df**	**p-value**
Asexual ~ Biome	3.2992	3	0.3598	3.9668	3	0.2651	3.2139	3	0.3598

Table 3 Bray-Curtis Dissimilarity metrics for sexuals vs. asexuals by biome and overall.

	Bray-Curtis dissimilarity					
	Composition			**Dispersion**		
	F	**df**	**p-value**	**F**	**df**	**p-value**
WNAD ~ Reproduction	2.5606	1,132	***0.015***	0.114	1,132	0.7362
TTSP ~ Reproduction	3.7727	1,9	***0.011***	0.0219	1,9	***0.8857***
Sexual ~ Biome	4.6019	1,105	***0.001***	52.685	1,105	***7.065E-11***
Asexual ~ Biome	4.3047	3,56	***0.001***	8.2626	3,56	***1.216E-04***
	Weighted UniFrac					

	Bray-Curtis dissimilarity					
	Composition			**Dispersion**		
	F	**df**	**p-value**	**F**	**df**	**p-value**
	Composition			**Dispersion**		
	F	**df**	**p-value**	**F**	**df**	**p-value**
WNAD ~ Reproduction	3.4152	1,132	***0.014***	4.8965	1,132	***0.02863***
TTSP ~ Reproduction	2.3268	1,9	0.071	0.0586	1,9	0.8142
Sexual ~ Biome	6.4106	1,105	***0.002***	21.266	1,105	***1.132E-05***
Asexual ~ Biome	5.384	3,56	***0.001***	36.078	3,56	***4.087E-13***
	Unweighted UniFrac					
	Composition			**Dispersion**		
	F	**df**	**p-value**	**F**	**df**	**p-value**
WNAD ~ Reproduction	1.4063	1,132	0.096	0.1716	1,132	0.6794
TTSP ~ Reproduction	0.73577	1,9	0.776	4.1478	1,9	0.07216
Sexual ~ Biome	2.2571	1,105	***0.011***	0.261	1,105	0.6105
Asexual ~ Biome	2.4572	3,56	***0.001***	18.774	3,56	***1.497E-08***

Table 4 Differentially abundant Families and Phyla in sexuals asexuals vs sexuals in the WNAD

Phylum	**p-value**	**t-value**	
Campylobacterota	1.470000E-08	6.046	Higher in sexuals than asexuals
Family	**p_value**	**t-value**	
Nocardiaceae	3.3000E-04	-3.688	Lower in sexuals than asexuals
Enterobacteriaceae	1.8300E-03	-3.181	Lower in sexuals than asexuals
Moraxellaceae	2.0000E-03	-3.154	Lower in sexuals than asexuals
Corynebacteriaceae	1.1500E-03	3.324	Higher in sexuals than asexuals
Monoglobaceae	1.0700E-03	3.348	Higher in sexuals than asexuals
Helicobacteraceae	4.2800E-06	4.800	Higher in sexuals than asexuals
Brevibacteriaceae	5.9900E-07	5.251	Higher in sexuals than asexuals

Table 5 Significance testing of pairwise comparisons of beta-diversity between asexuals across biomes.

	Bray-Curtis dissimilarity	Unweighted UniFrac	Weighted UniFrac
Comparison	**p-value**	**p-value**	**p-value**
MC ~ SCSP	0.178	0.301	0.144
MC ~ TTSP	***0.002***	***0.007***	***0.001***
MC ~ WNAD	***0.001***	***0.001***	***0.001***
SCSP ~ TTSP	0.5	1	0.5
SCSP ~ WNAD	0.891	0.665	1
TTSP ~ WNAD	0.087	0.497	0.092

Table 6 Differentially abundant Phyla and Families in asexuals between biomes

Phylum	**MC vs:**				**SCSP vs:**	
	WNAD p-value	**WNAD t-value**	**TTSP p-value**	**TTSP t-value**	**WNAD p-value**	**WNAD t-value**
Actinobacteriota	2.1301E-07	5.188	1.4289E-05	4.339	-	-
Firmicutes	1.4711E-07	-5.256	3.0698E-04	-3.609	-	-
Bacteroidota	2.0965E-04	-3.707	9.7714E-04	-3.297	-	-
Campylobacterota	5.4078E-06	-4.548	-	-	1.9878E-03	-3.092
Family	**MC vs:**					
	WNAD p-value	**WNAD t-value**	**TTSP p-value**	**TTSP t-value**	**SCSP p-value**	**SCSP t-value**
Oscillospiraceae	6.5209E-08	-5.404	2.6263E-03	-3.008	-	-
Dermabacteraceae	5.4986E-05	-4.033	-	-	-	-
Nocardiaceae	-	-	-	-	1.7854E-04	3.748
Intrasporangiaceae	-	-	1.5662E-10	6.399	-	-
Ruminococcaceae	2.8560E-06	-4.681	-	-	-	-
Diplorickettsiaceae	3.2626E-06	-4.654	-	-	-	-
Micrococcaceae	-	-	-	-	-	-
Bacteroidaceae	2.3120E-06	-4.724	4.1948E-03	-2.863	-	-
Micrococcacea			9.9835E-05	3.891	8.7106E-08	5.352
Geodermatophilaceae	-	-	-	-	-	-

Lachnospiraceae	4.6268E-12	-6.917	2.9545E-04	-3.619	-	-
Brevibacteriaceae	4.7596E-06	-4.575	-	-	-	-

Family	SCSP vs:				TTSP vs:	
	TTSP p-value	TTSP t-value	WNAD p-value	WNAD t-value	WNAD p-value	WNAD t-value
Oscillospiraceae	1.3114E-07	-5.277	-	-	-	-
Dermabacteraceae	-	-	2.9570E-03	-2.972	7.6553E-04	-3.365
Nocardiaceae	-	-	-	-	-	-
Intrasporangiaceae	-	-	-	-	1.9073E-04	-3.731
Ruminococcaceae	4.9983E-04	-3.481	-	-	-	-
Diplorickettsiaceae	-	-	-	-	-	-
Micrococcaceae	1.9235E-03	-3.102	-	-	-	-
Bacteroidaceae	4.2782E-10	-6.244	-	-	-	-
Micrococcacea	-	-	-	-	-	-
Geodermatophilacea	2.4368E-03	-3.031	-	-	-	-
Lachnospiraceae	2.1325E-04	-3.703	-	-	-	-
Brevibacteriaceae	-	-	2.0476E-14	-7.648	-	-

Table 7 Differentially abundant families in sexuals between TTSP and WNAD

Family	p TTSP vs. WNAD	t TTSP vs. WNAD	
Intrasporangiaceae	1.058581E-05	-4.405	Lower in WNAD
Dermabacteraceae	1.408837E-05	-4.342	Lower in WNAD
Brevibacteriaceae	1.316753E-05	-4.357	Lower in WNAD

Figures

Figure 1 Locality map for specimens collected in this study, notated as percent of total individuals at each locality as either sexual or asexual species. MC=Mediterranean California; WNAD= Warm North

American Deserts; TTSP= Tamaulipas-Texas Semiarid Plains; SCSP= South Central Semiarid Prairies.

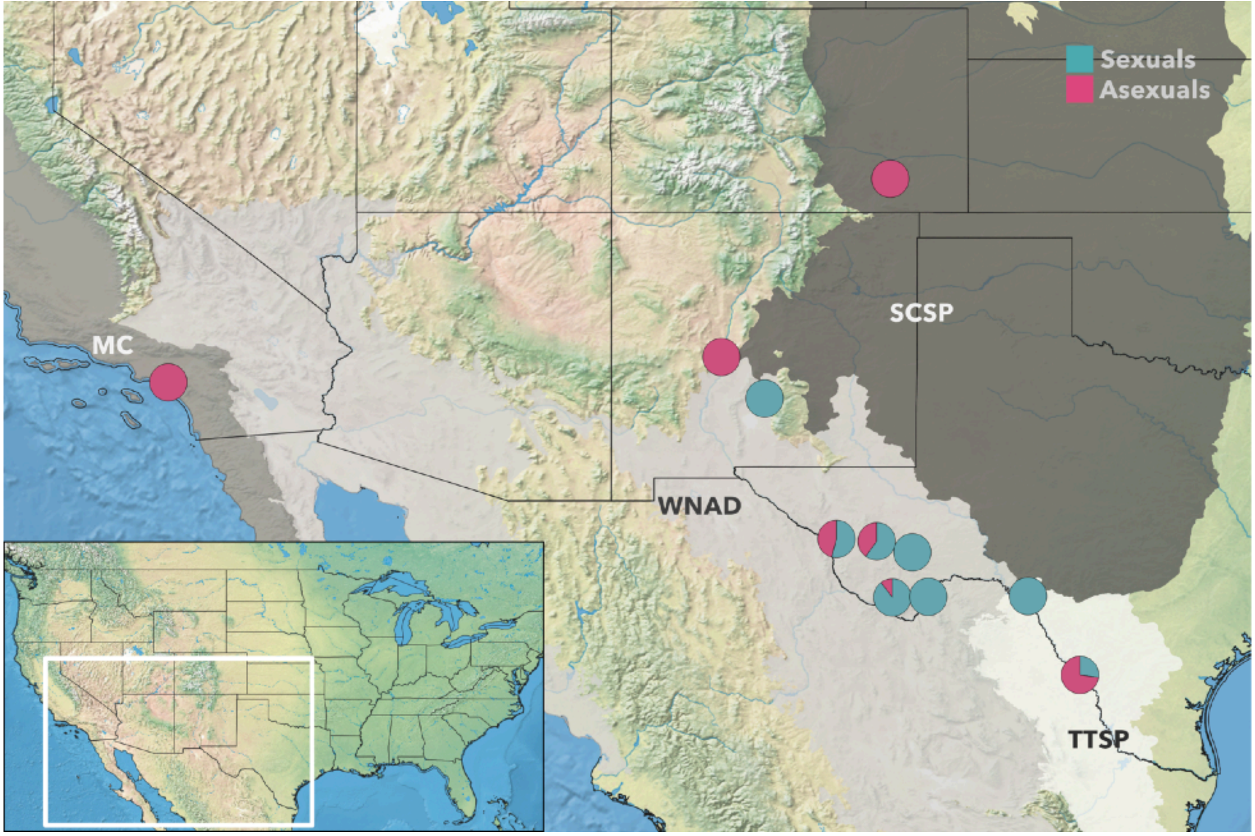


Figure 2 Mean Shannon Diversity Index (SDI) in sexual vs asexuals by biome.

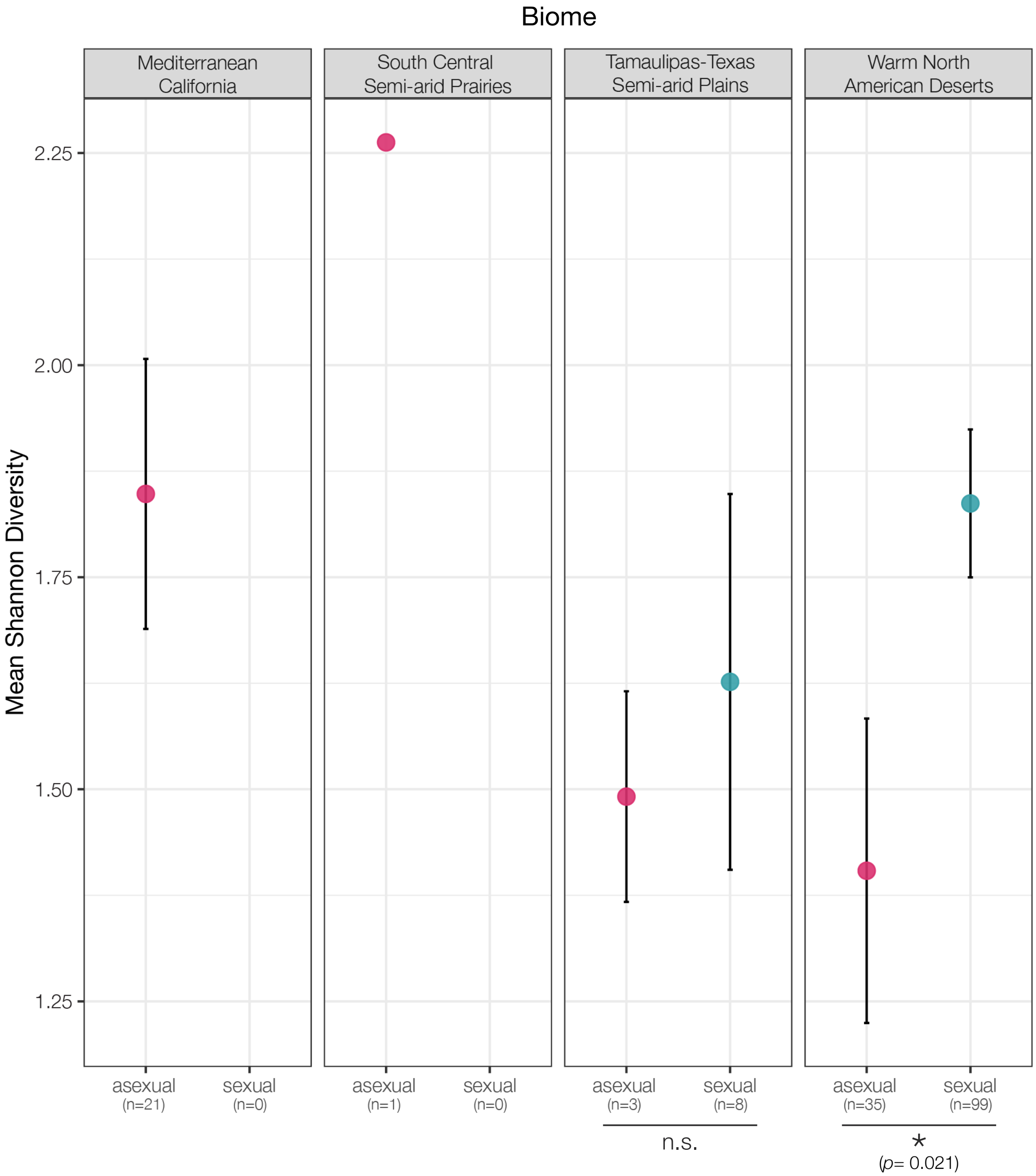


Figure 3 Mean observed species richness in sexual vs. asexuals by biome.

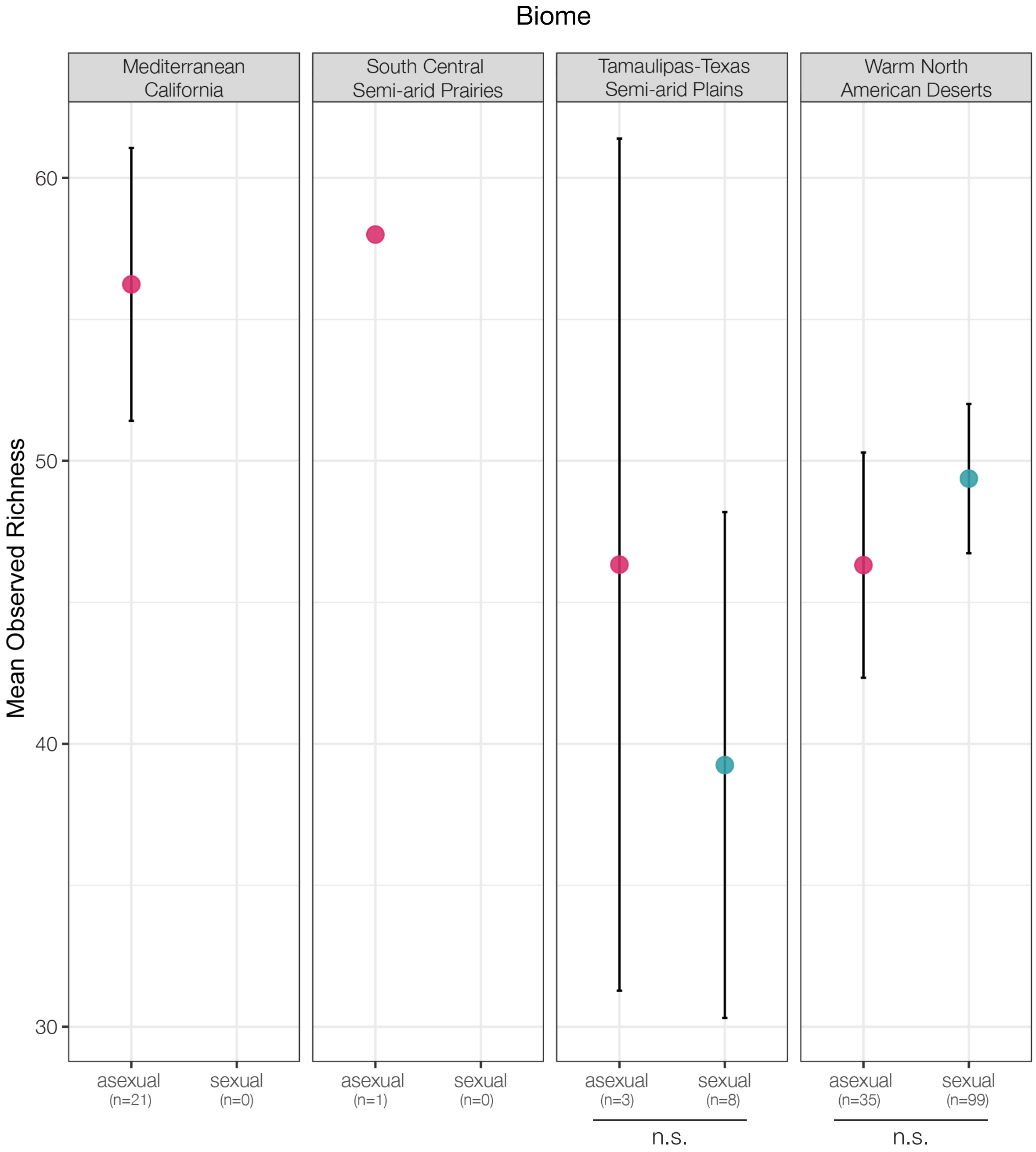


Figure 4 Mean Phylogenetic Diversity (PD) in sexual vs asexuals by biome.

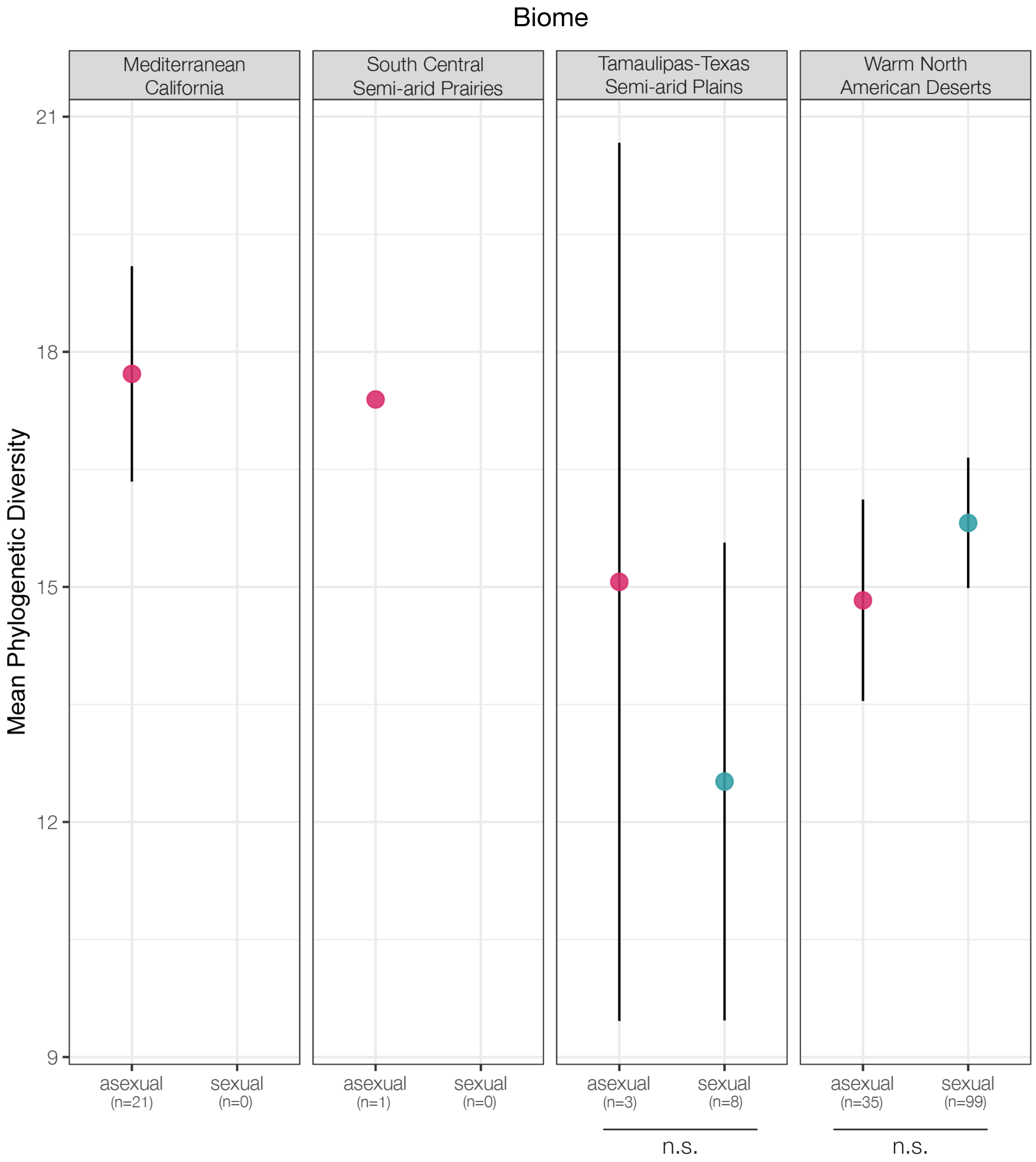


Figure 5 Mean percent composition of each Phyla present in sexual vs asexuals by biome.

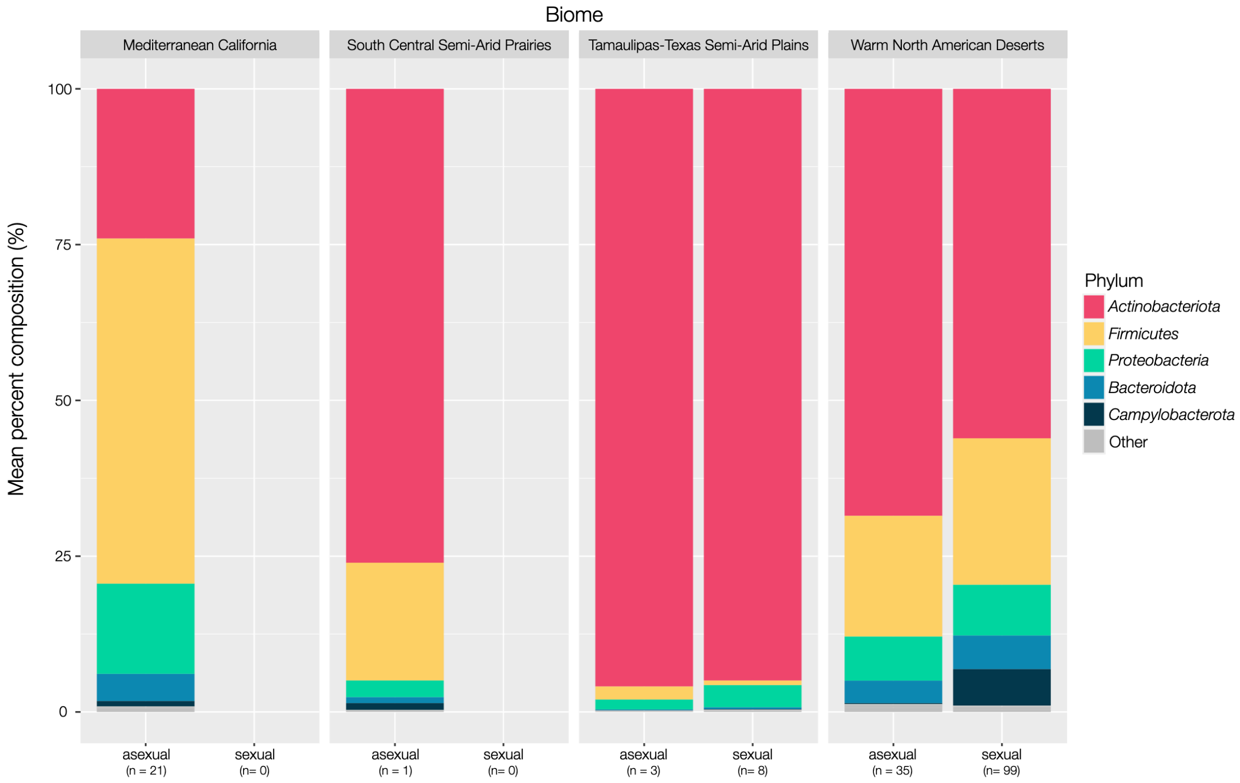


Figure 6 Mean percent composition of each Family present in sexual vs asexuals by biome.

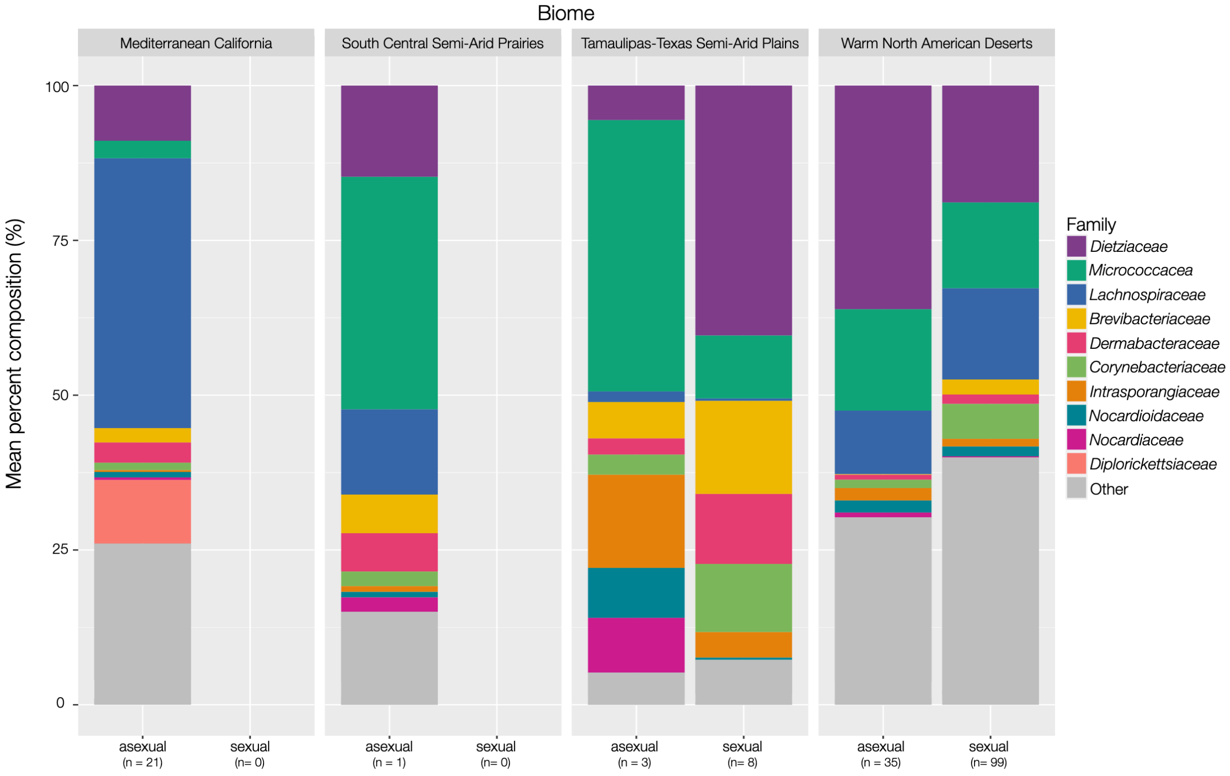
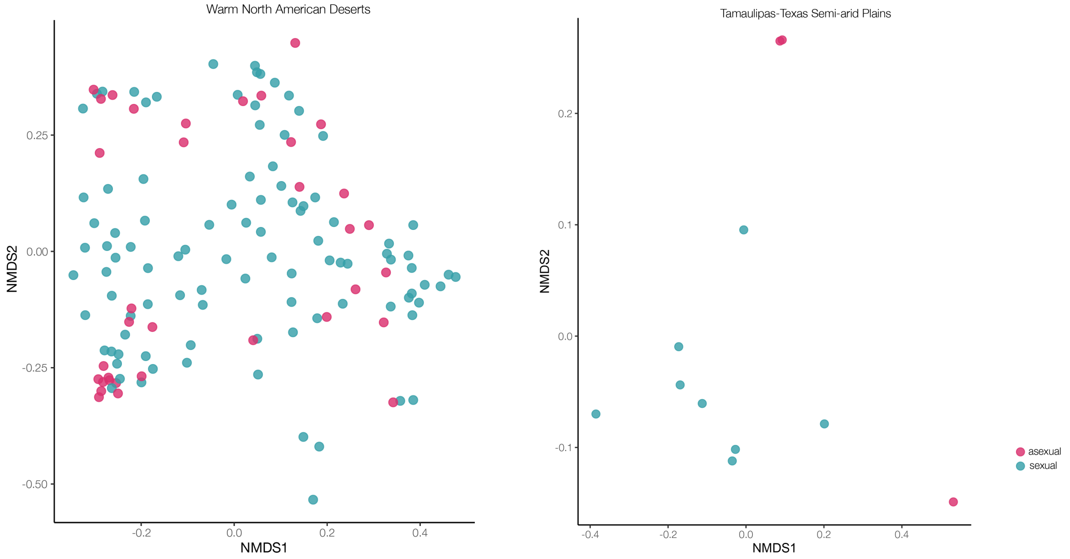


Figure 7 Beta diversity: Non-metric multidimensional scaling (NMDS) plots created using Bray-Curtis dissimilarity distances.

Sexuals and asexuals within a biome



Sexuals and asexuals between biomes

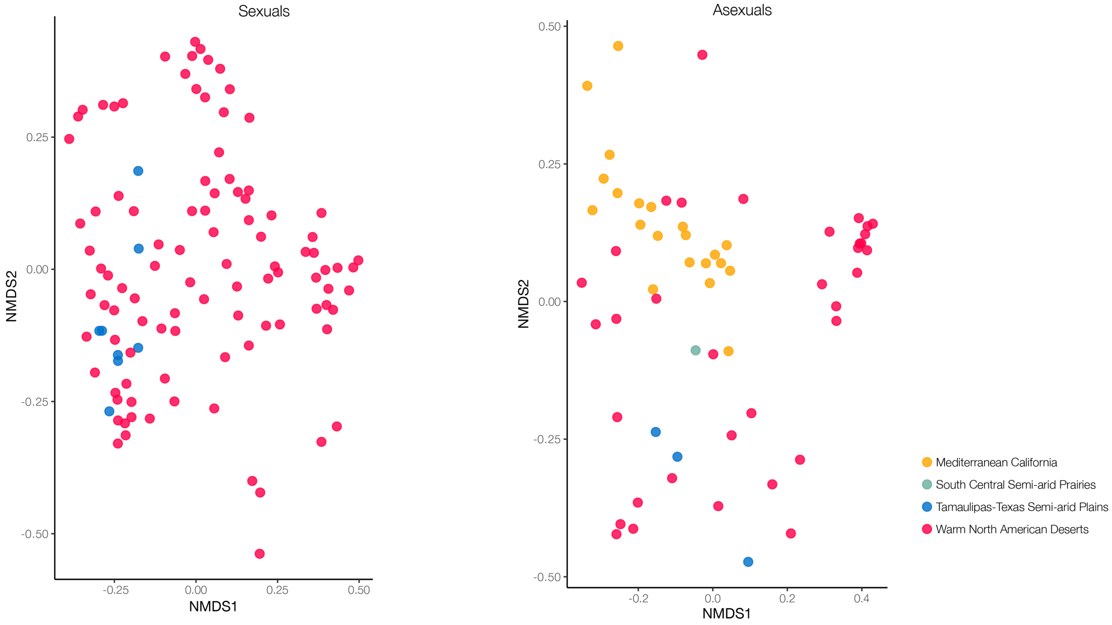
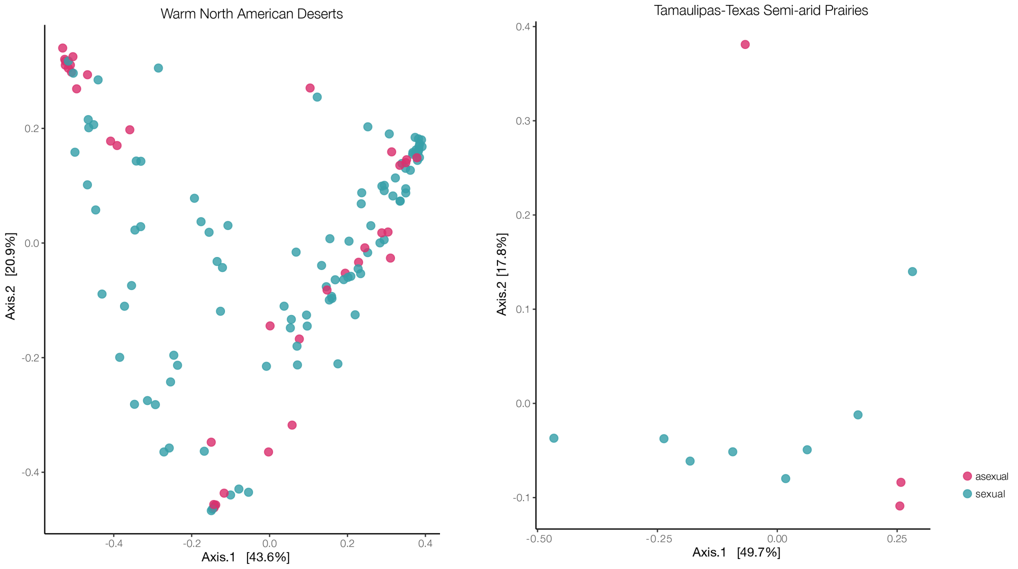


Figure 8 Beta diversity: PCoA plots based on weighted UniFrac distances.

Sexuals and asexuals within a biome



Sexuals and asexuals between biomes

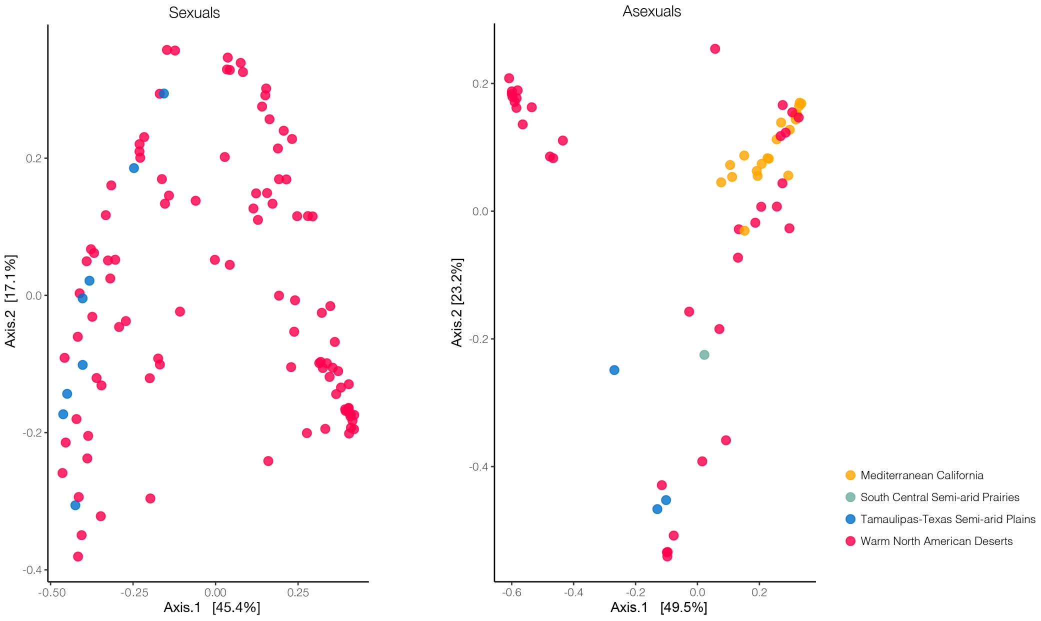
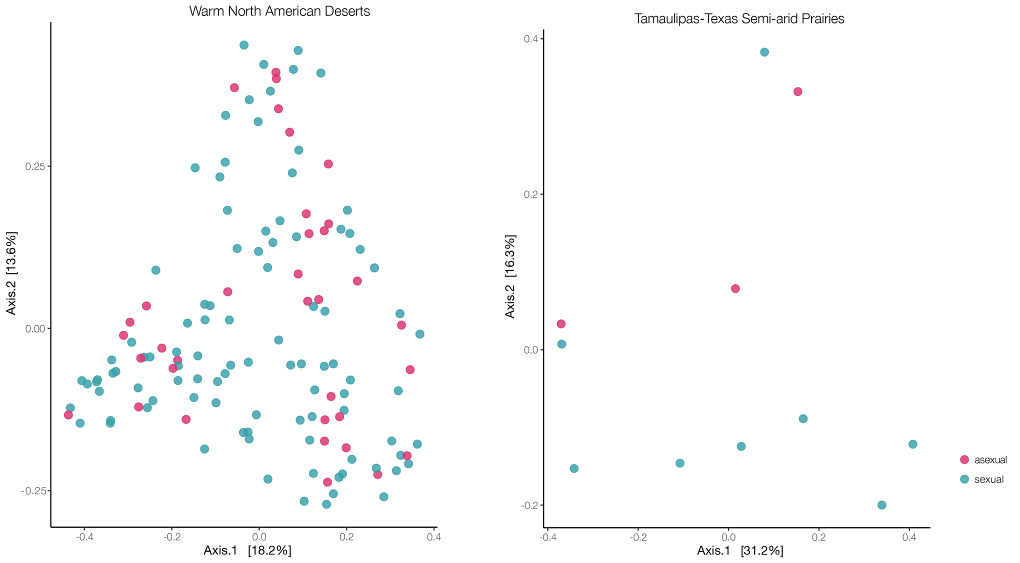
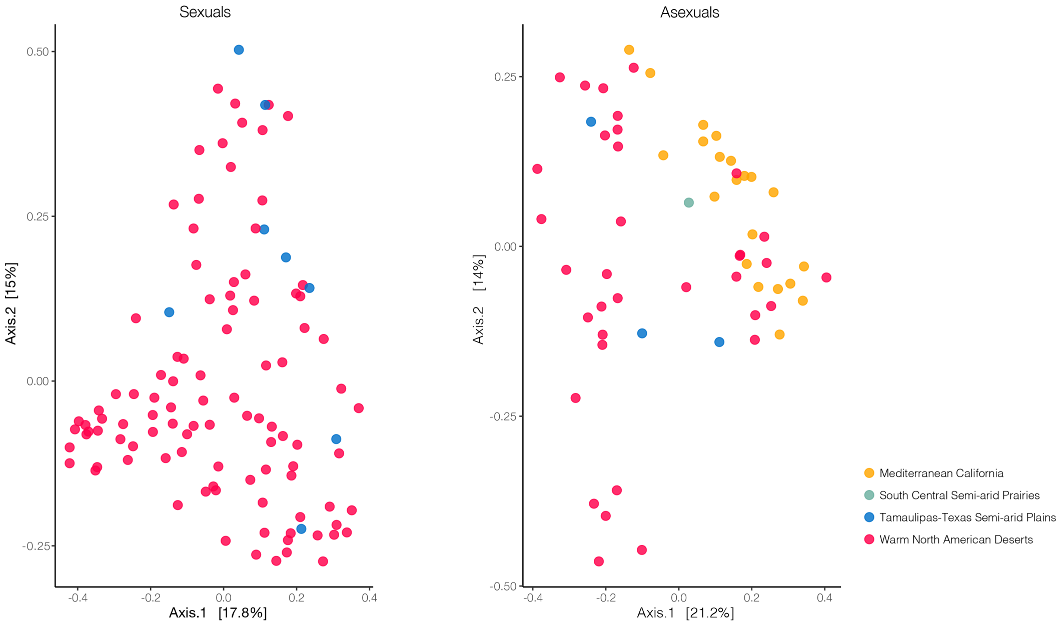


Figure 9 Beta diversity: PCoA plots based on unweighted UniFrac distances.

Sexuals and asexuals within a biome



Sexuals and asexuals between biomes



Chapter 2: Host Genetic Variation and the Cloacal Microbiome Diversity of Whiptail Lizards (Aspidoscelis)

Introduction

The microbiome is the collection of microbial organisms (bacteria, archaea, unicellular eukaryotes, and viruses) that inhabit a given environment. The composition of the microbiome depends on a multitude of factors; microbiomes of the environment depend heavily on climate, for instance (Rothschild et al. 2018), while those in the guts of animal hosts are largely determined by diet (Knutie et al. 2017). The microbiome is seeing increasing scrutiny because of its role in many aspects of a host's physiology, including immunological health, aging, and digestion (Turnbaugh et al. 2006; Ley et al. 2006; Mazmanian et al. 2005). An enduring question in microbiome research is how do environmental and host genetic factors influence microbial diversity? One hallmark study found that a significant component to human gut microbiome was due to environmental factors (e.g. diet; Rothschild et al. 2018). On the other hand, human genetic variation - particularly at pathways involved in immunity - has also been associated with microbial diversity (Blekhman et al. 2015). Thus, the relative roles of environment and host genetics in shaping microbiome composition is still an important research avenue. However, most of these studies largely relied on very controlled experiments or were performed with model organisms or humans. In this study, we investigate the role of host genetic variation on gut microbiome composition.

Our previous study (Chapter 1) heavily suggested that environment plays the most important role in shaping the diversity of the gut microbiome in wild populations. This conclusion is consistent with numerous studies in wild populations. For example, Wu et al. (2018) found that the gut microbiome of swan geese (*Anser cygnoides*) was altered significantly in a population from their wintering area - a pond with heavily altered water quality caused by human activities. In addition, Warne et al. (2017) found that the gut microbiota of amphibians (wood frogs: *Lithobates sylvaticus*, green frogs: *L. clamitans*, and bullfrogs: *L. catesbeianus*) was greatly effected by different species' change across larval ontogeny, and accounted for much of this change to be associated with alteration of diet, host morphology, and ecology. Lastly, Kohl et al. (2017) found that viviparous lizards' (*Liolaemus parvus*, *L. ruibali*, and *Phymaturus williamsi*) microbiome compositions were greatly effected by their environments, sharing about 35% of their gut bacteria diversity with that of their mothers within 24 hours after birth, and sharing a large portion (about 40%) of bacterial diversity with plant material from their environments.

On the other hand, host genetics has also been implicated in influencing microbiome composition. In humans, variation at immunity-related genes are largely correlated with gut microbiome (Blekhman et al. 2015). This variation has also shown to be due to local adaptation and human population structure, complicating the relationship between the relative roles of environmental factors and host genetics on microbiome composition (Blekhman et al. 2015). Other studies in humans used genome-wide association studies to identify genes that influence microbial diversity, though only a few loci have been significantly linked to microbiome composition (reviewed in Sanna et al. 2022). Investigating the role of host genetics has also been pursued in wild populations as well. A recent paper found a correlation between genetic distance and microbiome dissimilarity in the seaweed *Phyllospora comosa* (Wood et al. 2022), though this again has the confounding factor of population structure in the host. Another study also found that particular alleles at the major histocompatibility complex (MHC), and not simply absolute allelic diversity, strongly correlated with microbiome composition in natural populations of the Seychelles warbler (Davies et al. 2022).

Several studies that have investigated microbiome composition in wild populations have suggested practical implications for understanding host microbial diversity, including the conservation of imperiled populations. For example, a recent study found that microbiomes varied across the landscape in koalas, but were mismatched with host genetic variation (Littleford-Colquhoun et al. 2022), implicating that this “hidden” component to population structure should influence conservation strategies, such as reintroduction efforts. Indeed, there has been a recent effort to quantify microbial diversity in wild host populations for the specific purpose of understanding how the microbiome can inform conservation policy and practice (Trevelline et al. 2019; Wood et al. 2022). In this study, we investigate the microbiome composition in sexual and asexual whiptail lizards. While not a candidate for conservation efforts, asexual whiptails exhibit very little genetic diversity and thus can mimic the genetic signature of small populations that are in need of conservation.

Whiptail lizards of the genus *Aspidoscelis* are a complex of both sexual and asexual species with distributions in the United States, Mexico, and Central America. The parthenogenetic lineages arose through hybridization events between divergent sexual species; for example, hybridization between *Aspidoscelis septemvittatus* and *Aspidoscelis marmoratus* produced the diploid *Aspidoscelis tesselatus* (Figure 1). Despite having highly heterozygous genomes, populations of parthenogenetic lineages lack the variation seen in sexual populations (Jaron et al. 2021; Maldonado et al. 2022), setting up natural experiments to test how sexual reproduction and/or clonal reproduction differ with regard to genome and organismal evolution (Fujita et al. 2020). In this study, we leverage the *A. tesselatus* parthenogenetic system to investigate whether host genetic variation correlates with microbial diversity. We sampled both parthenogenetic and sexual species for their microbiome and collected Restriction site-associated DNA sequencing (RADseq) data to quantify genetic variation. We set out to address the question: does host genetic diversity influence the gut microbiome?

The goals of this chapter are to:

1. Use RADseq data from host populations to understand the genetic ancestry of both sexual and asexual populations of whiptail lizards in Texas, and
2. Investigate the relationship between host genetic diversity and microbiome composition.

Methods

Field work and sampling

Sampling for this study took place across Texas (Presidio Co., Brewster Co., Webb Co., Jeff Davis Co., and Potter Co.), New Mexico (Otero Co. and Socorro Co.), Colorado (Otero Co.), and California (Orange Co.). We categorized regions by biome as follows the Commission for Environmental Cooperation (Mumme and Duncan 1997): Mediterranean California (MC), South Central Semi-arid Prairies (SCSP), Tamaulipas-Texas Semi-arid Plains (TTSP), and Warm North American Deserts (WNAD). For the asexual species we targeted *Aspidoscelis exsanguis*, *A. laredoensis*, *A. neomexicanus*, *A. neotesselatus*, *A. sonorae*, *A. tesselatus*, and *A. uniparens*. For the sexual species we targeted *A. gularis*, *A. inornatus*, *A. marmoratus*, and *A. septemvittatus*.

Immediately following verification of euthanasia (IACUC protocol A13.010), lizards were prepared for bacterial sampling by cleaning the vent and surrounding area with an ethanol wipe. A sterile swab (Puritan 253316U Ultra Flocked Swab) was then inserted into the cloaca and rotated back and forth ~10 times, followed by collection of a second swab done in the same manner (Colston, Noonan, and Jackson 2015). Each swab was placed in a sterile cryovial and immediately stored in liquid nitrogen until returned to the lab where they were transferred to a -80ºC freezer until further processing. Once microbial sampling was complete, the liver was collected for use in this study and stored in RNAlater, while other tissues (heart, skeletal muscle, spleen, stomach, and hind-gut containing fecal matter) were collected for use in future studies and stored in either RNAlater or liquid nitrogen. All individuals were then prepared as museum specimens and deposited in the collection at the Amphibian and Reptile Diversity Research Center (ARDRC) at University of Texas at Arlington.

Microbiome sequencing

We extracted DNA from all cloacal swabs using the DNEasy PowerSoil Pro Kit (Qiagen) and also included one “blank” extraction from each kit used in order to correct for any potential contaminates from the extraction process. We then assessed DNA yield using the dsDNA High Sensitivity Assay Kit on a Qubit Fluorometer 2.0. The V3V4 region of the 16S rRNA gene was amplified via polymerase chain reaction using indexed primers. Each 25ul reaction contained: 5ul of Q5 reaction buffer (5x), 5ul of Q5 high GC enhancer (5x), 0.2ul of 25mM dNTP, 1ul of both primers (5uM), 0.2ul of Q5 Hot Start DNA polymerase (NEB), 1-10ng DNA and water to reach the final 25ul volume. Each reaction was done in triplicate and run under the following thermocycler conditions: 98ºC for 2 min (initial denaturation), followed by 32 cycles of 98ºC for 2 min (denaturation), 53.6ºC for 20s (annealing), 72ºC for 20s (extension), and final extension at 72ºC for 2 min. Once PCR products were verified on a 1% agarose gel, the triplicates were pooled for each individual sample and quantified again using the Qubit. Amplicons were then pooled at equal concentrations (2ng per sample) into a single library. Sequencing was performed at the UTA Life Sciences Core Facility on an Illumina MiSeq (300 PE).

RADseq sequencing

We followed the general protocols established in the Fujita lab to generate RAD data using the samples listed in Table 1; these samples also had their microbiome sequenced as described above. First, DNA was extracted from liver samples using the Qiagen DNeasy Blood and Tissue kit. Second, 500 ng of DNA was digested with the restriction enzymes SbfI (20 units; New England Biolabs) and MspI (20 units; New England Biolabs) by incubating them for four hours at 37 C in 1X CutSmart buffer (New England Biolabs) followed by an inactivation incubation at 65 C for 30 min. The digestions were then cleaned using Serapure beads (Faircloth 2014). Third, Illumina-compatible adapters with sticky ends for the remnant restriction sites were ligated onto the DNA fragments. Ligations were carried out using 400 units of T4 DNA Ligase and incubating at 23 C for 30 minutes before a deactivation incubation at 65 C for 15 min. The ligation reactions were cleaned using Serapure beads. Fourth, the fragments were uniquely double-indexed with i5 and i7 indexing primers by PCR using 10 units of Q5 polymerase; the PCR consisted of 20 cycles and an annealing temperature of 55 C. The amplified individual libraries were cleaned with Serapure beads and quantified using the Qubit 2.0 High-Sensitivity kit before pooling together in equimolar amounts. Fifth, we size-selected for total length (fragment + adapter) of 435-535 bp using the Blue Pippin machine and the 1.5% agarose cassette and R2 standard (Sage Science). This size-selected library was then sequenced at Novogene on a HiSeq2500 (150 PE; Novogene Corp, Sacramento, CA).

Data Processing

Microbiome sequences were received demultiplexed. We used cutadapt to remove primers and then imported them to R for further processing. The DADA2 package was used for quality filtering and trimming of sequences, merging paired reads, constructing an Amplicon Sequence Variant (ASV) table, removing chimeras, and assigning taxonomy using the Silva 138 reference database (Callahan et al, 2016). Once taxonomy and ASV count tables were generated, potential contaminants were removed based on the sequences that were returned for the two negative controls (decontam). Sequences were aligned using the R package DECIPHER (Wright 2016) and an unrooted tree was inferred from the alignment using the neighbor-joining algorithm in the R package phangorn (Schliep 2011). This tree served as the starting point for a maximum likelihood analysis using the function optim.pml() employing the GTR model with NNI branch swapping. Using the phyloseq package (McMurdie and Holmes 2013), the sample metadata, ASV count table, taxonomy table, sequences, and tree were all combined package into a single object. Finally, all ASVs assigned to Chloroplast or Mitochondria were filtered out and the resulting object was used for all further analyses.

RADseq data were processed using a series of custom scripts and Stacks v. 2.60 (Rochette et al. 2019). Our adapters include an 8-bp “unique molecular identifier” (UMI) that is sequenced to help improve the diversity of the flow cell. This UMI, along with remnant restriction sites, were removed before identifying loci using *ustacks*. For *ustacks*, we required each stack to have a minimum coverage of 5X (-m 5) and the maximum distance of 5 nucleotides (-M 5). For the remainder of the Stacks pipeline, we conducted several alternative processing steps based on different sampling schemes. The first sampling scheme included all samples (“ALL”). Based on the population stratification results from ALL (see below), we then re-ran the Stacks pipeline on individual clusters to try and identify further partitioning; this amounted to two additional data schemes for all *marmoratus* (“MARM”), all *gularis* (“GUL”), and all *septemvittatus* (“SEP”). The pipeline was similar for each dataset: *cstacks* builds a catalog of RAD loci (we set the distance between sample for each locus to 6 nucleotides; -n 6), *sstacks* reconciles the individual loci (from *ustacks*) with the catalog, *tsv2bam* incorporates the second read from paired-end sequencing, and *gstacks* genotypes each individual for every locus (Rochette et al. 2019). Finally, *populations* produces output files and summary statistics related to each population identified in the dataset (observed heterozygosity, Fst, and Dxy). Most importantly, populations can filter loci based on missing data; we only allowed 70% missing data for any locus. We then used a custom script to further filter the data to only include biallelic loci (loci that have just two haplotypes) and to randomly identify one SNP in the haplotype for downstream analyses.

Population stratification

To identify putative populations, we ran the program Admixture v. 1.3.0 (Alexander et al. 2009). The program admixture estimates allele and genotype frequencies and ancestry in order to identify the maximum likelihood population assignments of individuals. So that we can identify the most likely clustering, we conducted 20 separate runs for each value of K up to K=10, where K is the number of populations.

We then used CLUMPAK (Kopelman et al. 2015) to summarize the admixture results. CLUMPAK identifies sets of results within replicate runs of a given K, based on population assignments of individuals. It utilizes the program CLUMPP to provide an average representation for each of these sets (Jakobsson and Rosenberg 2007). It will then identify the best clustering model (the best K). We used the Evanno method (Evanno et al. 2005) to identify the K value that resulted in the largest difference in likelihood value; this K is the predicted number of populations from each dataset. However, because we did not want to over-interpret these results (Cullingham et al. 2020), we sometimes erred on the conservative side and chose a smaller K based on the likelihood scores and known biology of the species; we point these instances out in the results.

Correlations with microbiome composition

To assess community structure in microbial samples, we first used phyloseq to calculate alpha diversity (observed richness and Shannon index) for all individuals. Then, samples were grouped into their respective populations within each species (MARM, GUL, SEP). For each of these populations, we then calculated the mean, min, median, max, and standard deviation for the alpha diversity metrics. We then tested for correlations between alpha diversity and host genetic diversity (observed heterozygosity, H_{obs}) using linear regression. Next, vegan was used to create Bray-Curtis dissimilarity matrices between populations for each species on relative abundances. Finally, we tested for correlations between genetic diversity (both Fst and Dxy) and microbial community beta diversity (Bray-Curtis) using Mantel tests.

Results

RADseq summary

We used Stacks v. 2.6.0 to process the raw data and to work with four different datasets. We filtered each dataset to ensure a “70%” threshold: every locus had at least 70% samples represented, and every individual had been sequenced for least 70% of the loci. The “ALL” dataset included all species, including *Aspidoscelis tesselatus*, and had 532 loci and 88 individuals. For each of the remaining datasets, we re-ran *cstacks*, *sstacks*, *tsv2bam*, and *gstacks* to maximize the number of loci. The “GUL” dataset, which included those individuals identified as *A. gularis* from ALL, included 572 loci and 17 individuals. The “MARM” dataset, which included those individuals identified as *A. marmoratus* from ALL, included 1,751 loci and 31 individuals. The “SEP” dataset, which included those individuals identified as *A. septemvittatus* from ALL, included 2,156 loci and 27 individuals.

Population stratification

We used the program Admixture v. 1.3.0 to identify population units in our dataset. For the ALL dataset, which contained all individuals from all species, the best-supported (most likely) scenario had seven populations (K=7; Figure 2A). *Aspidoscelis tesselatus* was its own group, with 2 to 3 populations within each of the other species. Within *A. marmoratus*, every individual was inferred to be parts of two different populations, indicating that this result may be due to over-stratification. Similar results were obtained with K=5 and K=6, where *A. tesselatus* was its own population. We then explored K=3 and K=4, as we anticipated that each of the sexual species would be inferred to have its own population while not over splitting; these represent conservative inferences. For K=3, we are illustrating one of the likely models where *A. marmoratus*, *A. gularis*, and *A. septemvittatus* are each their own populations, while *A. tesselatus* is admixed between *A. marmoratus* and *A. septemvittatus* (Figure 2B). The other likely scenario that was inferred clumped *A. gularis* and *A. septemvittatus* together and put *A. tesselatus* in its own group (results not shown). For K = 4, we are illustrating one of the likely models that further splits *A. gularis* into two groups, but maintains *A. marmoratus* and *A. septemvittatus* as their own respective groups, with *A. tesselatus* admixed between *A. marmoratus* and *A. septemvittatus* (Figure 2C). The other likely scenarios infer *A. tesselatus* as its own group and either (1) split *A. gularis* into two groups that includes *A. septemvittatus* or (2) splits all the sexual species into their own respective groups (results not shown).

With the results from ALL, we split the data into individual species datasets so that we could maximize the number of markers for each species from Stacks. For *A. gularis*, admixture results illustrated there are three population (K=3; Figure 3A). For *A. marmoratus*, admixture results illustrated there are six population (K=6; Figure 3B). And for *A. septemvittatus*, admixture results illustrated there are two population (K=2; Figure 3C). These populations served as our groupings for microbiome correlations among genetic groups (see below).

Microbiome diversities

Summary statistics for the alpha diversities for each species (MARM, GUL, SEP) are summarized in Table 2.

Host genetic diversity and microbiome composition

We used linear regression to investigate the relationship between genetic diversity within the host whiptail lizards and alpha diversity of their microbiome. For each measure of alpha diversity, we found a negative relationship with observed heterozygosity (species richness, Figure 4A; Shannon Diversity, Figure 4B; Phylogenetic Diversity, Figure 4C). However, none of these relationships were significant. We did not pursue analyses with *A. tesselatus* because it represented only a single population for all of our stratification analyses. To investigate whether distinct populations had characteristic microbiome compositions, we used Mantel tests to examine the relationship between Fst and microbiome dissimilarity and Dxy and microbiome dissimilarity; both Fst and Dxy are measure of population differentiation. We were only able to do this with *A. marmoratus* and *A. gularis* because *A. septemvittatus* had only two populations. Correlations were high in *A. gularis* and only significant with Fst, while correlations in *A. marmoratus* were low and not significant (Table 3).

Discussion

Population stratification

The RADseq data was clearly able to distinguish between the sexual species and the asexual species (Figure 2A). The Evanno method identified K=7 as the most likely stratification, though *A. marmoratus* appears to be overspilt as every individual is assigned to at least two distinct populations. While this is not impossible, our subsequent hierarchical analyses which focused on individual species did identify finer population structure that did not involve individuals belonging to distinct groups (and hence looking as if they were admixed individuals; Figure 3B). These results highlights the caution that has been voiced recently regarding the interpretation of population stratification analyses from programs such as Admixture. For instance, Lawson et al. (2018) specifically stated that genetic data just may not identify fine-scale structure, as evidenced in our ALL dataset. Novembre (2018) also emphasizes how these analyses, while very helpful, should primarily be used as an exploratory tool, and not used as an absolute metric. For example, as K increases, the analyses adds more parameters with the ultimate consequence of overfitting noise in the data, even if those over-parametrized models are inferred to be the optimal model.

As part of the exploratory feature of population stratification interpretation, we examined results for lower K values. For instance, our a priori expectation is for there to be three clusters among our samples: one for *A. marmoratus*, one for *A. gularis*, and one for *A. septemvittatus*; *A. tesselatus* would be inferred to be admixed with A.

marmoratus and either *A. gularis* or *A. septemvittatus*. When looking at the K=3 results, we did find sets among the twenty replicate analyses that identified *A. tesselatus* as being an admixed population between *A. marmoratus* and *A. septemvittatus*. Similarly, we observed *A. tesselatus* having contributions from these same sexual species with the K=4 results. However, several CLUMPAK sets also identified *A. tesselatus* as its own group (similar to to the K=7 result); this may be due to the limited number of markers in the ALL dataset. Going forward, we will explore additional population stratification analyses, such as principal components analysis, to confirm the admixed nature of *A. tesselatus*. We did explore further stratification analyses with only *A. marmoratus*, *A. septemvittatus*, and *A. tesselatus* in order to see if we can further identify the genomic origins of parthenogenesis at a finer scale, but these results mirrored those of the ALL dataset. Thus, despite some mixed signals, we view our results as a strong indication that *A. tesselatus* originated from hybridization between *A. marmoratus* and *A. septemvittatus*.

Host genetics and microbiome correlations

Despite a consistent negative trend between observed host heterozygosity and the various measure of microbiome diversity, none of the correlations were significant (Figure 4). This supports a large volume of literature that demonstrates that in many cases, host genetics does not play an important role in shaping microbial diversity (Kurilshikov et al. 2017; Rothschild et al. 2018). In Chapter 1, we concluded that environment likely shapes the microbiome in whiptail lizards, and the lack of relationship with alpha diversity and host genetic diversity shown in this study supports that conclusion. There are several important caveats that need to be pointed out, however. First, our population-level sampling for the hosts was quite small in some cases. For example, one population of *A. gularis* was represented by a single individual, and two populations of *A. marmoratus* were represented by two individuals. Such a small sample size may be insufficient to accurately estimate the diversity of a population. Second, many of the studies that have argued for a role of host genetics in determining microbiome diversity have focused on specific candidate genes, such as those involved in immunity (Igartua et al. 2017), or have identified genes with specific functions that are important through genome-wide association studies (Bonder et al. 2016). Our genetic data is a random sampling across the genome at very low density, and thus finding a single marker that is statistically associated with microbiome diversity would be very difficult. Third, even if specific genes or markers were associated with microbial diversity, additional studies would be needed to dissect the causality of that relationship.

The one significant association we found was an association of population structure and microbiome dissimilarity in *Aspidoscelis gularis*, indicating that different populations have distinct microbiome compositions (Table 3). Again, our sample size was small for some *A. gularis* populations, but this can support our previous conclusions that environment has a major effect on microbial diversity if the different genetic *A. gularis* groups occupy distinct geographic regions. This result also highlights the importance of looking at microbiome composition in natural populations that may have significant structure, as this could influence conservation planning (Bahrndorff et al. 2016).

In conclusion, we identified that *A. marmoratus* and *A. septemvittatus* are the likely the parental species of *A. tesselatus* using RADseq data. This study also supports the conclusion from Chapter 1 that the environment likely plays a more important role in microbiome composition than host genetic variation. However, a more in-depth study, with denser marker sampling or with specific loci, such as immune genes, is needed before completely ruling out the influence of host genetics.

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Tables

Table 1 Sample locality information for the specimens used in this study.

Sample	Population	Latitude	Longitude	Locality	County	State
KLC_001	gularis					
KLC_007	tesselatus	29.5570	-103.7858	Dalquest Desert Research Institute - Canyon	Presidio	TX
KLC_008	tesselatus	29.5570	-103.7858	Dalquest Desert Research Institute - Canyon	Presidio	TX
KLC_009	tesselatus	29.5570	-103.7858	Dalquest Desert Research Institute - Canyon	Presidio	TX
KLC_010	tesselatus	29.5570	-103.7858	Dalquest Desert Research Institute - Canyon	Presidio	TX
KLC_011	tesselatus	29.5570	-103.7858	Dalquest Desert Research Institute - Canyon	Presidio	TX
KLC_012	tesselatus	29.5570	-103.7858	Dalquest Desert Research Institute - Canyon	Presidio	TX
KLC_013	tesselatus	29.5570	-103.7858	Dalquest Desert Research Institute - Canyon	Presidio	TX
KLC_014	tesselatus	29.5570	-103.7858	Dalquest Desert Research Institute - Canyon	Presidio	TX
KLC_016	marmoratus	29.4496	-102.8237	Black Gap WMA	Brewster	TX
KLC_027	marmoratus	29.4496	-102.8237	Black Gap WMA	Brewster	
KLC_029	gularis	27.9145	-99.8463	Trevino Ranch	Webb	TX
KLC_030	gularis	27.9145	-99.8463	Trevino Ranch	Webb	TX
KLC_032	gularis	27.9145	-99.8463	Trevino Ranch	Webb	TX
KLC_034	gularis	27.9145	-99.8463	Trevino Ranch	Webb	TX
KLC_035	gularis	27.9145	-99.8463	Trevino Ranch	Webb	TX
KLC_036	gularis	27.9145	-99.8463	Trevino Ranch	Webb	TX
KLC_037	gularis	27.9145	-99.8463	Trevino Ranch	Webb	TX
KLC_039	gularis	27.9145	-99.8463	Trevino Ranch	Webb	TX
KLC_040	gularis	27.9145	-99.8463	Trevino Ranch	Webb	TX

Sample	Population	Latitude	Longitude	Locality	County	State
KLC_041	gularis	30.5405	-103.8373	Chihuahuan Desert Research Institute	Jeff Davis	TX
KLC_045	gularis	30.5405	-103.8373	Chihuahuan Desert Research Institute	Jeff Davis	TX
KLC_046	gularis	30.5405	-103.8373	Chihuahuan Desert Research Institute	Jeff Davis	TX
KLC_048	gularis	30.5405	-103.8373	Chihuahuan Desert Research Institute	Jeff Davis	TX
KLC_049	gularis	30.5405	-103.8373	Chihuahuan Desert Research Institute	Jeff Davis	TX
KLC_050	gularis	30.5405	-103.8373	Chihuahuan Desert Research Institute	Jeff Davis	TX
KLC_051	gularis	30.5405	-103.8373	Chihuahuan Desert Research Institute	Jeff Davis	TX
KLC_066	tesselatus	30.5494	-104.6617	Miller Ranch - fort	Presidio	TX
KLC_080	septemvittatus	29.4634	-100.8663	Dead Horse Ranch	Brewster	TX
KLC_081	septemvittatus	29.4634	-100.8663	Dead Horse Ranch	Brewster	TX
KLC_082	septemvittatus	29.4634	-100.8663	Dead Horse Ranch	Brewster	TX
KLC_083	septemvittatus	29.4634	-100.8663	Dead Horse Ranch	Brewster	TX
KLC_084	septemvittatus	29.4634	-100.8663	Dead Horse Ranch	Brewster	TX
KLC_085	septemvittatus	29.4634	-100.8663	Dead Horse Ranch	Brewster	TX
KLC_086	septemvittatus	29.4634	-100.8663	Dead Horse Ranch	Brewster	TX
KLC_087	septemvittatus	29.4634	-100.8663	Dead Horse Ranch	Brewster	TX
KLC_088	septemvittatus	29.4634	-100.8663	Dead Horse Ranch	Brewster	TX
KLC_089	septemvittatus	29.4634	-100.8663	Dead Horse Ranch	Brewster	TX
KLC_090	septemvittatus	29.4634	-100.8663	Dead Horse Ranch	Brewster	TX
KLC_091	septemvittatus	29.4634	-100.8663	Dead Horse Ranch	Brewster	TX
KLC_092	septemvittatus	29.4634	-100.8663	Dead Horse Ranch	Brewster	TX
KLC_093	septemvittatus	29.4634	-100.8663	Dead Horse Ranch	Brewster	TX
KLC_094	septemvittatus	29.4561	-103.4125	Christmas Mountains	Brewster	TX
KLC_097	marmoratus	29.4368	-103.5060	Darryl Eby's property	Brewster	TX
KLC_098	septemvittatus	29.4368	-103.5060	Darryl Eby's property	Brewster	TX

Sample	Population	Latitude	Longitude	Locality	County	State
KLC_099	marmoratus	29.4368	-103.5060	Darryl Eby's property	Brewster	TX
KLC_100	marmoratus	29.4368	-103.5060	Darryl Eby's property	Brewster	TX
KLC_101	marmoratus	29.4368	-103.5060	Darryl Eby's property	Brewster	TX
KLC_102	marmoratus	29.4368	-103.5060	Darryl Eby's property	Brewster	TX
KLC_103	marmoratus	29.4368	-103.5060	Darryl Eby's property	Brewster	TX
KLC_104	marmoratus	29.4368	-103.5060	Darryl Eby's property	Brewster	TX
KLC_105	marmoratus	29.4368	-103.5060	Darryl Eby's property	Brewster	TX
KLC_106	marmoratus	29.4368	-103.5060	Darryl Eby's property	Brewster	TX
KLC_107	marmoratus	29.4368	-103.5060	Darryl Eby's property	Brewster	TX
KLC_108	marmoratus	29.4368	-103.5060	Darryl Eby's property	Brewster	TX
KLC_109	marmoratus	29.4368	-103.5060	Darryl Eby's property	Brewster	TX
KLC_110	marmoratus	29.4368	-103.5060	Darryl Eby's property	Brewster	TX
KLC_111	marmoratus	29.4368	-103.5060	Darryl Eby's property	Brewster	TX
KLC_112	marmoratus	29.4368	-103.5060	Darryl Eby's property	Brewster	TX
KLC_114	marmoratus	29.4368	-103.5060	Darryl Eby's property	Brewster	TX
KLC_115	marmoratus	29.4368	-103.5060	Darryl Eby's property	Brewster	TX
KLC_116	marmoratus	29.4368	-103.5060	Darryl Eby's property	Brewster	TX
KLC_117	marmoratus	29.4368	-103.5060	Darryl Eby's property	Brewster	TX
KLC_118	septemvittatus	29.4368	-103.5060	Darryl Eby's property	Brewster	TX
KLC_119	septemvittatus	29.4558	-103.4125	Christmas Mountains	Brewster	TX
KLC_120	septemvittatus	29.4558	-103.4125	Christmas Mountains	Brewster	TX
KLC_121	marmoratus	29.4558	-103.4125	Christmas Mountains	Brewster	TX
KLC_122	septemvittatus	29.4558	-103.4125	Christmas Mountains	Brewster	TX
KLC_123	septemvittatus	29.4558	-103.4125	Christmas Mountains	Brewster	TX
KLC_124	septemvittatus	29.4558	-103.4125	Christmas Mountains	Brewster	TX
KLC_125	septemvittatus	29.4558	-103.4125	Christmas Mountains	Brewster	TX
KLC_129	septemvittatus	29.4558	-103.4125	Christmas Mountains	Brewster	TX
KLC_130	septemvittatus	29.4558	-103.4125	Christmas Mountains	Brewster	TX

Sample	Population	Latitude	Longitude	Locality	County	State
KLC_131	septemvittatus	29.4558	-103.4125	Christmas Mountains	Brewster	TX
KLC_132	marmoratus	29.4558	-103.4125	Christmas Mountains	Brewster	TX
KLC_133	marmoratus	29.4558	-103.4125	Christmas Mountains	Brewster	TX
KLC_135	septemvittatus	29.4558	-103.4125	Christmas Mountains	Brewster	TX
KLC_136	septemvittatus	29.4544	-103.4927	Christmas Mountains	Brewster	TX
KLC_137	marmoratus	29.4544	-103.4927	Christmas Mountains	Brewster	TX
KLC_138	marmoratus	29.4544	-103.4927	Christmas Mountains	Brewster	TX
KLC_139	marmoratus	29.4544	-103.4927	Christmas Mountains	Brewster	TX
KLC_140	marmoratus	29.4544	-103.4927	Christmas Mountains	Brewster	TX
KLC_142	marmoratus	29.4544	-103.4927	Christmas Mountains	Brewster	TX
KLC_143	septemvittatus	29.4544	-103.4927	Christmas Mountains	Brewster	TX
KLC_145	marmoratus	29.4544	-103.4927	Christmas Mountains	Brewster	TX
KLC_146	marmoratus	29.4558	-103.4839	Christmas Mountains	Brewster	TX
KLC_147	septemvittatus	29.4558	-103.4839	Christmas Mountains	Brewster	TX
KLC_149	marmoratus	29.4558	-103.4839	Christmas Mountains	Brewster	TX
KLC_150	marmoratus	29.4558	-103.4839	Christmas Mountains	Brewster	TX
KLC_151	marmoratus	29.4558	-103.4839	Christmas Mountains	Brewster	TX
KLC_162	tesselatus	37.6597	-103.5703	Picketwire Canyon Trail	Otero	CO
KLC_163	tesselatus	37.6597	-103.5703	Picketwire Canyon Trail	Otero	CO
KLC_165	gularis	30.3232	-103.1369	Nature Conservancy	Brewster	TX
KLC_166	gularis	30.3232	-103.1369	Nature Conservancy	Brewster	TX
KLC_167	gularis	30.3232	-103.1369	Nature Conservancy	Brewster	TX
KLC_168	tesselatus	35.5129	-101.7947	Kritser Ranch	Potter	TX

Table 2 Summary statistics for the alpha diversities for each species' populations as inferred by Admixture.

	Population	n	Heterozygosity (obs)	Shannon Mean	Shannon SD
1	gularis1	2	0.00295	2.9430	0.2128
2	gularis2	1	0.00515	1.8620	NA

3	gularis3	6	0.00236	1.4082	0.2832
4	gularis4	5	0.00264	1.7220	0.8023
5	marmoratus1	9	0.00211	2.5176	1.3820
6	marmoratus2	2	0.00206	3.5176	0.4750
7	marmoratus3	4	0.00214	2.9971	0.6425
8	marmoratus4	6	0.00215	2.3593	1.2196
9	marmoratus5	1	0.00232	1.7146	NA
10	marmoratus6	3	0.00193	3.6560	0.1148
11	septemvittatus1	13	0.00137	1.4909	1.0756
12	septemvittatus2	13	0.00137	2.8947	0.7074

	Population	Richness Mean	Richness SD	PD Mean	PD SD
1	gularis1	120.5000	62.9325	27.8215	15.7407
2	gularis2	49.0000	NA	12.1688	NA
3	gularis3	39.3333	28.9390	10.1947	6.8230
4	gularis4	76.8000	47.5784	18.5821	10.8157
5	marmoratus1	82.4444	32.2572	20.3054	7.1116
6	marmoratus2	110.5000	7.7782	25.5609	1.5795
7	marmoratus3	78.2500	13.0990	20.4647	0.9851
8	marmoratus4	85.5000	25.9287	20.1284	5.6541
9	marmoratus5	61.0000	NA	17.3750	NA
10	marmoratus6	121.6667	30.0056	26.9444	4.0743
11	septemvittatus1	55.3077	30.8501	13.3540	5.7924
12	septemvittatus2	95.5385	43.3294	22.8930	9.6378

Obs. Het. x alpha diversity (linear regression)

		equation	R^2	F-statistic	p
	Shannon	y=2.9-185x	$R^2 = 0.054$	$F_{(1,10)} = 0.5701$	0.4676
	Richness	y=99.8-7780x	$R^2 = 0.079$	$F_{(1,10)} = 0.8522$	0.3777
	Phylogenetic diversity	y=23.8-1754x	$R^2 = 0.091$	$F_{(1,10)} = 1.002$	0.3405

Table 3 Fst and Dxy for each species.

	Fst		Dxy	
Population	**Mantel r**	**p**	**Mantel r**	**p**
gularis	0.9664	0.041667	0.8771	0.16667
marmoratus	0.04511	0.375	-0.07873	0.60278
septemvittatus	*NA*	*NA*	*NA*	*NA*

Figures

Figure 1 The origins of *Aspidoscelis tesselatus*, a parthenogenetic lineage of whiptail lizards. Sexual species *A. marmoratus* and *A. septemvittatus* hybridized, producing an offspring with the capability to reproduce clonally. As a result, *A. tesselatus* has a perpetually hybrid genome, one complement from *A. marmoratus* and one complement from *A. septemvittatus*.

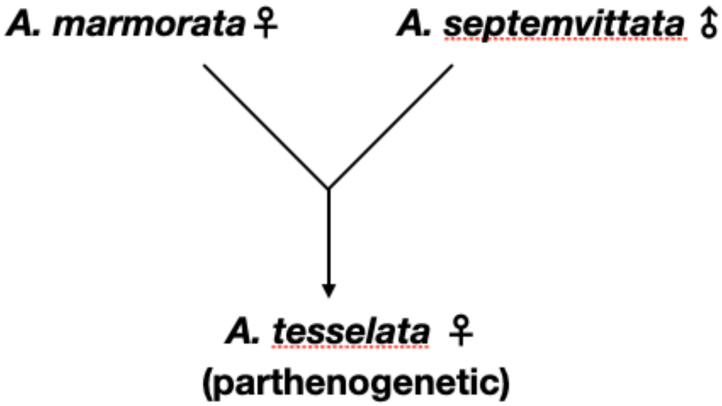


Figure 2 Population stratification results using admixture using the ALL dataset. (A) Results for K=7, the optimal number of clusters as determined by the Evanno method. (B) Results for K=3, based on *a priori* expectations for which each sexual species is inferred as its own cluster. (C) Results for K=4, where two clusters are given to *A. gularis* as seen in multiple admixture analyses.

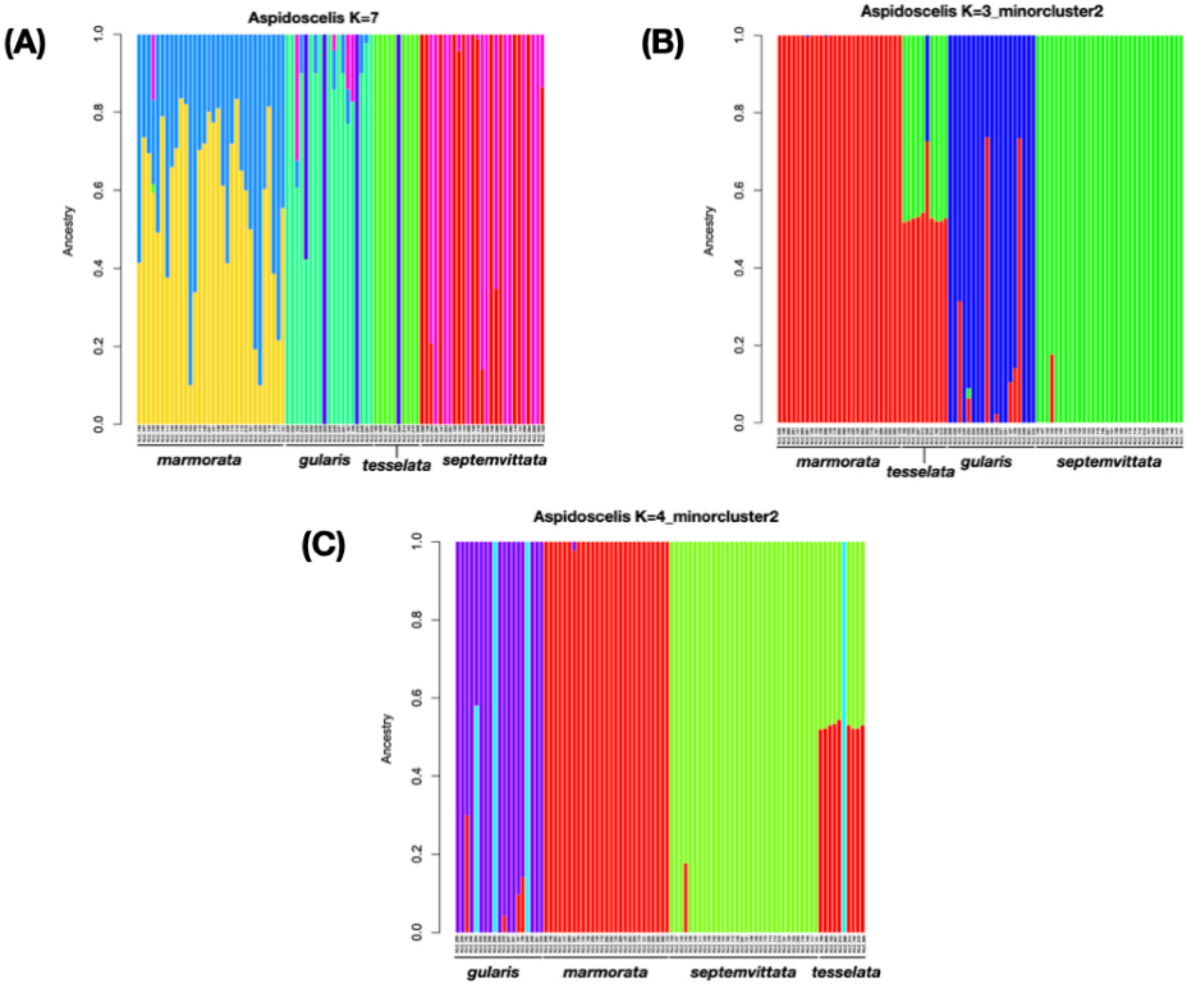


Figure 3 Admixture results for each individual species, with each K inferred based on the Evanno method. (A) *Aspidoscelis gularis*, (B), *A. marmoratus*, and (C) *A. septemvittatus*.

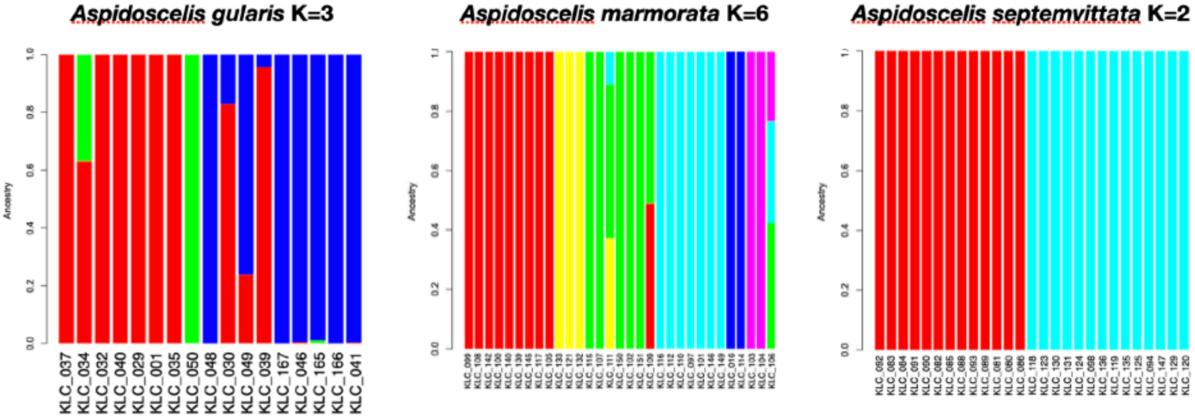
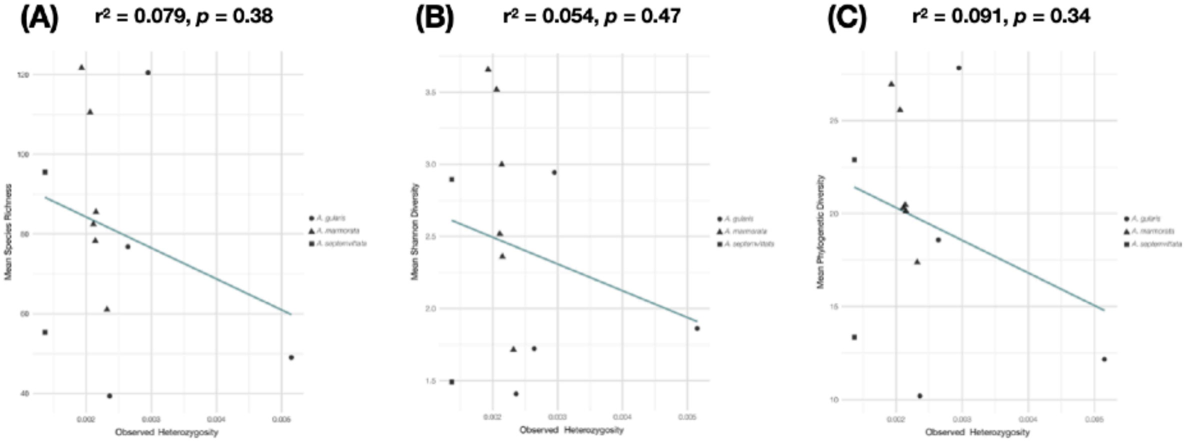


Figure 4 Linear regressions of observed heterozygosity of sexual populations (as inferred from admixture) and various measures of microbiome alpha diversity. None of these regressions were statistically significant. (A) Mean species richness, (B) Shannon Diversity, and (C) Phylogenetic Diversity against observed heterozygosity.



Chapter 3: Characterization of MHC II Beta Genes in Whiptail Lizards (*Aspidoscelis)*

Introduction

The major histocompatibility complex (MHC) is a pivotal player in innate immunity in vertebrates by presenting foreign antigens to T cells, thereby initiating an immune response. Three MHC classes have distinct roles; MHC class I present antigens originating intracellularly (such as from viruses), MHC class II present extracellular antigens, and MHC class III lacks antigen-presenting functions and instead is involved in signaling pathways (Juris 2021). Both class I and class II MHC are composed of two subunits, called the alpha and beta chains. The structure of MHC class I and class II genes are different though their functions are similar. Each are transmembrane complexes that present antigens that are attached to the antigen-binding site (ABS). In class I complexes, only the alpha chain contributes to the ABS. In class II complexes, both the alpha and beta chains contribute to the ABS (Figure 1). Each chain is encoded by a single gene, though multiple copies exist of each chain in vertebrate genomes; for example, the dozens of human MHC genes are all located in a single region in the human genome (“Complete Sequence and Gene Map of a Human Major

Histocompatibility Complex. The MHC Sequencing Consortium" 1999). The potential pairing of multiple different alpha and beta chains produces substantial diversity in both MHC classes that allows the immune system to initiate a response to nearly any pathogen. In addition, each of the alpha and beta chains often have tens to hundreds of alleles that exist in a population, making MHC genes some of the most polymorphic genes in the genome; the human MHC gene HLA-B has more than 2,000 alleles (Trowsdale and Knight 2013).

The MHC complexes are often a focus in conservation genetics largely because they can harbor substantial genetic variation. This variation directly reflects the selection pressures on the MHC: pathogen antigen presentation and sexual selection (Jan Ejsmond, Radwan, and Wilson 2014). Because pathogens are so diverse and come from all domains (viruses, bacteria, eukaryotes), genetic variation at MHC is crucial for recognizing any pathogen as a foreign entity. Thus, measures of MHC diversity are often used as a proxy for the immunological health of populations, especially those of potential conservation concern that may already exhibit low genetic variation. For example, Langefors et al. (2001) studies variation at the MHC IIB locus as correlated with disease susceptibility in salmon, and found that one particular allele was highly associated with resistance to the bacterial pathogen *Aeromonas salmonicida*. A more recent study by Manlik et al. (2019) found that bottlenose dolphins populations with higher MHC Class II variation were more viable (higher reproductive output) than a population that were less viable (lower reproductive output), compared to neutral markers. In reptiles, Santonastaso et al. (2017) found that MHC II variation in island populations of the wall lizard (*Podarcis erhardii*) is largely affected by effective population size, despite these genes being influenced by balancing selection. A second hypothesis regarding the extreme variation at MHC loci is that they play an important role in sexual selection, including humans, whereby individuals are attracted to others with similar allelic combinations (Chaix, Cao, and Donnelly 2008).

MHC complexes have been studied mostly in mammals, birds, fish, and even amphibians (reviewed in Kaufman 2018), though several recent studies have characterized both complex I and complex II chains in reptiles (Hacking et al. 2018; Reed and Settlage 2021; Olivieri, Mirete-Bachiller, and Gambón-Deza 2020; Miller et al. 2006). Because the great majority of the microbiome is extracellular, I will focus on characterizing MHC class II as part of my dissertation. In particular, I will identify the class II beta chains in an attempt to understand their copy number and variation within and between different species of whiptails. This characterization will be a foundation to investigate further genetic variation within and between parthenogenetic and sexual lineages, and how that variation correlates with gut microbiome diversity.

Whiptail lizards (genus *Aspidoscelis*) are widespread throughout the United States, Mexico, and Central America. They belong to the family Teiidae, and contain a large number of clonal lineages that reproduce by parthenogenesis. Parthenogenetic lineages arose via hybridization events between two divergent sexual species; these hybridization events occurred within the Pleistocene (Maldonado et al. 2022). Further backcrossing of the diploid parthenogens to the parentals is possible, and even hybridization with a third species produce triploid lineages. The establishment of parthenogenetic lineages via hybridization is a severe bottleneck such that the genetic variation is initially limited to that present in the maternal and paternal individuals involved in the initial cross; subsequent mutation, intergenomic recombination, and gene conversion can further act to increase or decrease variation. Because of their unique histories, reproductive mode, and genomic composition, whiptails are an exciting and exemplary group to investigate evolution in the absence of sex (Fujita et al. 2020; Maldonado et al. 2022).

Understanding MHC dynamics in whiptails could provide important insight into several aspects of their biology. First, parthenogens are expected to harbor high MHC heterozygosity, perhaps even higher than in sexuals because the alleles from asexual individuals come from divergent parentals. In contrast, the allelic diversity in parthenogenetic populations is expected to be low. Furthermore mechanisms such as intergenomic recombination could produce novel alleles, while gene conversion could remove alleles. Nevertheless, understanding MHC variation is important in parthenogens, which are expected to be particularly vulnerable to pathogens given their static genetic variation (Sommer 2005). Second, whiptails display reproductive behavior linked to hormones and pheromones that may play a role in sexual selection (e.g. Crews et al. 1996). It is unknown if the MHC plays a role as well, though a recent study demonstrated that follicular glands of lizards are enriched with MHC transcripts (and whiptails, both male and female, have femoral follicular glands). Third, it is unknown whether MHC variation has any effect on gut microbiome composition. Parthenogenetic whiptails are an excellent system to investigate this given they have (theoretically) static genetic variation in contrast to sexual populations that constantly shuffle and generate alleles among individuals. However, to investigate MHC dynamics first requires understanding the genomic architecture of the genes. The purpose of this chapter is to provide an initial characterization of MHC class II beta genes. To attain this goal, I will:

1. Sequence the liver and femoral gland transcriptomes from 20 lizards.
2. Identify putative MHC loci.
3. Infer potential gene models using the newly-release *Aspidoscelis tigris* genome
4. Infer a minimum copy number of beta chain loci using the genome and phylogenetic analysis

Methods

Sampling

We collected 20 individuals across 9 species during our field work in Texas, including the parthenogenetic species (numbers are in parentheses) *Aspidoscelis tesselatus* (diploid, 9), *A. neotesselatus* (triploid, 1), *A. neomexicanus* (diploid, 1), and *A. exsanguis* (triploid, 1), and the sexual species *A. marmoratus* (5), *A. inornatus* (3), *A. gularis* (1), and *A. sexlineata* (1). Localities are provided in Table 1. All samples were humanely collected by lasso or hand and processed under IACUC protocol A13.010. Liver tissue and femoral glands was stored in RNALater (Qiagen) using the manufacturer's guidelines, stored under refrigeration for 1-7 days, before permanent storage at -20 C. Specimens were preserved with formalin and lodged at UTA's Amphibian and Reptile Diversity Research Center. We sequenced liver transcriptomes for most individuals, though for four individuals we sequenced the transcriptomes of femoral glands (two *A. inornatus*, one *A. exsanguis*, and one *A. tesselatus*). All transcriptomes were processed and analyzed in the same manner for the purposes of this study.

RNA library preparation

RNA was extracted using the Promega SV Total RNA Extraction kit (Promega) following the manufacturer's protocol. Briefly, this extraction method requires manual losing of cells in the presence of beta mercaptoethanol (which deactivated RNases). We used Qiagen's bead beater (Qiagen) with a setting of 20 Hz to disrupt cells in the presence of the lysis buffer for 10 minutes with a 3 mm stainless steel ball bearing. RNA is then captured on a silica filter in a spin column, at which time DNase is added to remove contaminating DNA. RNA is then eluted in water. The concentration of RNA was estimated using the Qubit 2.0. While we did some additional quality control steps (such as running a few samples on the Bioanalyzer), we found that the library kit used for sequencing was adequate for both high-quality and intact RNA preparations as well as degraded samples.

To construct the RNA libraries for sequencing, I used the Kapa Biosystems RNA HyperPlus with RiboErase (HMR) kit (Roche). This kit uses sequence capture to remove ribosomal RNA from the RNA preparations before using the remaining mRNA to build the sequencing library. A benefit of this approach is that degraded RNA (e.g. those preparations where the 3' A-tail has been degraded) can be used for library preparation. Despite the kit being optimized for human, mouse, and rat genomes, we found that reptiles and amphibians can be used with the kit with high sequencing efficiency. We used at least 500 ng of input RNA but aimed for 1 µg, and followed the manufacturer’s protocol with some slight modifications regarding adapter ligation. We used our own adapters based off of Glenn et al. (“Adapterama”; 2019), which are compatible with Illumina sequencing technologies. Each sample was then uniquely dual-indexed by PCR; that is, each sample had a unique i5 and a unique i7 index. This unique dual-indexed system avoids issues with index swapping that can happen on Novaseq sequencers (“Minimizing Index Hopping” 2022). We pooled equimolar amounts of each prepared library and sequenced the pool at the UTA North Texas Genome Center (150 PE).

Transcriptome assembly

Transcriptomes for each sample were generated by de novo assembly using Trinity v. 2.14.0 (Grabherr et al. 2011; Haas et al. 2013) with Trimmomatic v.0.39 (Bolger et al. 2014) and default parameters. Trimmomatic filters the raw data for adapter contamination and low-quality reads, while also trimming reads of low-quality bases. Trinity takes the filtered reads and uses de Bruijn graphs and assembly algorithms optimized for coding regions to produce an initial transcriptome, which usually consists of tens of thousands of putative transcripts. I then used Transdecoder v. 5.5.0 (Haas et al. 2013) to filter the initial Trinity assembly for the longest and most probable transcripts, using default parameters. This optimized transcriptome was further processed using cd-hit v. 4.8.1 and default parameters (Fu et al. 2012), which collapses similar transcripts into putative orthologs, resulting in the working transcriptomes for each individual. I recognize that cd-hit potentially merges transcripts from distinct genes, though I proceeded with this version of the transcriptome knowing that the results likely underestimate the diversity of class II beta chain genes.

To quantify the completeness of each transcriptome, we ran BUSCO v. 5.3.2 using the vertebrate gene set (vertebrata_odb10_; Manni et al. 2021). We aligned the trimmed and filtered reads back to the transcriptome using bowtie2 v.2.4.5 (Langmead and Salzberg 2012) in order to estimate the average coverage per sample using the function coverage in samtools v.1.15.1 (Danecek et al. 2021).

Identification of MHC class II beta genes

To identify putative MHC class II beta chain transcripts in the transcriptome, we performed blast (tblastx) searches against beta chain sequences from the green anole lizard (*Anolis carolinensis*; GenBank Accession XM_008121064), the marine iguana (*Amblyrhynchus cristatus*; GenBank Accession FJ623746), the tuatara (*Sphenodon punctatus*; DQ124233), and the axolotl (*Ambystoma mexicanum*; GenBank Accession AF209117). We used a stringent e-value cutoff of 1e-50 for each search. There were some lizards on GenBank that had MHC II beta chains that were more closely related to *Aspidoscelis* (*Podarcis muralis* and *Lacerta agilis*), but these were computationally annotated rather than experimentally identified; we did not use these in the blast searches but did include them in the phylogenetic analysis described below.

One of our goals was to determine the gene structure of the MHC II beta genes, as this will provide foundational information for future work. Because transcripts only provide coding sequences, we used external information to identify the exon boundaries. The first source of information were gene models predicted from the *Anolis*, *Podarcis*, and *Lacerta* genomes (see below). The second source of information was the *Aspidoscelis tigris* genome (GCA_023333555.1) that is available on GenBank. To our knowledge, the genome is unannotated. Thus, to identify the MHC genes in the *A. tigris* genome, we used tblastx searches with the whiptail MHC II beta transcripts. These searches returned one scaffold from the *A. tigris* genome; thus, subsequent work focused solely on this one scaffold. We used Augustus v. 3.4.0 (Stanke et al. 2008) to identify putative genes, including their exon/intron structures. We then identified the putative MHC loci using our transcripts in blastx searches against the translated Augustus genes.

We aligned all of the MHC II beta genes from our transcripts, *Anolis*, *Lacerta*, *Amblyrhynchus*, and *A. tigris* using translation-guided algorithms as implemented in Geneious (see below under Phylogenetic Analysis for more details). While the alignments identified a core region in all the genes that were obviously homologous, several of the *A. tigris* genes had large 3’ and 5’ sequences that did not align to our transcripts. We made the conservative decision to remove these sequences even though they represent distinct loci in the *A. tigris* genome. After removing these genes, we had a set of six genes from the *A. tigris* genome that aligned well with the rest of the MHC II beta sequences. We consider this set of six the minimum number of MHC II beta genes in the *Aspidoscelis* genome.

Manual annotation of MHC class II beta gene models

We used annotations from the *Anolis*, *Lacerta*, and *Podarcis* genomes as well as the Augustus gene predictions of the *Aspidoscelis* tigris genome to identify the exons within our transcripts. We downloaded exon sequences from *Anolis*, *Lacerta*, and *Podarcis* from NCBI and used these to identify the exon boundaries in the multiple sequence alignment. We also identified the exon boundaries using the Augustus annotations of the six genes we retained from the *A. tigris* genome as these are most likely to reflect the gene structure in our transcripts.

To visualize and validate the gene structures of our transcripts, we aligned them to the *A. tigris* scaffold using GMAP (Wu and Watanabe 2005).

Phylogenetic analysis

We conducted a phylogenetic analysis that included the six predicted MHC II beta genes from the *Aspidoscelis* tigris genome, our transcriptomes, and four sequences from GenBank (*Anolis* and *Amblyrhynchus*, as well as MHC II beta genes annotated from draft genomes of *Podarcis muralis*, (XM_028716159_, and *Lacerta agilis*, XM_033141761_). In total the analysis included 53 sequences.

We generated an alignment of the lizard MHC II beta genes using translation-guided algorithms as implemented in Geneious Prime 2022.1.1 (Biomatters). Geneious offers several multiple sequence alignments programs, and we explored several that permitted translation-guided alignments (including muscle v5 - Edgar 2021; MAFFT v 7.490 - Katoh and Standley 2013; and the Geneious algorithms). For each we used default parameters. While all three approaches produced similar alignments, we still adjusted the alignments by eye. In so doing, we understand that we are making judgements about the homology of aligned bases, but by doing so we were able to produce alignments where the 3’ and 5’ ends (in particular, the start and stop codons) were aligned. Note some of the sequences were incomplete and lacked start and stop codons, though these sequences were generally well-aligned.

We conducted a Bayesian phylogenetic analysis as implemented in BEAST 2.6.7 (Bouckaert et al. 2019). The constrained the tree to have a monophyletic Teiidae + Lacertidae; that is, the *Aspidoscelis*, *Podarcis*, and *Lacerta* would be the ingroup and *Anolis* and *Amblyrhynchus* (families Polychrotidae and Iguanidae, respectively) are the outgroups. We implemented the GTR+G (6 gamma variables) for the first, second, and third codon positions, which were allowed to have distinct rates (log-normal distributions). We ran four different analyses to make sure we sampled from the global optimum of the posterior; each run was 20,000,000 generations, sampling every 20,000 generations (this resulted in posterior sampling of 10,000 trees). We checked each run with LogCombiner to make sure they all converged to the same optimum after removing the first 1,000 trees as burn-in (10% of the posterior), and then combined the posterior distributions by resampling every 8000 generations (for a total of 9004 trees of the combined posterior sampling). We summarized the trees using TreeAnnotator to produce a MCC tree.

Results

Sequencing and assemblies

Sequencing and assembly summaries are provided in Table 1. Average length of transcripts across all assemblies, after refining using Transdecoder and cd-hit, is 648.1 bp. The completeness of the transcriptomes ranged from 11.1% to 81.9% of the 3,354 vertebrate genes that BUSCO uses. This result roughly correlates with the size of the transcriptome (as measured by the size of the transcriptome after all refinement). The average sequence coverage among the samples ranged from 22.34X - 121.58X.

Identification of MHC class II beta genes

The initial tblastx searches of known MHC class II beta chain genes from *Anolis*, *Amblyrhynchus*, *Sphenodon*, and *Ambystoma* against the transcriptomes yielded between 0 and 5 hits per sample. The one sample that yielded 0 hits (KLC 168) sequenced poorly, but our sampling had other representatives of *A. tesselatus*. Our searches were stringent and thus *Sphenodon* and *Ambystoma* did not hit with any of the transcripts. However, the same transcripts from each individual were consistently returned when blasted with the lizards, *Anolis* and *Amblyrhynchus*. When combined, the total number of MHC II beta chain genes across *Aspidoscelis* samples totaled 43.

Our tblastx searches against the *A. tigris* genome yielded a single scaffold (JALMGA010000024). blastx searches against Augustus-predicted genes on this scaffold returned 10 hits, indicating 10 distinct putative MHC II beta genes in the *A.*

tigris genome. We refined these 10 genes down to 6 after removing 4 that had 3' or 5' ends that extended beyond the start and stop codons of our transcripts. Thus, while we focus on these six genes in the *A. tigris* genome, there are at least four other potential MHC II beta genes.

The multiple sequence alignment between all of the sequences (our *Aspidoscelis* transcripts, *Anolis*, *Lacerta*, *Podarcis*, and the six genes from *A. tigris*) was translation-guided. Several transcripts as well as some of the *A. tigris* genes did not not have obvious start or stop codons, or were missing some parts of the 3' and 5' ends. Nevertheless, the alignment did not have any internal stop codons.

There is strong evidence that the MHC II beta transcripts represent five exons. The exon boundaries are predicted to be the same in *Podarcis* and *Lacerta*, which also coincided with predicted exons in the *A. tigris* genome. In fact, all six of the MHC II beta genes in the *A. tigris* genome had the same exon-intron structures (though some had additional exons and introns at the 5' end). This was even the case for the one copy that was oriented in the opposite direction as the others (g583). Thus, we are confident that the exon structures in our transcripts follow the same patterns as those found in the *A. tigris* genome, *Podarcis*, and *Lacerta* (Figure 2). Interestingly, *Anolis* was annotated to have a very different exon-intron structure that did not match those found in the other lizards.

Phylogenetic Analysis

The multiple sequence alignment of 53 MHC II beta genes is 837 nucleotides long. Using LogCombiner, we checked that the four independent runs converged to the same optimum before combining them into a single posterior. To make sure that the sampled trees were not autocorrelated, we checked to make sure the ESS value for the likelihood was >200. For all parameters, including the likelihood and rate parameters, ESS values were much larger than 200. We then summarized the posterior as an MCC tree (Figure 3).

The MCC tree shows important patterns of diversity MHC II beta genes within whiptails. First, the transcripts are monophyletic with respect to *Podarcis* and *Lacerta*. Second, there are two major clades within *Aspidoscelis* (which are labeled as “Clade A” and “Clade B” in Figure 3). Third, genes that were predicted from the *A. tigris* genome using Augustus occur in both clades (g234, g229, and g247 are in Clade A and g583, g541, and g276 are in Clade B). Similarly, transcripts assembled within individuals also occurred in both clades, indicating that gene duplication and subsequent divergence occurred before the diversification of *Aspidoscelis* species.

Discussion

Our initial survey of MHC genes in the *Aspidoscelis tigris* genome identified 10 putative class II beta chain genes that are all located on one scaffold. Because Augustus inferred some of these genes to be very large due to their extended 3’ (the initial ATG start codon was far upstream of annotated MHC genes) or 5’ (there was a lack of stop codon compared to annotated MHC genes) ends, we removed these for our phylogenetic analysis, leaving six putative genes. The long genes predicted from Augustus may be an artifact of matching the start of one gene with the end of a different gene; thus, there may be more than 10 MHC II genes, and this requires further refinement in annotation. The phylogenetic analysis placed these six genes in both major groups, though it is clear that some genes are closely related to each other given their affinities in the tree. We consider the 6 genes the minimum number of class II MHC beta chain genes.

For the *A. tigris* genome, which was sequenced using both HiFi PacBio reads and HiC scaffolding, all 10 of the putative MHC II beta genes occurred on a single scaffold. This is consistent with most other vertebrates where the MHC region, often spanning a few megabases, includes all MHC genes, including MHC I and MHC III complexes (reviewed in Kaufman 2018). Paralogous regions do exist in some genomes, though we did not find any evidence of this in whiptails. Because all MHC classes tend to exist in the same region (as well as other immune genes; Kumánovics, Takada, and Lindahl 2003), we fully expect to find other classes of MHC on this scaffold. It is important to note that we do not know whether our transcripts represent distinct loci, alleles at a single locus, or perhaps even misassemblies from different loci resulting in a chimeric annotation. This is especially true in the parthenogens whose genomes are a hybrid between two divergent sexuals. However, we did not see any evidence that loci were misassembled between the two phylogenetic groups within a parthenogen.

MHC and the Red Queen

Parthenogenetic systems provide an interesting system to examine an important hypothesis in evolutionary biology, the Red Queen Hypothesis first proposed by Van Valen (1973). The Red Queen predicts that genotypes will fluctuate over time due to frequency-dependent selection as a result of a constantly-changing environment.

Populations that are more genetically diverse will be more capable to adapt to changing environments than populations that are less genetically diverse. One common scenario that invokes the Red Queen is the relationship between hosts and pathogens (Bell 1982), with the prediction that populations with more genetic diversity will harbor fewer pathogens. We can thus predict that parthenogenetic lineages - with their limited genetic diversity - will harbor more pathogen loads than their sexual counterparts. One genetic system that is a candidate for Red Queen dynamics is the MHC complex because of its role in adaptive immunity and recognizing previously-exposed pathogens. A recent study by Gösser et al. (2019) examined MHC I variation in asexual and sexual populations of the fish *Poecilia* but found no correlation between allelic diversity and parasite (trematode) load. One explanation given for this was the high heterozygosity of the hybrid clones provided the protection against the trematodes via the innate immune system. One issue that should be investigated further is whether MHC II should have been used, as this complex is typically presents the extracellular antigens (which presumably would be proteins from parasites).

It has been shown that parasite loads are higher in some parthenogenetic lizards (e.g. the Bynoe’s gecko, *Heteronotia binoei*; Moritz et al. 1991) but not others (the mourning gecko, *Lepidodactylus lugubris*; Hanley, Fisher, and Case 1995). One potential explanation for this is that *Lepidodactylus* are island lizards, and thus we expect that even the sexual populations have reduced genetic variation that might reflect on normalizing parasite loads with parthenogenetic relatives. *Heteronotia* is a mainland species with extensive genetic diversity in the sexuals (Fujita et al. 2010), perhaps with the variation necessary for the Red Queen to operate. In whiptails, one study found higher mite loads in parthenogenetic lizards compared to sexuals (Jackson and Bateman, 2018). Missing from all of these studies is a genetic component. One exciting avenue of research is the integration of parasite and pathogen studies with the quantification of genetic diversity of both neutral and immune genes, such as the MHC, in these studies.

Phylogenetic analysis

We included *Podarcis* and *Lacerta* in order to understand when the diversity of MHC alleles arose within whiptails. Because whiptail MHC II beta alleles are monophyletic, this indicates that diversity arose after the divergence between the lizard families Teiidae (*Aspidoscelis*) and Lacertidae (*Podarcis* and *Lacerta*). However, given the identical gene structures between the MHC II beta genes across Teiidae and Lacertidae, it may be that the gene copies arose before the two families diverged and that homogenizing mechanisms, such as gene conversion, are responsible for the monophyly of the genes within *Aspidoscelis*. Gene conversion has been shown to be an important aspect of MHC variation (reviewed in Martinsohn et al. 1999; Bahr and Wilson 2012; Chen, Bei, and Li 2015), and can even generate new alleles (Högstrand and Böhme 1999). One of our future goals is to investigate the frequency of gene conversion in parthenogenetic lizards and how this mechanism might generate or remove genetic variation, including at MHC loci.

Most of the smaller clades near the tips of the tree only contain transcripts from a few species. For instance, one clade that contains g541 only has transcripts from *inornatus* and *sexlineata*. This may be due to several, non-mutually exclusive reasons.

First, our sequencing effort may have missed some MHC alleles. This is entirely possible given many of our samples had low BUSCO “complete” scores. Second, Trinity may have found it difficult to assemble exact alleles, an issue with multi-gene families in general. Indeed, our study is unable to distinguish between potential chimaeras or true alleles. Long-read sequencing of either transcriptomes or genomes will be necessary to definitively identify the different genes within the genome.

The antigen binding site of MHC II is located in exon 2; thus, we expect that exon 2 will harbor the most variation in the gene. In our sampling, exon 2 has an average pairwise distance of 0.27, while exon 3 has an average pairwise distance of 0.19. Thus, our data confirm that exon 2 has more extensive variation. Our alignments are among paralogous copies, and thus we might expect to see even more extreme differences in alignments of orthologous exons 2 and 3. The importance of this difference is that exon 2 is typically sequenced for non-model organisms in conservation studies because of its expansive variation. This variation also makes it amenable to detecting the contributions of mutation, recombination and gene conversion in generating the patterns of diversity.

Future Directions

The primary purpose of this study was to provide a preliminary look at MHC II structure and diversity in whiptail lizards. While we have accomplished this task and provided discussion on the implications of our results, this project opens up multiple avenues of future research, with two of them being immediate foci of the lab. First, our bioinformatics pipeline and approach is amenable to characterizing other gene complexes, and we intend to pursue MHC Class I genes as well as other immunity genes, such as those involved in innate immunity (Toll-like receptors). We predict that the MHC Class I genes will reside on the same scaffold from the *tigris* genome. Along with identifying the additional genes, we hope to provide a precise and detailed annotation of the MHC region in whiptail lizards. Second, we will use our annotations of the MHC II to design primers to sequence exon 2, which is the exon that has the ABS and is thus highly polymorphic. With population-level sequencing of exon 2, we will be able to infer many of the genomic and evolutionary mechanisms that govern patterns of MHC II polymorphisms between sexual and asexual lizards. MHC variation has been studied in sexual and parthenogenetic *Lepidodactylus* geckos (Radtkey et al. 1996), finding that parthenogenetic lineages had limited variation compared to sexual relatives. This study had limited sequencing and assayed variation through restriction fragments. With next-generation sequencing, we will have the ability to massively scale up our sequencing to test this hypothesis and to explore the mechanisms that limit the variation in parthenogenetic lineages. Third, we will investigate the relationship between MHC variation and gut microbiome diversity in parthenogenetic and sexual populations. A recent study in the Seychelles warbler (*Acrocephalus schellensis*) found that particular alleles - rather than absolute diversity - in both MHC I and MHC II influence gut microbiome composition (Davies et al. 2022). While our studies have shown that the environment is largely responsible for microbiome diversity, we have not yet pursued investigations of individual genes.

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Tables

Table 1 Sample locality information, and associated transcriptome data.

Sample	species	Latitude	Longitude	Locality	# MHC after initial tblastx
JAM_014	tesselatus				4
KLC_066	tesselatus	30.5494	-104.6617	Miller Ranch - fort	2
KLC_136	septemvittatus	29.4544	-103.4927	Christmas Mountains	4
KLC_145	marmoratus	29.4544	-103.4927	Christmas Mountains	1
KLC_146	marmoratus	29.4558	-103.4839	Christmas Mountains	2
KLC_148	inornatus	29.4558	-103.4839	Christmas Mountains	3
KLC_149	marmoratus	29.4558	-103.4839	Christmas Mountains	3
KLC_150	marmoratus	29.4558	-103.4839	Christmas Mountains	1
KLC_151	marmoratus	29.4558	-103.4839	Christmas Mountains	1
KLC_157	sexlineata	37.7697	-103.5130	Vogel Canyon Rec. Center	4
KLC_160	neotesselatus	37.7697	-103.5130	Vogel Canyon Rec. Center	1
KLC_162	tesselatus	37.6597	-103.5703	Picketwire Canyon Trail	3
KLC_163	tesselatus	37.6597	-103.5703	Picketwire Canyon Trail	3
KLC_167	gularis	30.3232	-103.1369	Nature Conservancy	3
KLC_168	tesselatus	35.5129	-101.7947	Kritser Ranch	0
MKF_01006	inornatus	30.551961	-104.646825	Miller Ranch, Valentine, T	5
MKF_01011	inornatus	30.551961	-104.646825	Miller Ranch, Valentine, T	3
MKF_01012	exsanguis	30.551961	-104.646825	Miller Ranch, Valentine, T	2
MKF_01013	tesselatus	30.551961	-104.646825	Miller Ranch, Valentine, T	3
RLK_089	neomexicanus				1
Sample	**Total # cd-hit transcripts**	**Average length of cd-hit transcript (bp)**	**Average coverage**	**Raw reads (forward only)**	**BUSCO complete percentage**

JAM_014	59470	669.6	47.57	76235418	66.9
KLC_066	34464	685.7	89.71	56527052	46.8
KLC_136	63995	592.9	52.54	141040594	51.6
KLC_145	36967	668.3	54.27	68598213	46.4
KLC_146	46876	694.9	58.59	90564746	62.1
KLC_148	55284	664.9	62.54	100380008	64.4
KLC_149	22808	565.7	44.70	70352813	17.7
KLC_150	26822	584.7	40.76	71570089	21.2
KLC_151	16169	542.0	29.83	55105448	11.1
KLC_157	45234	725.2	57.60	72422214	65.5
KLC_160	42886	659.3	72.32	75838488	56.1
KLC_162	64064	601.9	53.41	127107483	57.7
KLC_163	40117	617.9	57.06	142712126	34.3
KLC_167	48325	671.3	50.27	107324864	57.7
KLC_168	21772	711.8	95.78	68310836	41.4
MKF_01006	65101	695.8	121.58	107636522	79.2
MKF_01011	68152	686.3	72.42	84258478	81.9
MKF_01012	46108	679.4	85.87	187559306	47.9
MKF_01013	75323	604.6	77.17	115312995	63.8
RLK_089	45460	639.2	22.34	31164439	48.7

Sample	BUSCO complete S (of 3354)	BUSCO complete D	BUSCO fragmented	BUSCO missing	
JAM_014	2133	110	8	1103	
KLC_066	1510	59	684	1101	
KLC_136	1654	76	86	1538	
KLC_145	1492	65	866	931	
KLC_146	1990	93	579	692	
KLC_148	2061	99	552	642	
KLC_149	573	22	819	1940	
KLC_150	678	32	908	1736	
KLC_151	357	16	613	2368	
KLC_157	2093	105	478	678	

KLC_160	1822	59	630	843	
KLC_162	1860	76	87	1331	
KLC_163	1100	49	970	1235	
KLC_167	1859	75	619	801	
KLC_168	1338	49	667	1300	
MKF_01006	2502	153	231	468	
MKF_01011	2591	156	274	333	
MKF_01012	1518	89	921	826	
MKF_01013	2023	117	366	848	
RLK_089	1584	50	743	977	

Figures

Figure 1 An example of an MHC II complex, which is a dimer formed from an alpha and beta polypeptide. They are similar in structure and both contribute to the antigen binding site. This study is focused on characterizing the beta chains.

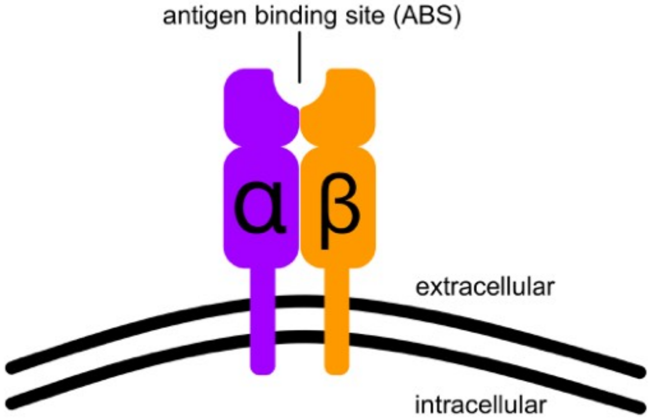


Figure 2 Alignment of the beta chains found in the transcriptomes and genome of whiptail (Aspidoscelis). The exon structures were inferred from Augustus gene predictions and GMAP alignments.

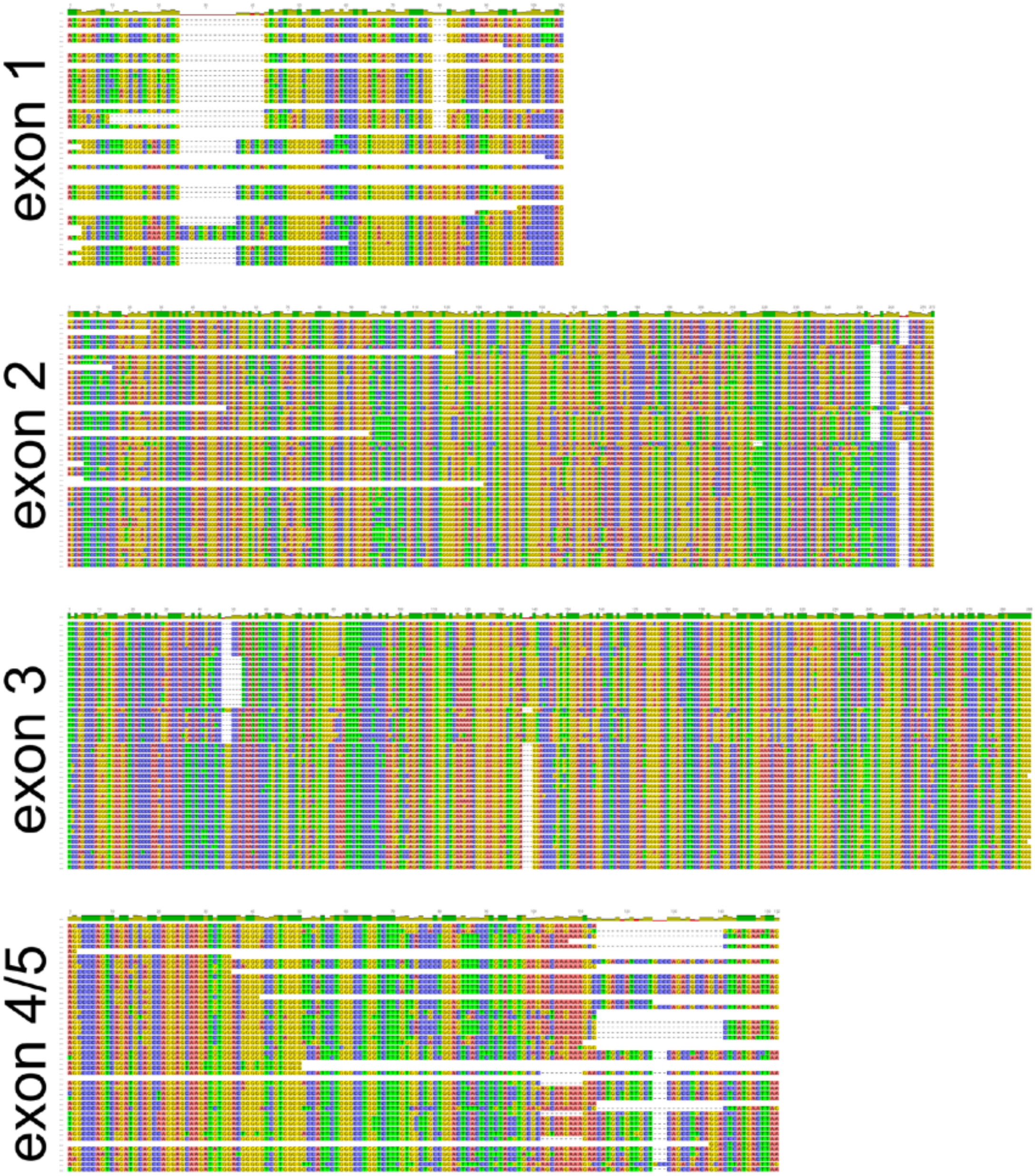
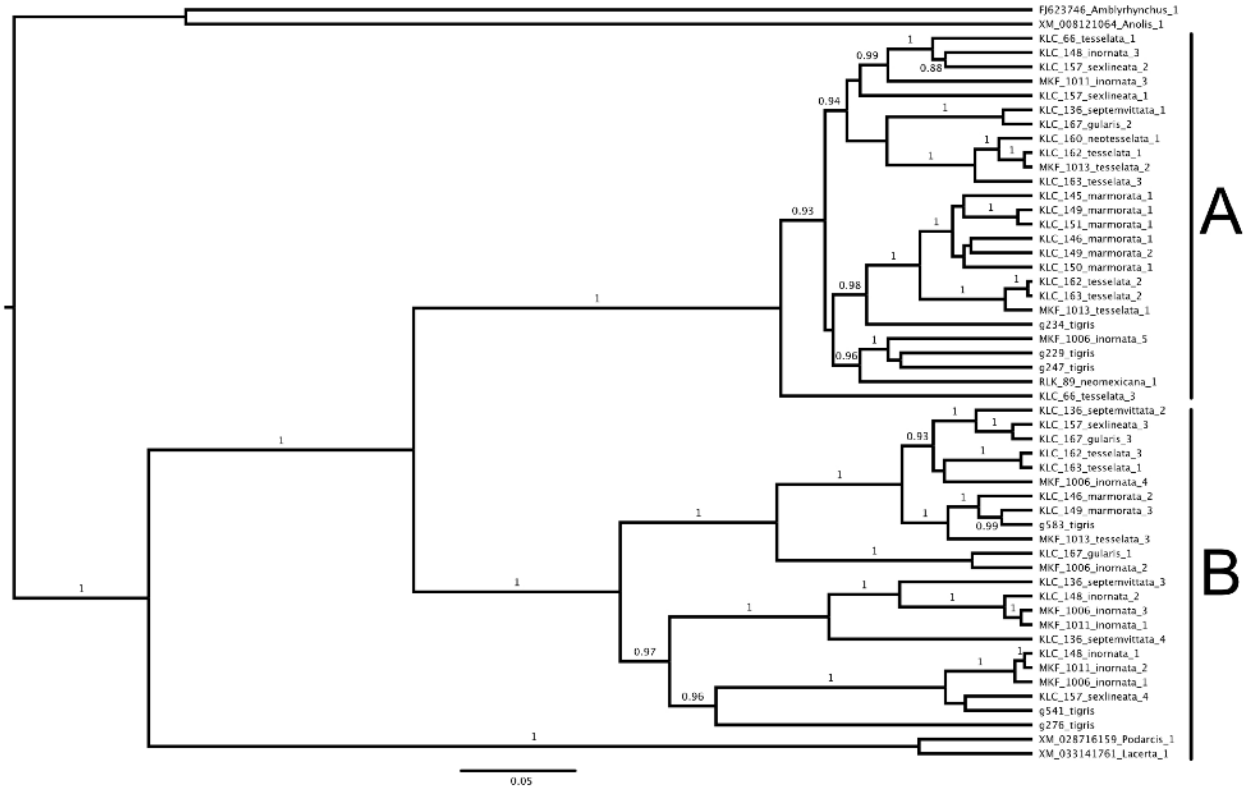

exon 1
exon 2
exon 3
exon 4/5

Figure 3 Phylogeny of the beta chain genes of MHC II in whiptails. The genes from the *Aspidoscelis tigris* genome are indicated with a “g.” There are two clades and every species and individual has genes from both, indicating that the gene copies originated before the diversification of *Aspidoscelis*.



Appendix I

Specimen locality information for all samples used in this study. Rep=Reproduction mode; S=Season collected.

ID	Genus	Species	Rep	Sex	County	State	Year	Month	S
KLC002	*Aspidoscelis*	*inornatus*	sexual	NA	Presidio	TX	2016	6	Summer
KLC004	*Aspidoscelis*	*inornatus*	sexual	NA	Presidio	TX	2016	6	Summer
KLC005	*Aspidoscelis*	*inornatus*	sexual	NA	Presidio	TX	2016	6	Summer
KLC006	*Aspidoscelis*	*inornatus*	sexual	NA	Presidio	TX	2016	6	Summer
KLC007	*Aspidoscelis*	*tesselatus*	asexual	female	Presidio	TX	2016	6	Summer
KLC009	*Aspidoscelis*	*tesselatus*	asexual	female	Presidio	TX	2016	6	Summer

KLC010	*Aspidoscelis*	*tesselatus*	asexual	female	Presidio	TX	2016	6	Summer
KLC011	*Aspidoscelis*	*tesselatus*	asexual	female	Presidio	TX	2016	6	Summer
KLC014	*Aspidoscelis*	*tesselatus*	asexual	female	Presidio	TX	2016	6	Summer
KLC015	*Aspidoscelis*	*tesselatus*	asexual	female	Presidio	TX	2016	6	Summer
KLC016	*Aspidoscelis*	*marmoratus*	sexual	NA	Brewster	TX	2016	6	Summer
KLC017	*Aspidoscelis*	*inornatus*	sexual	NA	Brewster	TX	2016	6	Summer
KLC018	*Aspidoscelis*	*inornatus*	sexual	NA	Brewster	TX	2016	6	Summer
KLC020	*Aspidoscelis*	*inornatus*	sexual	NA	Brewster	TX	2016	6	Summer
KLC021	*Aspidoscelis*	*inornatus*	sexual	NA	Brewster	TX	2016	6	Summer
KLC022	*Aspidoscelis*	*inornatus*	sexual	NA	Brewster	TX	2016	6	Summer
KLC023	*Aspidoscelis*	*inornatus*	sexual	NA	Brewster	TX	2016	6	Summer
KLC024	*Aspidoscelis*	*inornatus*	sexual	NA	Brewster	TX	2016	6	Summer
KLC025	*Aspidoscelis*	*inornatus*	sexual	NA	Brewster	TX	2016	6	Summer
KLC026	*Aspidoscelis*	*inornatus*	sexual	NA	Brewster	TX	2016	6	Summer
KLC027	*Aspidoscelis*	*marmoratus*	sexual	NA	Brewster	TX	2016	6	Summer
KLC029	*Aspidoscelis*	*gularis*	sexual	male	Webb	TX	2017	4	Spring
KLC031	*Aspidoscelis*	*laredoensis*	asexual	female	Webb	TX	2017	4	Spring
KLC032	*Aspidoscelis*	*gularis*	sexual	female	Webb	TX	2017	4	Spring
KLC033	*Aspidoscelis*	*laredoensis*	asexual	female	Webb	TX	2017	4	Spring
KLC034	*Aspidoscelis*	*gularis*	sexual	male	Webb	TX	2017	4	Spring
KLC035	*Aspidoscelis*	*gularis*	sexual	male	Webb	TX	2017	4	Spring
KLC036	*Aspidoscelis*	*gularis*	sexual	female	Webb	TX	2017	4	Spring
KLC037	*Aspidoscelis*	*gularis*	sexual	male	Webb	TX	2017	4	Spring
KLC038	*Aspidoscelis*	*laredoensis*	asexual	female	Webb	TX	2017	4	Spring
KLC039	*Aspidoscelis*	*gularis*	sexual	male	Webb	TX	2017	4	Spring
KLC040	*Aspidoscelis*	*gularis*	sexual	female	Webb	TX	2017	4	Spring
KLC041	*Aspidoscelis*	*gularis*	sexual	female	JeffDavis	TX	2017	6	Summer
KLC042	*Aspidoscelis*	*exsanguis*	asexual	female	JeffDavis	TX	2017	6	Summer
KLC043	*Aspidoscelis*	*exsanguis*	asexual	female	JeffDavis	TX	2017	6	Summer
KLC044	*Aspidoscelis*	*exsanguis*	asexual	female	JeffDavis	TX	2017	6	Summer
KLC046	*Aspidoscelis*	*gularis*	sexual	male	JeffDavis	TX	2017	6	Summer
KLC047	*Aspidoscelis*	*exsanguis*	asexual	female	JeffDavis	TX	2017	6	Summer

KLC048	*Aspidoscelis*	*gularis*	sexual	NA	JeffDavis	TX	2017	6	Summer
KLC049	*Aspidoscelis*	*gularis*	sexual	male	JeffDavis	TX	2017	6	Summer
KLC050	*Aspidoscelis*	*gularis*	sexual	female	JeffDavis	TX	2017	6	Summer
KLC051	*Aspidoscelis*	*gularis*	sexual	male	JeffDavis	TX	2017	6	Summer
KLC052	*Aspidoscelis*	*inornatus*	sexual	NA	JeffDavis	TX	2017	6	Summer
KLC053	*Aspidoscelis*	*inornatus*	sexual	male	JeffDavis	TX	2017	6	Summer
KLC054	*Aspidoscelis*	*inornatus*	sexual	male	JeffDavis	TX	2017	6	Summer
KLC055	*Aspidoscelis*	*inornatus*	sexual	male	JeffDavis	TX	2017	6	Summer
KLC056	*Aspidoscelis*	*inornatus*	sexual	male	JeffDavis	TX	2017	6	Summer
KLC057	*Aspidoscelis*	*inornatus*	sexual	male	JeffDavis	TX	2017	6	Summer
KLC060	*Aspidoscelis*	*inornatus*	sexual	male	JeffDavis	TX	2017	6	Summer
KLC061	*Aspidoscelis*	*inornatus*	sexual	NA	JeffDavis	TX	2017	6	Summer
KLC062	*Aspidoscelis*	*inornatus*	sexual	male	JeffDavis	TX	2017	6	Summer
KLC063	*Aspidoscelis*	*inornatus*	sexual	female	JeffDavis	TX	2017	6	Summer
KLC064	*Aspidoscelis*	*exsanguis*	asexual	female	Presidio	TX	2017	6	Summer
KLC065	*Aspidoscelis*	*exsanguis*	asexual	female	Presidio	TX	2017	6	Summer
KLC066	*Aspidoscelis*	*tesselatus*	asexual	female	Presidio	TX	2017	6	Summer
KLC067	*Aspidoscelis*	*exsanguis*	asexual	female	Presidio	TX	2017	6	Summer
KLC068	*Aspidoscelis*	*exsanguis*	asexual	female	Presidio	TX	2017	6	Summer
KLC069	*Aspidoscelis*	*exsanguis*	asexual	female	Presidio	TX	2017	6	Summer
KLC070	*Aspidoscelis*	*exsanguis*	asexual	female	Presidio	TX	2017	6	Summer
KLC071	*Aspidoscelis*	*exsanguis*	asexual	female	Presidio	TX	2017	6	Summer
KLC072	*Aspidoscelis*	*exsanguis*	asexual	female	Presidio	TX	2017	6	Summer
KLC073	*Aspidoscelis*	*exsanguis*	asexual	female	Presidio	TX	2017	6	Summer
KLC074	*Aspidoscelis*	*inornatus*	sexual	female	Presidio	TX	2017	6	Summer
KLC075	*Aspidoscelis*	*exsanguis*	asexual	female	Presidio	TX	2017	6	Summer
KLC076	*Aspidoscelis*	*inornatus*	sexual	male	Presidio	TX	2017	6	Summer
KLC077	*Aspidoscelis*	*inornatus*	sexual	NA	Presidio	TX	2017	6	Summer
KLC080	*Aspidoscelis*	*septemvitta*	sexual	NA	Brewster	TX	2017	6	Summer
KLC081	*Aspidoscelis*	*septemvitta*	sexual	female	Brewster	TX	2017	6	Summer
KLC082	*Aspidoscelis*	*septemvitta*	sexual	male	Brewster	TX	2017	6	Summer
KLC083	*Aspidoscelis*	*septemvitta*	sexual	male	Brewster	TX	2017	6	Summer

KLC084	*Aspidoscelis*	*septemvitta*	sexual	male	Brewster	TX	2017	6	Summer
KLC085	*Aspidoscelis*	*septemvitta*	sexual	male	Brewster	TX	2017	6	Summer
KLC086	*Aspidoscelis*	*septemvitta*	sexual	male	Brewster	TX	2017	6	Summer
KLC087	*Aspidoscelis*	*septemvitta*	sexual	male	Brewster	TX	2017	6	Summer
KLC088	*Aspidoscelis*	*septemvitta*	sexual	female	Brewster	TX	2017	6	Summer
KLC089	*Aspidoscelis*	*septemvitta*	sexual	male	Brewster	TX	2017	6	Summer
KLC090	*Aspidoscelis*	*septemvitta*	sexual	male	Brewster	TX	2017	6	Summer
KLC091	*Aspidoscelis*	*septemvitta*	sexual	NA	Brewster	TX	2017	6	Summer
KLC092	*Aspidoscelis*	*septemvitta*	sexual	NA	Brewster	TX	2017	6	Summer
KLC093	*Aspidoscelis*	*septemvitta*	sexual	NA	Brewster	TX	2017	6	Summer
KLC094	*Aspidoscelis*	*septemvitta*	sexual	female	Brewster	TX	2018	5	Spring
KLC095	*Aspidoscelis*	*inornatus*	sexual	NA	Brewster	TX	2018	5	Spring
KLC096	*Aspidoscelis*	*inornatus*	sexual	NA	Brewster	TX	2018	5	Spring
KLC097	*Aspidoscelis*	*marmoratus*	sexual	NA	Brewster	TX	2018	5	Spring
KLC098	*Aspidoscelis*	*septemvitta*	sexual	male	Brewster	TX	2018	5	Spring
KLC099	*Aspidoscelis*	*marmoratus*	sexual	male	Brewster	TX	2018	5	Spring
KLC100	*Aspidoscelis*	*marmoratus*	sexual	NA	Brewster	TX	2018	5	Spring
KLC101	*Aspidoscelis*	*marmoratus*	sexual	NA	Brewster	TX	2018	5	Spring
KLC102	*Aspidoscelis*	*marmoratus*	sexual	NA	Brewster	TX	2018	5	Spring
KLC103	*Aspidoscelis*	*marmoratus*	sexual	NA	Brewster	TX	2018	5	Spring
KLC104	*Aspidoscelis*	*marmoratus*	sexual	male	Brewster	TX	2018	5	Spring
KLC105	*Aspidoscelis*	*marmoratus*	sexual	male	Brewster	TX	2018	5	Spring
KLC106	*Aspidoscelis*	*marmoratus*	sexual	NA	Brewster	TX	2018	5	Spring
KLC107	*Aspidoscelis*	*marmoratus*	sexual	NA	Brewster	TX	2018	5	Spring
KLC108	*Aspidoscelis*	*marmoratus*	sexual	NA	Brewster	TX	2018	5	Spring
KLC109	*Aspidoscelis*	*marmoratus*	sexual	NA	Brewster	TX	2018	5	Spring
KLC112	*Aspidoscelis*	*marmoratus*	sexual	NA	Brewster	TX	2018	5	Spring
KLC116	*Aspidoscelis*	*marmoratus*	sexual	male	Brewster	TX	2018	5	Spring
KLC117	*Aspidoscelis*	*marmoratus*	sexual	NA	Brewster	TX	2018	5	Spring
KLC118	*Aspidoscelis*	*septemvitta*	sexual	male	Brewster	TX	2018	5	Spring
KLC119	*Aspidoscelis*	*septemvitta*	sexual	male	Brewster	TX	2018	5	Spring
KLC120	*Aspidoscelis*	*septemvitta*	sexual	NA	Brewster	TX	2018	5	Spring

KLC121	*Aspidoscelis*	*marmoratus*	sexual	female	Brewster	TX	2018	5	Spring
KLC122	*Aspidoscelis*	*septemvitta*	sexual	NA	Brewster	TX	2018	5	Spring
KLC123	*Aspidoscelis*	*septemvitta*	sexual	female	Brewster	TX	2018	5	Spring
KLC124	*Aspidoscelis*	*septemvitta*	sexual	female	Brewster	TX	2018	5	Spring
KLC125	*Aspidoscelis*	*septemvitta*	sexual	NA	Brewster	TX	2018	5	Spring
KLC126	*Aspidoscelis*	*inornatus*	sexual	NA	Brewster	TX	2018	5	Spring
KLC127	*Aspidoscelis*	*inornatus*	sexual	male	Brewster	TX	2018	5	Spring
KLC129	*Aspidoscelis*	*septemvitta*	sexual	male	Brewster	TX	2018	5	Spring
KLC130	*Aspidoscelis*	*septemvitta*	sexual	male	Brewster	TX	2018	5	Spring
KLC133	*Aspidoscelis*	*marmoratus*	sexual	female	Brewster	TX	2018	5	Spring
KLC134	*Aspidoscelis*	*inornatus*	sexual	male	Brewster	TX	2018	5	Spring
KLC135	*Aspidoscelis*	*septemvitta*	sexual	male	Brewster	TX	2018	5	Spring
KLC136	*Aspidoscelis*	*septemvitta*	sexual	male	Brewster	TX	2018	5	Spring
KLC137	*Aspidoscelis*	*marmoratus*	sexual	male	Brewster	TX	2018	5	Spring
KLC138	*Aspidoscelis*	*marmoratus*	sexual	male	Brewster	TX	2018	5	Spring
KLC139	*Aspidoscelis*	*marmoratus*	sexual	male	Brewster	TX	2018	5	Spring
KLC140	*Aspidoscelis*	*marmoratus*	sexual	male	Brewster	TX	2018	5	Spring
KLC141	*Aspidoscelis*	*inornatus*	sexual	male	Brewster	TX	2018	5	Spring
KLC142	*Aspidoscelis*	*marmoratus*	sexual	male	Brewster	TX	2018	5	Spring
KLC143	*Aspidoscelis*	*septemvitta*	sexual	male	Brewster	TX	2018	5	Spring
KLC145	*Aspidoscelis*	*marmoratus*	sexual	male	Brewster	TX	2018	5	Spring
KLC146	*Aspidoscelis*	*marmoratus*	sexual	male	Brewster	TX	2018	5	Spring
KLC147	*Aspidoscelis*	*septemvitta*	sexual	male	Brewster	TX	2018	5	Spring
KLC148	*Aspidoscelis*	*inornatus*	sexual	male	Brewster	TX	2018	5	Spring
KLC149	*Aspidoscelis*	*marmoratus*	sexual	female	Brewster	TX	2018	5	Spring
KLC151	*Aspidoscelis*	*marmoratus*	sexual	male	Brewster	TX	2018	5	Spring
KLC166	*Aspidoscelis*	*gularis*	sexual	male	Brewster	TX	2019	5	Spring
KLC167	*Aspidoscelis*	*gularis*	sexual	male	Brewster	TX	2019	5	Spring
KLC170	*Aspidoscelis*	*neotesselat*	asexual	female	Otero	CO	2019	6	Summer
KLC172	*Aspidoscelis*	*sonorae*	asexual	female	Orange	CA	2019	9	Autumn
KLC173	*Aspidoscelis*	*sonorae*	asexual	female	Orange	CA	2019	9	Autumn
KLC174	*Aspidoscelis*	*sonorae*	asexual	female	Orange	CA	2019	9	Autumn

KLC175	*Aspidoscelis*	*sonorae*	asexual	female	Orange	CA	2019	9	Autumn
KLC176	*Aspidoscelis*	*sonorae*	asexual	female	Orange	CA	2019	9	Autumn
KLC177	*Aspidoscelis*	*sonorae*	asexual	female	Orange	CA	2019	9	Autumn
KLC178	*Aspidoscelis*	*sonorae*	asexual	female	Orange	CA	2019	9	Autumn
KLC179	*Aspidoscelis*	*sonorae*	asexual	female	Orange	CA	2019	9	Autumn
KLC180	*Aspidoscelis*	*sonorae*	asexual	female	Orange	CA	2019	9	Autumn
KLC181	*Aspidoscelis*	*sonorae*	asexual	female	Orange	CA	2019	9	Autumn
KLC182	*Aspidoscelis*	*sonorae*	asexual	female	Orange	CA	2019	9	Autumn
KLC183	*Aspidoscelis*	*sonorae*	asexual	female	Orange	CA	2019	9	Autumn
KLC185	*Aspidoscelis*	*sonorae*	asexual	female	Orange	CA	2019	9	Autumn
KLC186	*Aspidoscelis*	*sonorae*	asexual	female	Orange	CA	2019	9	Autumn
KLC187	*Aspidoscelis*	*sonorae*	asexual	female	Orange	CA	2019	9	Autumn
KLC190	*Aspidoscelis*	*sonorae*	asexual	female	Orange	CA	2019	9	Autumn
KLC191	*Aspidoscelis*	*sonorae*	asexual	female	Orange	CA	2019	9	Autumn
KLC192	*Aspidoscelis*	*sonorae*	asexual	female	Orange	CA	2019	9	Autumn
KLC193	*Aspidoscelis*	*sonorae*	asexual	female	Orange	CA	2019	9	Autumn
KLC194	*Aspidoscelis*	*sonorae*	asexual	female	Orange	CA	2019	9	Autumn
KLC195	*Aspidoscelis*	*sonorae*	asexual	female	Orange	CA	2019	9	Autumn
RLK072	*Aspidoscelis*	*marmoratus*	sexual	NA	Otero	NM	2018	6	Summer
RLK079	*Aspidoscelis*	*uniparens*	asexual	female	Socorro	NM	2018	6	Summer
RLK080	*Aspidoscelis*	*exsanguis*	asexual	female	Socorro	NM	2018	6	Summer
RLK081	*Aspidoscelis*	*exsanguis*	asexual	female	Socorro	NM	2018	6	Summer
RLK083	*Aspidoscelis*	*uniparens*	asexual	female	Socorro	NM	2018	6	Summer
RLK084	*Aspidoscelis*	*exsanguis*	asexual	female	Socorro	NM	2018	6	Summer
RLK085	*Aspidoscelis*	*neomexican*	asexual	female	Socorro	NM	2018	6	Summer
RLK086	*Aspidoscelis*	*neomexican*	asexual	female	Socorro	NM	2018	6	Summer
RLK087	*Aspidoscelis*	*neomexican*	asexual	female	Socorro	NM	2018	6	Summer
RLK089	*Aspidoscelis*	*neomexican*	asexual	female	Socorro	NM	2018	6	Summer
RLK090	*Aspidoscelis*	*neomexican*	asexual	female	Socorro	NM	2018	6	Summer
RLK097	*Aspidoscelis*	*neomexican*	asexual	female	Socorro	NM	2018	6	Summer
RLK099	*Aspidoscelis*	*neomexican*	asexual	female	Socorro	NM	2018	6	Summer
RLK100	*Aspidoscelis*	*neomexican*	asexual	female	Socorro	NM	2018	6	Summer

RLK102	*Aspidoscelis*	*neomexican*	asexual	female	Socorro	NM	2018	6	Summer

SampleID	Biome	Elevation (ft)	Latitude	Longitude
KLC002	Warm North American Deserts	4529	29.5570	-103.7939
KLC004	Warm North American Deserts	4529	29.5570	-103.7939
KLC005	Warm North American Deserts	4529	29.5570	-103.7939
KLC006	Warm North American Deserts	4529	29.5570	-103.7939
KLC007	Warm North American Deserts	4111	29.5570	-103.7939
KLC009	Warm North American Deserts	4111	29.5570	-103.7939
KLC010	Warm North American Deserts	4111	29.5570	-103.7939
KLC011	Warm North American Deserts	4111	29.5570	-103.7939
KLC014	Warm North American Deserts	4111	29.5570	-103.7939
KLC015	Warm North American Deserts	4111	29.5570	-103.7939
KLC016	Warm North American Deserts	1841	29.4496	-102.8237
KLC017	Warm North American Deserts	1841	29.4496	-102.8237
KLC018	Warm North American Deserts	1841	29.4496	-102.8237
KLC020	Warm North American Deserts	1841	29.4496	-102.8237
KLC021	Warm North American Deserts	1841	29.4496	-102.8237
KLC022	Warm North American Deserts	1841	29.4496	-102.8237
KLC023	Warm North American Deserts	1841	29.4496	-102.8237
KLC024	Warm North American Deserts	1841	29.4496	-102.8237
KLC025	Warm North American Deserts	1841	29.4496	-102.8237
KLC026	Warm North American Deserts	1841	29.4496	-102.8237
KLC027	Warm North American Deserts	1841	29.4496	-102.8237
KLC029	Tamaulipas - Texas Semiarid Plains	592	27.9145	-99.8463
KLC031	Tamaulipas - Texas Semiarid Plains	592	27.9145	-99.8463
KLC032	Tamaulipas - Texas Semiarid Plains	592	27.9145	-99.8463
KLC033	Tamaulipas - Texas Semiarid Plains	592	27.9145	-99.8463
KLC034	Tamaulipas - Texas Semiarid Plains	592	27.9145	-99.8463
KLC035	Tamaulipas - Texas Semiarid Plains	592	27.9145	-99.8463
KLC036	Tamaulipas - Texas Semiarid Plains	592	27.9145	-99.8463
KLC037	Tamaulipas - Texas Semiarid Plains	592	27.9145	-99.8463
KLC038	Tamaulipas - Texas Semiarid Plains	592	27.9145	-99.8463

KLC039	Tamaulipas - Texas Semiarid Plains	592	27.9145	-99.8463
KLC040	Tamaulipas - Texas Semiarid Plains	592	27.9145	-99.8463
KLC041	Warm North American Deserts	4932	30.5405	-103.8373
KLC042	Warm North American Deserts	4932	30.5405	-103.8373
KLC043	Warm North American Deserts	4932	30.5405	-103.8373
KLC044	Warm North American Deserts	4932	30.5405	-103.8373
KLC046	Warm North American Deserts	4932	30.5405	-103.8373
KLC047	Warm North American Deserts	4932	30.5405	-103.8373
KLC048	Warm North American Deserts	4932	30.5405	-103.8373
KLC049	Warm North American Deserts	4932	30.5405	-103.8373
KLC050	Warm North American Deserts	4932	30.5405	-103.8373
KLC051	Warm North American Deserts	4932	30.5405	-103.8373
KLC052	Warm North American Deserts	4400	30.5857	-104.6273
KLC053	Warm North American Deserts	4400	30.5857	-104.6273
KLC054	Warm North American Deserts	4400	30.5857	-104.6273
KLC055	Warm North American Deserts	4400	30.5857	-104.6273
KLC056	Warm North American Deserts	4400	30.5857	-104.6273
KLC057	Warm North American Deserts	4400	30.5857	-104.6273
KLC060	Warm North American Deserts	4400	30.5857	-104.6273
KLC061	Warm North American Deserts	4400	30.5857	-104.6273
KLC062	Warm North American Deserts	4400	30.5857	-104.6273
KLC063	Warm North American Deserts	4400	30.5857	-104.6273
KLC064	Warm North American Deserts	5000	30.5494	-104.6617
KLC065	Warm North American Deserts	5000	30.5494	-104.6617
KLC066	Warm North American Deserts	5000	30.5494	-104.6617
KLC067	Warm North American Deserts	5000	30.5494	-104.6617
KLC068	Warm North American Deserts	5000	30.5494	-104.6617
KLC069	Warm North American Deserts	5000	30.5494	-104.6617
KLC070	Warm North American Deserts	5000	30.5494	-104.6617
KLC071	Warm North American Deserts	5000	30.5494	-104.6617
KLC072	Warm North American Deserts	5000	30.5494	-104.6617
KLC073	Warm North American Deserts	5000	30.5494	-104.6617

KLC074	Warm North American Deserts	5000	30.5494	-104.6617
KLC075	Warm North American Deserts	4400	30.5857	-104.6617
KLC076	Warm North American Deserts	4400	30.5857	-104.6617
KLC077	Warm North American Deserts	4400	30.5857	-104.6617
KLC080	Warm North American Deserts	4017	29.4634	-100.8663
KLC081	Warm North American Deserts	4017	29.4634	-100.8663
KLC082	Warm North American Deserts	4017	29.4634	-100.8663
KLC083	Warm North American Deserts	4017	29.4634	-100.8663
KLC084	Warm North American Deserts	4017	29.4634	-100.8663
KLC085	Warm North American Deserts	4017	29.4634	-100.8663
KLC086	Warm North American Deserts	4017	29.4634	-100.8663
KLC087	Warm North American Deserts	4017	29.4634	-100.8663
KLC088	Warm North American Deserts	4017	29.4634	-100.8663
KLC089	Warm North American Deserts	4017	29.4634	-100.8663
KLC090	Warm North American Deserts	4017	29.4634	-100.8663
KLC091	Warm North American Deserts	4017	29.4634	-100.8663
KLC092	Warm North American Deserts	4017	29.4634	-100.8663
KLC093	Warm North American Deserts	4017	29.4634	-100.8663
KLC094	Warm North American Deserts	3800	29.4561	-103.4125
KLC095	Warm North American Deserts	3800	29.4561	-103.4125
KLC096	Warm North American Deserts	3800	29.4561	-103.4125
KLC097	Warm North American Deserts	3367	29.4368	-103.5060
KLC098	Warm North American Deserts	3367	29.4368	-103.5060
KLC099	Warm North American Deserts	3367	29.4368	-103.5060
KLC100	Warm North American Deserts	3367	29.4368	-103.5060
KLC101	Warm North American Deserts	3367	29.4368	-103.5060
KLC102	Warm North American Deserts	3367	29.4368	-103.5060
KLC103	Warm North American Deserts	3367	29.4368	-103.5060
KLC104	Warm North American Deserts	3367	29.4368	-103.5060
KLC105	Warm North American Deserts	3367	29.4368	-103.5060
KLC106	Warm North American Deserts	3367	29.4368	-103.5060
KLC107	Warm North American Deserts	3367	29.4368	-103.5060

KLC108	Warm North American Deserts	3367	29.4368	-103.5060
KLC109	Warm North American Deserts	3367	29.4368	-103.5060
KLC112	Warm North American Deserts	3367	29.4368	-103.5060
KLC116	Warm North American Deserts	3367	29.4368	-103.5060
KLC117	Warm North American Deserts	3367	29.4368	-103.5060
KLC118	Warm North American Deserts	3840	29.4558	-103.4125
KLC119	Warm North American Deserts	3840	29.4558	-103.4125
KLC120	Warm North American Deserts	3840	29.4558	-103.4125
KLC121	Warm North American Deserts	3840	29.4558	-103.4125
KLC122	Warm North American Deserts	3840	29.4558	-103.4125
KLC123	Warm North American Deserts	3840	29.4558	-103.4125
KLC124	Warm North American Deserts	3840	29.4558	-103.4125
KLC125	Warm North American Deserts	3840	29.4558	-103.4125
KLC126	Warm North American Deserts	3840	29.4558	-103.4125
KLC127	Warm North American Deserts	3840	29.4558	-103.4125
KLC129	Warm North American Deserts	3840	29.4558	-103.4125
KLC130	Warm North American Deserts	3840	29.4558	-103.4125
KLC133	Warm North American Deserts	3840	29.4558	-103.4125
KLC134	Warm North American Deserts	3840	29.4558	-103.4125
KLC135	Warm North American Deserts	3840	29.4558	-103.4125
KLC136	Warm North American Deserts	3500	29.4544	-103.4927
KLC137	Warm North American Deserts	3500	29.4544	-103.4927
KLC138	Warm North American Deserts	3500	29.4544	-103.4927
KLC139	Warm North American Deserts	3500	29.4544	-103.4927
KLC140	Warm North American Deserts	3500	29.4544	-103.4927
KLC141	Warm North American Deserts	3500	29.4544	-103.4927
KLC142	Warm North American Deserts	3500	29.4544	-103.4927
KLC143	Warm North American Deserts	3500	29.4544	-103.4927
KLC145	Warm North American Deserts	3500	29.4544	-103.4927
KLC146	Warm North American Deserts	3690	29.4558	-103.4839
KLC147	Warm North American Deserts	3690	29.4558	-103.4839
KLC148	Warm North American Deserts	3690	29.4558	-103.4839

KLC149	Warm North American Deserts	3690	29.4558	-103.4839
KLC151	Warm North American Deserts	3690	29.4558	-103.4839
KLC166	Warm North American Deserts	4380	30.3232	-103.1369
KLC167	Warm North American Deserts	4380	30.3232	-103.1369
KLC170	South Central Semiarid Prairies	4576	37.6597	-103.5703
KLC172	Mediterranean California	233	33.6614317	-117.7444432
KLC173	Mediterranean California	233	33.6614317	-117.7444432
KLC174	Mediterranean California	233	33.6614317	-117.7444432
KLC175	Mediterranean California	233	33.6614317	-117.7444432
KLC176	Mediterranean California	233	33.6614317	-117.7444432
KLC177	Mediterranean California	233	33.6614317	-117.7444432
KLC178	Mediterranean California	233	33.6614317	-117.7444432
KLC179	Mediterranean California	233	33.6614317	-117.7444432
KLC180	Mediterranean California	233	33.6614317	-117.7444432
KLC181	Mediterranean California	233	33.6614317	-117.7444432
KLC182	Mediterranean California	239	33.7216587	-117.7549618
KLC183	Mediterranean California	239	33.7216587	-117.7549618
KLC185	Mediterranean California	263	33.7249813	-117.7523282
KLC186	Mediterranean California	32	33.6840365	-117.8303131
KLC187	Mediterranean California	32	33.6840365	-117.8303131
KLC190	Mediterranean California	32	33.6840365	-117.8303131
KLC191	Mediterranean California	32	33.6840365	-117.8303131
KLC192	Mediterranean California	32	33.6840365	-117.8303131
KLC193	Mediterranean California	32	33.6840365	-117.8303131
KLC194	Mediterranean California	32	33.6840365	-117.8303131
KLC195	Mediterranean California	133	33.6597916	-117.7804713
RLK072	Warm North American Deserts	4790	33.34387	-106.03830
RLK079	Warm North American Deserts	4640	34.15864	-106.88740
RLK080	Warm North American Deserts	4640	34.15864	-106.88740
RLK081	Warm North American Deserts	4640	34.15864	-106.88740
RLK083	Warm North American Deserts	4640	34.15864	-106.88740
RLK084	Warm North American Deserts	4640	34.15864	-106.88740

RLK085	Warm North American Deserts	4640	34.15864	-106.88740
RLK086	Warm North American Deserts	4640	34.15864	-106.88740
RLK087	Warm North American Deserts	4640	34.15864	-106.88740
RLK089	Warm North American Deserts	4640	34.15864	-106.88740
RLK090	Warm North American Deserts	4640	34.15864	-106.88740
RLK097	Warm North American Deserts	4640	34.15864	-106.88740
RLK099	Warm North American Deserts	4640	34.15864	-106.88740
RLK100	Warm North American Deserts	4640	34.15864	-106.88740
RLK102	Warm North American Deserts	4620	34.12129	-106.89120

Appendix II

Mean relative abundances (Phylum) per Amplicon Sequence Variant (ASV).
Rep=Reproduction mode; SD=Standard Deviation; SE=Standard Error.

OTU	Biome	Reprodu	Phylum	Mean	N	SD	SE
ASV_7	Mediterranean California	asexual	Firmicutes	55.4135	21	27.0555	5.9040
ASV_1	Mediterranean California	asexual	Actinobacteriota	24.0043	21	21.5176	4.6955
ASV_18	Mediterranean California	asexual	Proteobacteria	14.4752	21	25.5273	5.5705
ASV_32	Mediterranean California	asexual	Bacteroidota	4.3577	21	3.1181	0.6804
ASV_3	Mediterranean California	asexual	Campylobacterota	0.8568	21	1.0479	0.2287
ASV_98	Mediterranean California	asexual	Desulfobacterota	0.5749	21	0.7137	0.1557
ASV_729	Mediterranean California	asexual	Gemmatimonadota	0.1696	21	0.5377	0.1173
ASV_624	Mediterranean California	asexual	Acidobacteriota	0.0499	21	0.1567	0.0342
ASV_255	Mediterranean California	asexual	Fusobacteriota	0.0270	21	0.0534	0.0116
ASV_439	Mediterranean California	asexual	Myxococcota	0.0250	21	0.0734	0.0160
ASV_272	Mediterranean California	asexual	Bdellovibrionota	0.0174	21	0.0578	0.0126
ASV_314	Mediterranean California	asexual	Chloroflexi	0.0119	21	0.0362	0.0079
ASV_213	Mediterranean California	asexual	Nitrospirota	0.0088	21	0.0279	0.0061
ASV_434	Mediterranean California	asexual	Verrucomicrobiota	0.0045	21	0.0122	0.0027
ASV_586	Mediterranean California	asexual	Patescibacteria	0.0022	21	0.0071	0.0015
ASV_621	Mediterranean California	asexual	Cyanobacteria	0.0012	21	0.0040	0.0009

ASV_236	Mediterranean California	asexual	Abditibacteriota	0.0000	21	0.0000	0.0000
ASV_423	Mediterranean California	asexual	Fibrobacterota	0.0000	21	0.0000	0.0000
ASV_525	Mediterranean California	asexual	Planctomycetota	0.0000	21	0.0000	0.0000
ASV_708	Mediterranean California	asexual	Synergistota	0.0000	21	0.0000	0.0000
ASV_848	Mediterranean California	asexual	Entotheonellaeota	0.0000	21	0.0000	0.0000
ASV_856	Mediterranean California	asexual	Elusimicrobiota	0.0000	21	0.0000	0.0000
ASV_981	Mediterranean California	asexual	Deinococcota	0.0000	21	0.0000	0.0000
ASV_1	South Central Semiarid Prairi	asexual	Actinobacteriota	76.0492	1	NA	NA
ASV_7	South Central Semiarid Prairi	asexual	Firmicutes	18.9018	1	NA	NA
ASV_18	South Central Semiarid Prairi	asexual	Proteobacteria	2.6821	1	NA	NA
ASV_3	South Central Semiarid Prairi	asexual	Campylobacterota	1.1045	1	NA	NA
ASV_32	South Central Semiarid Prairi	asexual	Bacteroidota	0.9377	1	NA	NA
ASV_439	South Central Semiarid Prairi	asexual	Myxococcota	0.1949	1	NA	NA
ASV_729	South Central Semiarid Prairi	asexual	Gemmatimonadota	0.0950	1	NA	NA
ASV_624	South Central Semiarid Prairi	asexual	Acidobacteriota	0.0310	1	NA	NA
ASV_856	South Central Semiarid Prairi	asexual	Elusimicrobiota	0.0039	1	NA	NA
ASV_213	South Central Semiarid Prairi	asexual	Nitrospirota	0.0000	1	NA	NA
ASV_236	South Central Semiarid Prairi	asexual	Abditibacteriota	0.0000	1	NA	NA
ASV_255	South Central Semiarid Prairi	asexual	Fusobacteriota	0.0000	1	NA	NA
ASV_272	South Central Semiarid Prairi	asexual	Bdellovibrionota	0.0000	1	NA	NA
ASV_314	South Central Semiarid Prairi	asexual	Chloroflexi	0.0000	1	NA	NA
ASV_423	South Central Semiarid Prairi	asexual	Fibrobacterota	0.0000	1	NA	NA
ASV_434	South Central Semiarid Prairi	asexual	Verrucomicrobiota	0.0000	1	NA	NA
ASV_525	South Central Semiarid Prairi	asexual	Planctomycetota	0.0000	1	NA	NA
ASV_586	South Central Semiarid Prairi	asexual	Patescibacteria	0.0000	1	NA	NA
ASV_621	South Central Semiarid Prairi	asexual	Cyanobacteria	0.0000	1	NA	NA
ASV_708	South Central Semiarid Prairi	asexual	Synergistota	0.0000	1	NA	NA
ASV_848	South Central Semiarid Prairi	asexual	Entotheonellaeota	0.0000	1	NA	NA
ASV_98	South Central Semiarid Prairi	asexual	Desulfobacterota	0.0000	1	NA	NA
ASV_981	South Central Semiarid Prairi	asexual	Deinococcota	0.0000	1	NA	NA
ASV_1	Tamaulipas - Texas Semiarid	asexual	Actinobacteriota	95.9114	3	1.3451	0.7766
ASV_7	Tamaulipas - Texas Semiarid	asexual	Firmicutes	2.0993	3	2.2810	1.3169

ASV_18	Tamaulipas - Texas Semiarid	asexual	Proteobacteria	1.5890	3	1.2092	0.6981
ASV_32	Tamaulipas - Texas Semiarid	asexual	Bacteroidota	0.1426	3	0.1325	0.0765
ASV_729	Tamaulipas - Texas Semiarid	asexual	Gemmatimonadota	0.0698	3	0.1210	0.0698
ASV_624	Tamaulipas - Texas Semiarid	asexual	Acidobacteriota	0.0539	3	0.0933	0.0539
ASV_621	Tamaulipas - Texas Semiarid	asexual	Cyanobacteria	0.0450	3	0.0779	0.0450
ASV_272	Tamaulipas - Texas Semiarid	asexual	Bdellovibrionota	0.0249	3	0.0431	0.0249
ASV_3	Tamaulipas - Texas Semiarid	asexual	Campylobacterota	0.0245	3	0.0425	0.0245
ASV_439	Tamaulipas - Texas Semiarid	asexual	Myxococcota	0.0225	3	0.0390	0.0225
ASV_236	Tamaulipas - Texas Semiarid	asexual	Abditibacteriota	0.0071	3	0.0123	0.0071
ASV_586	Tamaulipas - Texas Semiarid	asexual	Patescibacteria	0.0047	3	0.0082	0.0047
ASV_314	Tamaulipas - Texas Semiarid	asexual	Chloroflexi	0.0030	3	0.0051	0.0030
ASV_525	Tamaulipas - Texas Semiarid	asexual	Planctomycetota	0.0012	3	0.0021	0.0012
ASV_856	Tamaulipas - Texas Semiarid	asexual	Elusimicrobiota	0.0012	3	0.0021	0.0012
ASV_213	Tamaulipas - Texas Semiarid	asexual	Nitrospirota	0.0000	3	0.0000	0.0000
ASV_255	Tamaulipas - Texas Semiarid	asexual	Fusobacteriota	0.0000	3	0.0000	0.0000
ASV_423	Tamaulipas - Texas Semiarid	asexual	Fibrobacterota	0.0000	3	0.0000	0.0000
ASV_434	Tamaulipas - Texas Semiarid	asexual	Verrucomicrobiota	0.0000	3	0.0000	0.0000
ASV_708	Tamaulipas - Texas Semiarid	asexual	Synergistota	0.0000	3	0.0000	0.0000
ASV_848	Tamaulipas - Texas Semiarid	asexual	Entotheonellaeota	0.0000	3	0.0000	0.0000
ASV_98	Tamaulipas - Texas Semiarid	asexual	Desulfobacterota	0.0000	3	0.0000	0.0000
ASV_981	Tamaulipas - Texas Semiarid	asexual	Deinococcota	0.0000	3	0.0000	0.0000
ASV_1	Warm North American Desert	asexual	Actinobacteriota	68.5234	35	33.1060	5.5959
ASV_7	Warm North American Desert	asexual	Firmicutes	19.3798	35	27.2084	4.5991
ASV_18	Warm North American Desert	asexual	Proteobacteria	7.0765	35	10.1938	1.7231
ASV_32	Warm North American Desert	asexual	Bacteroidota	3.6092	35	6.5624	1.1092
ASV_98	Warm North American Desert	asexual	Desulfobacterota	0.6544	35	1.8026	0.3047
ASV_729	Warm North American Desert	asexual	Gemmatimonadota	0.2934	35	0.6267	0.1059
ASV_3	Warm North American Desert	asexual	Campylobacterota	0.1515	35	0.4642	0.0785
ASV_439	Warm North American Desert	asexual	Myxococcota	0.0945	35	0.3164	0.0535
ASV_624	Warm North American Desert	asexual	Acidobacteriota	0.0822	35	0.1720	0.0291
ASV_272	Warm North American Desert	asexual	Bdellovibrionota	0.0387	35	0.0959	0.0162
ASV_255	Warm North American Desert	asexual	Fusobacteriota	0.0359	35	0.1181	0.0200

ASV_621	Warm North American Desert	asexual	Cyanobacteria	0.0261	35	0.0693	0.0117
ASV_314	Warm North American Desert	asexual	Chloroflexi	0.0134	35	0.0527	0.0089
ASV_586	Warm North American Desert	asexual	Patescibacteria	0.0057	35	0.0229	0.0039
ASV_236	Warm North American Desert	asexual	Abditibacteriota	0.0041	35	0.0171	0.0029
ASV_525	Warm North American Desert	asexual	Planctomycetota	0.0031	35	0.0078	0.0013
ASV_213	Warm North American Desert	asexual	Nitrospirota	0.0026	35	0.0088	0.0015
ASV_434	Warm North American Desert	asexual	Verrucomicrobiota	0.0024	35	0.0143	0.0024
ASV_848	Warm North American Desert	asexual	Entotheonellaeota	0.0024	35	0.0140	0.0024
ASV_423	Warm North American Desert	asexual	Fibrobacterota	0.0008	35	0.0035	0.0006
ASV_708	Warm North American Desert	asexual	Synergistota	0.0000	35	0.0000	0.0000
ASV_856	Warm North American Desert	asexual	Elusimicrobiota	0.0000	35	0.0000	0.0000
ASV_981	Warm North American Desert	asexual	Deinococcota	0.0000	35	0.0000	0.0000
ASV_1	Tamaulipas - Texas Semiarid	sexual	Actinobacteriota	94.9527	8	6.6158	2.3391
ASV_18	Tamaulipas - Texas Semiarid	sexual	Proteobacteria	3.5756	8	5.3613	1.8955
ASV_7	Tamaulipas - Texas Semiarid	sexual	Firmicutes	0.7285	8	1.2347	0.4365
ASV_32	Tamaulipas - Texas Semiarid	sexual	Bacteroidota	0.2814	8	0.4552	0.1610
ASV_729	Tamaulipas - Texas Semiarid	sexual	Gemmatimonadota	0.2119	8	0.3733	0.1320
ASV_3	Tamaulipas - Texas Semiarid	sexual	Campylobacterota	0.0716	8	0.0954	0.0337
ASV_621	Tamaulipas - Texas Semiarid	sexual	Cyanobacteria	0.0401	8	0.0728	0.0257
ASV_439	Tamaulipas - Texas Semiarid	sexual	Myxococcota	0.0369	8	0.0594	0.0210
ASV_272	Tamaulipas - Texas Semiarid	sexual	Bdellovibrionota	0.0317	8	0.0604	0.0213
ASV_624	Tamaulipas - Texas Semiarid	sexual	Acidobacteriota	0.0253	8	0.0427	0.0151
ASV_213	Tamaulipas - Texas Semiarid	sexual	Nitrospirota	0.0140	8	0.0397	0.0140
ASV_255	Tamaulipas - Texas Semiarid	sexual	Fusobacteriota	0.0091	8	0.0258	0.0091
ASV_314	Tamaulipas - Texas Semiarid	sexual	Chloroflexi	0.0075	8	0.0211	0.0075
ASV_856	Tamaulipas - Texas Semiarid	sexual	Elusimicrobiota	0.0066	8	0.0188	0.0066
ASV_98	Tamaulipas - Texas Semiarid	sexual	Desulfobacterota	0.0030	8	0.0084	0.0030
ASV_236	Tamaulipas - Texas Semiarid	sexual	Abditibacteriota	0.0022	8	0.0064	0.0022
ASV_981	Tamaulipas - Texas Semiarid	sexual	Deinococcota	0.0017	8	0.0048	0.0017
ASV_423	Tamaulipas - Texas Semiarid	sexual	Fibrobacterota	0.0000	8	0.0000	0.0000
ASV_434	Tamaulipas - Texas Semiarid	sexual	Verrucomicrobiota	0.0000	8	0.0000	0.0000
ASV_525	Tamaulipas - Texas Semiarid	sexual	Planctomycetota	0.0000	8	0.0000	0.0000

ASV_586	Tamaulipas - Texas Semiarid	sexual	Patescibacteria	0.0000	8	0.0000	0.0000
ASV_708	Tamaulipas - Texas Semiarid	sexual	Synergistota	0.0000	8	0.0000	0.0000
ASV_848	Tamaulipas - Texas Semiarid	sexual	Entotheonellaeota	0.0000	8	0.0000	0.0000
ASV_1	Warm North American Desert	sexual	Actinobacteriota	56.0861	99	35.6871	3.5867
ASV_7	Warm North American Desert	sexual	Firmicutes	23.5105	99	29.8797	3.0030
ASV_18	Warm North American Desert	sexual	Proteobacteria	8.1392	99	11.8909	1.1951
ASV_3	Warm North American Desert	sexual	Campylobacterota	5.8497	99	17.3822	1.7470
ASV_32	Warm North American Desert	sexual	Bacteroidota	5.3789	99	9.4598	0.9507
ASV_729	Warm North American Desert	sexual	Gemmatimonadota	0.4246	99	0.8393	0.0843
ASV_624	Warm North American Desert	sexual	Acidobacteriota	0.2239	99	0.7119	0.0716
ASV_98	Warm North American Desert	sexual	Desulfobacterota	0.1736	99	0.6806	0.0684
ASV_439	Warm North American Desert	sexual	Myxococcota	0.0640	99	0.1680	0.0169
ASV_272	Warm North American Desert	sexual	Bdellovibrionota	0.0393	99	0.1307	0.0131
ASV_255	Warm North American Desert	sexual	Fusobacteriota	0.0293	99	0.1163	0.0117
ASV_314	Warm North American Desert	sexual	Chloroflexi	0.0210	99	0.0552	0.0055
ASV_621	Warm North American Desert	sexual	Cyanobacteria	0.0209	99	0.0679	0.0068
ASV_236	Warm North American Desert	sexual	Abditibacteriota	0.0117	99	0.0769	0.0077
ASV_708	Warm North American Desert	sexual	Synergistota	0.0061	99	0.0531	0.0053
ASV_213	Warm North American Desert	sexual	Nitrospirota	0.0052	99	0.0202	0.0020
ASV_434	Warm North American Desert	sexual	Verrucomicrobiota	0.0041	99	0.0381	0.0038
ASV_586	Warm North American Desert	sexual	Patescibacteria	0.0035	99	0.0177	0.0018
ASV_525	Warm North American Desert	sexual	Planctomycetota	0.0034	99	0.0130	0.0013
ASV_856	Warm North American Desert	sexual	Elusimicrobiota	0.0023	99	0.0133	0.0013
ASV_423	Warm North American Desert	sexual	Fibrobacterota	0.0015	99	0.0120	0.0012
ASV_848	Warm North American Desert	sexual	Entotheonellaeota	0.0009	99	0.0059	0.0006
ASV_981	Warm North American Desert	sexual	Deinococcota	0.0004	99	0.0037	0.0004

Appendix III

Mean relative abundances (Family) per Amplicon Sequence Variant (ASV).

OTU	Biome	Reprodu	Family	Mean	N	SD	SE
ASV_7	Mediterranean California	asexual	Lachnospiraceae	43.5945	21	22.9927	5.0174
ASV_23	Mediterranean California	asexual	Diplorickettsiaceae	10.2938	21	26.3903	5.7588
ASV_1	Mediterranean California	asexual	Dietziaceae	8.9116	21	9.6589	2.1077
ASV_12	Mediterranean California	asexual	Dermabacteraceae	3.2827	21	3.5432	0.7732
ASV_22	Mediterranean California	asexual	Ruminococcaceae	3.1150	21	6.5083	1.4202
ASV_11	Mediterranean California	asexual	Oscillospiraceae	2.9991	21	2.3306	0.5086
ASV_4	Mediterranean California	asexual	Micrococcacea	2.8211	21	3.3158	0.7236
ASV_8	Mediterranean California	asexual	Brevibacteriaceae	2.3026	21	2.6355	0.5751
ASV_129	Mediterranean California	asexual	Peptostreptococcaceae	2.0248	21	8.5248	1.8603
ASV_32	Mediterranean California	asexual	Bacteroidaceae	1.7256	21	1.6511	0.3603
ASV_6	Mediterranean California	asexual	Corynebacteriaceae	1.1913	21	1.3315	0.2906
ASV_69	Mediterranean California	asexual	Geodermatophilaceae	1.1877	21	3.3426	0.7294
ASV_38	Mediterranean California	asexual	Tannerellaceae	1.1582	21	0.9106	0.1987
ASV_139	Mediterranean California	asexual	Acetobacteraceae	0.9962	21	3.9383	0.8594
ASV_20	Mediterranean California	asexual	Nocardioidaceae	0.8834	21	1.4539	0.3173
ASV_3	Mediterranean California	asexual	Helicobacteraceae	0.8559	21	1.0465	0.2284
ASV_97	Mediterranean California	asexual	Beijerinckiaceae	0.7287	21	2.2058	0.4814
ASV_10	Mediterranean California	asexual	Clostridiaceae	0.7126	21	1.7130	0.3738
ASV_24	Mediterranean California	asexual	Micrococcaceae	0.6712	21	1.5171	0.3311
ASV_98	Mediterranean California	asexual	Desulfovibrionaceae	0.5645	21	0.7197	0.1570
ASV_162	Mediterranean California	asexual	Sphingomonadaceae	0.5472	21	0.7066	0.1542
ASV_250	Mediterranean California	asexual	Butyricicoccaceae	0.5418	21	0.9038	0.1972
ASV_117	Mediterranean California	asexual	Marinifilaceae	0.5241	21	0.4268	0.0931
ASV_86	Mediterranean California	asexual	Anaerovoracaceae	0.4806	21	0.4572	0.0998
ASV_18	Mediterranean California	asexual	Rhodobacteraceae	0.4772	21	0.6836	0.1492
ASV_420	Mediterranean California	asexual	Enterobacteriaceae	0.4719	21	1.6851	0.3677
ASV_19	Mediterranean California	asexual	Nocardiaceae	0.3990	21	0.4051	0.0884
ASV_153	Mediterranean California	asexual	Pseudonocardiaceae	0.3668	21	0.7474	0.1631
ASV_29	Mediterranean California	asexual	[Eubacterium] coprostar	0.3627	21	0.4129	0.0901
ASV_44	Mediterranean California	asexual	Rikenellaceae	0.3344	21	0.3592	0.0784
ASV_21	Mediterranean California	asexual	Intrasporangiaceae	0.2946	21	0.3533	0.0771

ASV_96	Mediterranean California	asexual	Christensenellaceae	0.2746	21	0.5624	0.1227
ASV_3453	Mediterranean California	asexual	Streptococcaceae	0.2434	21	1.0984	0.2397
ASV_142	Mediterranean California	asexual	Streptomycetaceae	0.2278	21	0.2746	0.0599
ASV_49	Mediterranean California	asexual	Microbacteriaceae	0.2156	21	0.2748	0.0600
ASV_660	Mediterranean California	asexual	Moraxellaceae	0.2008	21	0.3447	0.0752
ASV_214	Mediterranean California	asexual	Eggerthellaceae	0.1955	21	0.2541	0.0555
ASV_912	Mediterranean California	asexual	NA	0.1737	21	0.6354	0.1387
ASV_73	Mediterranean California	asexual	Cellulomonadaceae	0.1710	21	0.6914	0.1509
ASV_442	Mediterranean California	asexual	Rhizobiaceae	0.1469	21	0.2552	0.0557
ASV_57	Mediterranean California	asexual	Devosiaceae	0.1336	21	0.2393	0.0522
ASV_807	Mediterranean California	asexual	Gemmatimonadaceae	0.1186	21	0.3807	0.0831
ASV_163	Mediterranean California	asexual	Monoglobaceae	0.1152	21	0.1765	0.0385
ASV_121	Mediterranean California	asexual	NA	0.1109	21	0.2348	0.0512
ASV_309	Mediterranean California	asexual	Family XI	0.1100	21	0.1433	0.0313
ASV_126	Mediterranean California	asexual	NA	0.1090	21	0.1724	0.0376
ASV_1694	Mediterranean California	asexual	Marinococcaceae	0.1012	21	0.4639	0.1012
ASV_2104	Mediterranean California	asexual	NA	0.0992	21	0.2132	0.0465
ASV_259	Mediterranean California	asexual	Enterococcaceae	0.0981	21	0.1860	0.0406
ASV_347	Mediterranean California	asexual	Azospirillaceae	0.0932	21	0.3256	0.0711
ASV_538	Mediterranean California	asexual	Caulobacteraceae	0.0877	21	0.1305	0.0285
ASV_571	Mediterranean California	asexual	Flavobacteriaceae	0.0833	21	0.2588	0.0565
ASV_1110	Mediterranean California	asexual	Mycobacteriaceae	0.0753	21	0.1018	0.0222
ASV_1974	Mediterranean California	asexual	NA	0.0736	21	0.1723	0.0376
ASV_1715	Mediterranean California	asexual	Eubacteriaceae	0.0711	21	0.1269	0.0277
ASV_283	Mediterranean California	asexual	Micromonosporaceae	0.0688	21	0.2181	0.0476
ASV_604	Mediterranean California	asexual	Hydrogenoanaerobacter	0.0686	21	0.1160	0.0253
ASV_405	Mediterranean California	asexual	NA	0.0656	21	0.1845	0.0403
ASV_404	Mediterranean California	asexual	Kineosporiaceae	0.0621	21	0.0986	0.0215
ASV_3419	Mediterranean California	asexual	Dysgonomonadaceae	0.0588	21	0.1385	0.0302
ASV_1201	Mediterranean California	asexual	Sphingobacteriaceae	0.0580	21	0.1174	0.0256
ASV_468	Mediterranean California	asexual	Weeksellaceae	0.0562	21	0.0929	0.0203
ASV_91	Mediterranean California	asexual	Peptococcaceae	0.0552	21	0.0944	0.0206

ASV_2494	Mediterranean California	asexual	Thermicanaceae	0.0546	21	0.2425	0.0529
ASV_483	Mediterranean California	asexual	Hymenobacteraceae	0.0505	21	0.2001	0.0437
ASV_815	Mediterranean California	asexual	NA	0.0491	21	0.1655	0.0361
ASV_624	Mediterranean California	asexual	Bryobacteraceae	0.0474	21	0.1500	0.0327
ASV_729	Mediterranean California	asexual	Longimicrobiaceae	0.0470	21	0.1478	0.0323
ASV_456	Mediterranean California	asexual	Promicromonosporacea	0.0468	21	0.1034	0.0226
ASV_410	Mediterranean California	asexual	Ilumatobacteraceae	0.0434	21	0.0876	0.0191
ASV_512	Mediterranean California	asexual	Geminicoccaceae	0.0421	21	0.1106	0.0241
ASV_817	Mediterranean California	asexual	Porphyromonadaceae	0.0419	21	0.0962	0.0210
ASV_1150	Mediterranean California	asexual	NA	0.0350	21	0.0710	0.0155
ASV_3155	Mediterranean California	asexual	NA	0.0331	21	0.0850	0.0186
ASV_1107	Mediterranean California	asexual	Muribaculaceae	0.0319	21	0.1190	0.0260
ASV_740	Mediterranean California	asexual	NA	0.0315	21	0.0653	0.0142
ASV_161	Mediterranean California	asexual	Bacillaceae	0.0315	21	0.0623	0.0136
ASV_362	Mediterranean California	asexual	Thermomonosporaceae	0.0284	21	0.0500	0.0109
ASV_1285	Mediterranean California	asexual	NA	0.0255	21	0.0687	0.0150
ASV_4227	Mediterranean California	asexual	Halomonadaceae	0.0252	21	0.1008	0.0220
ASV_728	Mediterranean California	asexual	Xanthobacteraceae	0.0250	21	0.0675	0.0147
ASV_2554	Mediterranean California	asexual	Fusobacteriaceae	0.0238	21	0.0529	0.0115
ASV_1864	Mediterranean California	asexual	Anaerofustaceae	0.0230	21	0.0578	0.0126
ASV_2522	Mediterranean California	asexual	Beutenbergiaceae	0.0219	21	0.0815	0.0178
ASV_1445	Mediterranean California	asexual	NA	0.0216	21	0.0584	0.0127
ASV_1080	Mediterranean California	asexual	NA	0.0193	21	0.0751	0.0164
ASV_1563	Mediterranean California	asexual	Erysipelatoclostridiacea	0.0164	21	0.0282	0.0062
ASV_1162	Mediterranean California	asexual	Puniceispirillales Incerta	0.0157	21	0.0722	0.0157
ASV_867	Mediterranean California	asexual	Gaiellaceae	0.0154	21	0.0321	0.0070
ASV_941	Mediterranean California	asexual	Staphylococcaceae	0.0154	21	0.0364	0.0079
ASV_1575	Mediterranean California	asexual	Defluviitaleaceae	0.0152	21	0.0426	0.0093
ASV_474	Mediterranean California	asexual	Chitinophagaceae	0.0146	21	0.0472	0.0103
ASV_4022	Mediterranean California	asexual	Pseudomonadaceae	0.0139	21	0.0636	0.0139
ASV_2606	Mediterranean California	asexual	Euzebyaceae	0.0136	21	0.0419	0.0091
ASV_4747	Mediterranean California	asexual	Solirubrobacteraceae	0.0133	21	0.0588	0.0128

ASV_1275	Mediterranean California	asexual	Actinomycetaceae	0.0132	21	0.0412	0.0090
ASV_2726	Mediterranean California	asexual	Bdellovibrionaceae	0.0128	21	0.0437	0.0095
ASV_4700	Mediterranean California	asexual	Reyranellaceae	0.0122	21	0.0514	0.0112
ASV_753	Mediterranean California	asexual	[Clostridium] methylpen	0.0120	21	0.0286	0.0063
ASV_552	Mediterranean California	asexual	Propionibacteriaceae	0.0120	21	0.0308	0.0067
ASV_2506	Mediterranean California	asexual	Acidothermaceae	0.0114	21	0.0403	0.0088
ASV_4291	Mediterranean California	asexual	NA	0.0112	21	0.0491	0.0107
ASV_5924	Mediterranean California	asexual	Exiguobacteraceae	0.0106	21	0.0378	0.0083
ASV_2445	Mediterranean California	asexual	Streptosporangiales Inc	0.0106	21	0.0412	0.0090
ASV_4224	Mediterranean California	asexual	NA	0.0105	21	0.0481	0.0105
ASV_2156	Mediterranean California	asexual	Hyphomicrobiaceae	0.0091	21	0.0397	0.0087
ASV_2708	Mediterranean California	asexual	Bifidobacteriaceae	0.0090	21	0.0413	0.0090
ASV_5527	Mediterranean California	asexual	Comamonadaceae	0.0090	21	0.0412	0.0090
ASV_2133	Mediterranean California	asexual	Nitrospiraceae	0.0088	21	0.0279	0.0061
ASV_681	Mediterranean California	asexual	Sporichthyaceae	0.0088	21	0.0368	0.0080
ASV_5631	Mediterranean California	asexual	Sporomusaceae	0.0084	21	0.0243	0.0053
ASV_2986	Mediterranean California	asexual	Actinospicaceae	0.0079	21	0.0183	0.0040
ASV_5486	Mediterranean California	asexual	Microscillaceae	0.0077	21	0.0252	0.0055
ASV_7107	Mediterranean California	asexual	Bogoriellaceae	0.0076	21	0.0293	0.0064
ASV_979	Mediterranean California	asexual	Nakamurellaceae	0.0076	21	0.0214	0.0047
ASV_1813	Mediterranean California	asexual	D05-2	0.0072	21	0.0196	0.0043
ASV_795	Mediterranean California	asexual	Labraceae	0.0071	21	0.0324	0.0071
ASV_345	Mediterranean California	asexual	Dermacoccaceae	0.0068	21	0.0248	0.0054
ASV_1904	Mediterranean California	asexual	Cytophagaceae	0.0067	21	0.0309	0.0067
ASV_5915	Mediterranean California	asexual	env.OPS 17	0.0067	21	0.0202	0.0044
ASV_2146	Mediterranean California	asexual	NA	0.0066	21	0.0201	0.0044
ASV_7111	Mediterranean California	asexual	Family III	0.0066	21	0.0301	0.0066
ASV_5638	Mediterranean California	asexual	NA	0.0064	21	0.0295	0.0064
ASV_2306	Mediterranean California	asexual	NA	0.0061	21	0.0280	0.0061
ASV_481	Mediterranean California	asexual	Oxalobacteraceae	0.0056	21	0.0168	0.0037
ASV_7766	Mediterranean California	asexual	AKYH767	0.0056	21	0.0255	0.0056
ASV_7533	Mediterranean California	asexual	Saprospiraceae	0.0051	21	0.0236	0.0051

ASV_6091	Mediterranean California	asexual	JG30-KF-CM45	0.0051	21	0.0134	0.0029
ASV_4284	Mediterranean California	asexual	Ardenticatenaceae	0.0051	21	0.0207	0.0045
ASV_1664	Mediterranean California	asexual	NA	0.0049	21	0.0118	0.0026
ASV_5154	Mediterranean California	asexual	KF-JG30-B3	0.0048	21	0.0219	0.0048
ASV_3726	Mediterranean California	asexual	Rhodothermaceae	0.0046	21	0.0146	0.0032
ASV_4341	Mediterranean California	asexual	Simkaniaceae	0.0045	21	0.0122	0.0027
ASV_4655	Mediterranean California	asexual	Iamiaceae	0.0045	21	0.0147	0.0032
ASV_2211	Mediterranean California	asexual	NA	0.0042	21	0.0191	0.0042
ASV_439	Mediterranean California	asexual	Polyangiaceae	0.0039	21	0.0177	0.0039
ASV_9672	Mediterranean California	asexual	Methylopilaceae	0.0037	21	0.0119	0.0026
ASV_6397	Mediterranean California	asexual	NA	0.0036	21	0.0148	0.0032
ASV_9818	Mediterranean California	asexual	67-14	0.0035	21	0.0162	0.0035
ASV_994	Mediterranean California	asexual	NA	0.0035	21	0.0162	0.0035
ASV_2550	Mediterranean California	asexual	Spirosomaceae	0.0035	21	0.0099	0.0022
ASV_3064	Mediterranean California	asexual	Paludibacteraceae	0.0033	21	0.0153	0.0033
ASV_3442	Mediterranean California	asexual	NA	0.0033	21	0.0153	0.0033
ASV_4124	Mediterranean California	asexual	Leptotrichiaceae	0.0032	21	0.0147	0.0032
ASV_1246	Mediterranean California	asexual	NA	0.0031	21	0.0101	0.0022
ASV_7145	Mediterranean California	asexual	Haliangiaceae	0.0029	21	0.0133	0.0029
ASV_4184	Mediterranean California	asexual	Methyloligellaceae	0.0027	21	0.0094	0.0021
ASV_1340	Mediterranean California	asexual	Microtrichaceae	0.0027	21	0.0100	0.0022
ASV_8572	Mediterranean California	asexual	Nocardiopsaceae	0.0026	21	0.0119	0.0026
ASV_493	Mediterranean California	asexual	Frankiaceae	0.0026	21	0.0118	0.0026
ASV_8455	Mediterranean California	asexual	NA	0.0026	21	0.0118	0.0026
ASV_9488	Mediterranean California	asexual	NA	0.0026	21	0.0118	0.0026
ASV_4929	Mediterranean California	asexual	Erysipelotrichaceae	0.0025	21	0.0061	0.0013
ASV_9871	Mediterranean California	asexual	Nannocystaceae	0.0022	21	0.0103	0.0022
ASV_2172	Mediterranean California	asexual	Hungateiclostridiaceae	0.0022	21	0.0070	0.0015
ASV_2450	Mediterranean California	asexual	Prevotellaceae	0.0021	21	0.0097	0.0021
ASV_1096	Mediterranean California	asexual	UCG-010	0.0020	21	0.0072	0.0016
ASV_1554	Mediterranean California	asexual	Cryptosporangiaceae	0.0020	21	0.0089	0.0020
ASV_5396	Mediterranean California	asexual	Caloramatoraceae	0.0019	21	0.0089	0.0019

ASV_3376	Mediterranean California	asexual	Sandaracinaceae	0.0019	21	0.0088	0.0019
ASV_7146	Mediterranean California	asexual	Planococcaceae	0.0019	21	0.0088	0.0019
ASV_5152	Mediterranean California	asexual	Rickettsiaceae	0.0018	21	0.0084	0.0018
ASV_9715	Mediterranean California	asexual	Desulfitobacteriaceae	0.0018	21	0.0084	0.0018
ASV_1501	Mediterranean California	asexual	Sanguibacteraceae	0.0017	21	0.0079	0.0017
ASV_11833	Mediterranean California	asexual	BIrii41	0.0016	21	0.0074	0.0016
ASV_5823	Mediterranean California	asexual	Competibacteraceae	0.0016	21	0.0074	0.0016
ASV_3410	Mediterranean California	asexual	Selenomonadaceae	0.0014	21	0.0066	0.0014
ASV_7023	Mediterranean California	asexual	NA	0.0014	21	0.0057	0.0012
ASV_5351	Mediterranean California	asexual	NA	0.0013	21	0.0061	0.0013
ASV_586	Mediterranean California	asexual	Saccharimonadaceae	0.0013	21	0.0060	0.0013
ASV_9144	Mediterranean California	asexual	NA	0.0013	21	0.0059	0.0013
ASV_9161	Mediterranean California	asexual	Legionellaceae	0.0013	21	0.0059	0.0013
ASV_9517	Mediterranean California	asexual	Chloroflexaceae	0.0013	21	0.0059	0.0013
ASV_11196	Mediterranean California	asexual	Vulgatibacteraceae	0.0012	21	0.0056	0.0012
ASV_3457	Mediterranean California	asexual	Sedimentibacteraceae	0.0012	21	0.0056	0.0012
ASV_2687	Mediterranean California	asexual	Unknown Family	0.0011	21	0.0049	0.0011
ASV_758	Mediterranean California	asexual	Coriobacteriales Incerta	0.0010	21	0.0034	0.0007
ASV_166	Mediterranean California	asexual	Tsukamurellaceae	0.0010	21	0.0047	0.0010
ASV_12532	Mediterranean California	asexual	Bacteriovoracaceae	0.0010	21	0.0045	0.0010
ASV_4297	Mediterranean California	asexual	NA	0.0010	21	0.0045	0.0010
ASV_9515	Mediterranean California	asexual	Rhodomicrobiaceae	0.0010	21	0.0044	0.0010
ASV_6395	Mediterranean California	asexual	Campylobacteraceae	0.0010	21	0.0044	0.0010
ASV_13328	Mediterranean California	asexual	NA	0.0010	21	0.0044	0.0010
ASV_7906	Mediterranean California	asexual	LWQ8	0.0009	21	0.0041	0.0009
ASV_838	Mediterranean California	asexual	Erwiniaceae	0.0008	21	0.0039	0.0008
ASV_12595	Mediterranean California	asexual	Demequinaceae	0.0008	21	0.0037	0.0008
ASV_11493	Mediterranean California	asexual	Leptolyngbyaceae	0.0008	21	0.0036	0.0008
ASV_417	Mediterranean California	asexual	Streptosporangiaceae	0.0007	21	0.0033	0.0007
ASV_1996	Mediterranean California	asexual	Thermincolaceae	0.0006	21	0.0029	0.0006
ASV_11365	Mediterranean California	asexual	SM2D12	0.0006	21	0.0028	0.0006
ASV_11541	Mediterranean California	asexual	Crocinitomicaceae	0.0006	21	0.0028	0.0006

ASV_13507	Mediterranean California	asexual	Mycoplasmataceae	0.0006	21	0.0028	0.0006
ASV_3510	Mediterranean California	asexual	A0839	0.0006	21	0.0026	0.0006
ASV_13511	Mediterranean California	asexual	Methylophagaceae	0.0005	21	0.0022	0.0005
ASV_14535	Mediterranean California	asexual	NA	0.0004	21	0.0019	0.0004
ASV_7025	Mediterranean California	asexual	Cyclobacteriaceae	0.0004	21	0.0019	0.0004
ASV_9931	Mediterranean California	asexual	Caldilineaceae	0.0004	21	0.0019	0.0004
ASV_3627	Mediterranean California	asexual	Ethanoligenenaceae	0.0004	21	0.0018	0.0004
ASV_10092	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_10319	Mediterranean California	asexual	Neisseriaceae	0.0000	21	0.0000	0.0000
ASV_10336	Mediterranean California	asexual	Xanthomonadaceae	0.0000	21	0.0000	0.0000
ASV_10434	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_10439	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_10617	Mediterranean California	asexual	Aerococcaceae	0.0000	21	0.0000	0.0000
ASV_10922	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_11270	Mediterranean California	asexual	Caedibacteraceae	0.0000	21	0.0000	0.0000
ASV_11284	Mediterranean California	asexual	Salisediminibacteriacea	0.0000	21	0.0000	0.0000
ASV_11494	Mediterranean California	asexual	Magnetospiraceae	0.0000	21	0.0000	0.0000
ASV_11504	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_11538	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_11608	Mediterranean California	asexual	FFCH9454	0.0000	21	0.0000	0.0000
ASV_11668	Mediterranean California	asexual	Desulfobulbaceae	0.0000	21	0.0000	0.0000
ASV_11680	Mediterranean California	asexual	Atopobiaceae	0.0000	21	0.0000	0.0000
ASV_11787	Mediterranean California	asexual	Parachlamydiaceae	0.0000	21	0.0000	0.0000
ASV_11913	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_11956	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_12171	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_12229	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_12365	Mediterranean California	asexual	Elusimicrobiaceae	0.0000	21	0.0000	0.0000
ASV_12449	Mediterranean California	asexual	Steroidobacteraceae	0.0000	21	0.0000	0.0000
ASV_12453	Mediterranean California	asexual	B1-7BS	0.0000	21	0.0000	0.0000
ASV_12467	Mediterranean California	asexual	Coxiellaceae	0.0000	21	0.0000	0.0000
ASV_12517	Mediterranean California	asexual	Aquaspirillaceae	0.0000	21	0.0000	0.0000

ASV_12650	Mediterranean California	asexual	Morganellaceae	0.0000	21	0.0000	0.0000
ASV_12655	Mediterranean California	asexual	Sporolactobacillaceae	0.0000	21	0.0000	0.0000
ASV_12858	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_12860	Mediterranean California	asexual	Tepidisphaeraceae	0.0000	21	0.0000	0.0000
ASV_12984	Mediterranean California	asexual	Acidimicrobiaceae	0.0000	21	0.0000	0.0000
ASV_13067	Mediterranean California	asexual	AKAU3644	0.0000	21	0.0000	0.0000
ASV_1308	Mediterranean California	asexual	Desulfotomaculaceae	0.0000	21	0.0000	0.0000
ASV_13082	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_13085	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_13217	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_1325	Mediterranean California	asexual	Acidobacteriaceae (Sub	0.0000	21	0.0000	0.0000
ASV_13265	Mediterranean California	asexual	Veillonellaceae	0.0000	21	0.0000	0.0000
ASV_13268	Mediterranean California	asexual	Aeromonadaceae	0.0000	21	0.0000	0.0000
ASV_13269	Mediterranean California	asexual	Prolixibacteraceae	0.0000	21	0.0000	0.0000
ASV_13301	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_13305	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_13329	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_13344	Mediterranean California	asexual	vadinHA21	0.0000	21	0.0000	0.0000
ASV_13581	Mediterranean California	asexual	Terasakiellaceae	0.0000	21	0.0000	0.0000
ASV_13598	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_13609	Mediterranean California	asexual	Stappiaceae	0.0000	21	0.0000	0.0000
ASV_13614	Mediterranean California	asexual	Wohlfahrtiimonadaceae	0.0000	21	0.0000	0.0000
ASV_13670	Mediterranean California	asexual	Phycisphaeraceae	0.0000	21	0.0000	0.0000
ASV_13739	Mediterranean California	asexual	Koribacteraceae	0.0000	21	0.0000	0.0000
ASV_13753	Mediterranean California	asexual	Yersiniaceae	0.0000	21	0.0000	0.0000
ASV_13789	Mediterranean California	asexual	Zavarziniaceae	0.0000	21	0.0000	0.0000
ASV_13922	Mediterranean California	asexual	Thermoanaerobaculace	0.0000	21	0.0000	0.0000
ASV_13957	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_13965	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_14007	Mediterranean California	asexual	Rhodanobacteraceae	0.0000	21	0.0000	0.0000
ASV_14037	Mediterranean California	asexual	Magnetospirillaceae	0.0000	21	0.0000	0.0000
ASV_14123	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000

ASV_14142	Mediterranean California	asexual	Syntrophomonadaceae	0.0000	21	0.0000	0.0000
ASV_14155	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_14225	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_14349	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_14744	Mediterranean California	asexual	Alcaligenaceae	0.0000	21	0.0000	0.0000
ASV_14757	Mediterranean California	asexual	Gemmataceae	0.0000	21	0.0000	0.0000
ASV_152	Mediterranean California	asexual	3M1PL1-52 termite grou	0.0000	21	0.0000	0.0000
ASV_1571	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_1605	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_1686	Mediterranean California	asexual	Anaeromyxobacteracea	0.0000	21	0.0000	0.0000
ASV_2367	Mediterranean California	asexual	Abditibacteriaceae	0.0000	21	0.0000	0.0000
ASV_2482	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_2624	Mediterranean California	asexual	Unknown Family	0.0000	21	0.0000	0.0000
ASV_2819	Mediterranean California	asexual	Micropepsaceae	0.0000	21	0.0000	0.0000
ASV_282	Mediterranean California	asexual	Thermoactinomycetacea	0.0000	21	0.0000	0.0000
ASV_2892	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_2959	Mediterranean California	asexual	Phaselicystidaceae	0.0000	21	0.0000	0.0000
ASV_2996	Mediterranean California	asexual	Nitrosococcaceae	0.0000	21	0.0000	0.0000
ASV_3114	Mediterranean California	asexual	Solibacteraceae	0.0000	21	0.0000	0.0000
ASV_3144	Mediterranean California	asexual	Roseiflexaceae	0.0000	21	0.0000	0.0000
ASV_317	Mediterranean California	asexual	Hafniaceae	0.0000	21	0.0000	0.0000
ASV_3179	Mediterranean California	asexual	Sulfurospirillaceae	0.0000	21	0.0000	0.0000
ASV_3356	Mediterranean California	asexual	Caldalkalibacillaceae	0.0000	21	0.0000	0.0000
ASV_3501	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_3519	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_3549	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_3660	Mediterranean California	asexual	Paracaedibacteraceae	0.0000	21	0.0000	0.0000
ASV_3766	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_3769	Mediterranean California	asexual	Williamwhitmaniaceae	0.0000	21	0.0000	0.0000
ASV_3781	Mediterranean California	asexual	Coleofasciculaceae	0.0000	21	0.0000	0.0000
ASV_3972	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_4085	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000

ASV_4086	Mediterranean California	asexual	Nostocaceae	0.0000	21	0.0000	0.0000
ASV_4236	Mediterranean California	asexual	Fibrobacteraceae	0.0000	21	0.0000	0.0000
ASV_4399	Mediterranean California	asexual	Anaplasmataceae	0.0000	21	0.0000	0.0000
ASV_4558	Mediterranean California	asexual	Myxococcaceae	0.0000	21	0.0000	0.0000
ASV_4602	Mediterranean California	asexual	Lactobacillaceae	0.0000	21	0.0000	0.0000
ASV_4645	Mediterranean California	asexual	Dongiaceae	0.0000	21	0.0000	0.0000
ASV_4673	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_4785	Mediterranean California	asexual	Oxobacteraceae	0.0000	21	0.0000	0.0000
ASV_4894	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_4934	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_5057	Mediterranean California	asexual	Nitriliruptoraceae	0.0000	21	0.0000	0.0000
ASV_5059	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_5102	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_5177	Mediterranean California	asexual	Candidatus Jidaibacter	0.0000	21	0.0000	0.0000
ASV_5248	Mediterranean California	asexual	Phormidiaceae	0.0000	21	0.0000	0.0000
ASV_5250	Mediterranean California	asexual	WD2101 soil group	0.0000	21	0.0000	0.0000
ASV_5301	Mediterranean California	asexual	Glycomycetaceae	0.0000	21	0.0000	0.0000
ASV_5314	Mediterranean California	asexual	Marinilabiliaceae	0.0000	21	0.0000	0.0000
ASV_5389	Mediterranean California	asexual	Desulfotomaculales Ince	0.0000	21	0.0000	0.0000
ASV_5504	Mediterranean California	asexual	Alicyclobacillaceae	0.0000	21	0.0000	0.0000
ASV_5553	Mediterranean California	asexual	Rhizobiales Incertae Se	0.0000	21	0.0000	0.0000
ASV_5681	Mediterranean California	asexual	Rhodospirillaceae	0.0000	21	0.0000	0.0000
ASV_5887	Mediterranean California	asexual	Budviciaceae	0.0000	21	0.0000	0.0000
ASV_6102	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_6172	Mediterranean California	asexual	Inquilinaceae	0.0000	21	0.0000	0.0000
ASV_621	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_6308	Mediterranean California	asexual	Barnesiellaceae	0.0000	21	0.0000	0.0000
ASV_6394	Mediterranean California	asexual	Chroococcidiopsaceae	0.0000	21	0.0000	0.0000
ASV_6560	Mediterranean California	asexual	Rubrobacteriaceae	0.0000	21	0.0000	0.0000
ASV_6570	Mediterranean California	asexual	Oligoflexaceae	0.0000	21	0.0000	0.0000
ASV_6583	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_6643	Mediterranean California	asexual	Gemellaceae	0.0000	21	0.0000	0.0000

ASV_6732	Mediterranean California	asexual	Hyphomonadaceae	0.0000	21	0.0000	0.0000
ASV_6794	Mediterranean California	asexual	Carnobacteriaceae	0.0000	21	0.0000	0.0000
ASV_685	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_6978	Mediterranean California	asexual	Defluviicoccaceae	0.0000	21	0.0000	0.0000
ASV_7083	Mediterranean California	asexual	Synergistaceae	0.0000	21	0.0000	0.0000
ASV_711	Mediterranean California	asexual	Pleomorphomonadacea	0.0000	21	0.0000	0.0000
ASV_7238	Mediterranean California	asexual	AKIW781	0.0000	21	0.0000	0.0000
ASV_7358	Mediterranean California	asexual	Methylophilaceae	0.0000	21	0.0000	0.0000
ASV_7459	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_7464	Mediterranean California	asexual	Blastocatellaceae	0.0000	21	0.0000	0.0000
ASV_7490	Mediterranean California	asexual	COB P4-1 termite grour	0.0000	21	0.0000	0.0000
ASV_7838	Mediterranean California	asexual	Sulfuricellaceae	0.0000	21	0.0000	0.0000
ASV_7869	Mediterranean California	asexual	Silvanigrellaceae	0.0000	21	0.0000	0.0000
ASV_7964	Mediterranean California	asexual	AKYG1722	0.0000	21	0.0000	0.0000
ASV_7971	Mediterranean California	asexual	Vicinamibacteraceae	0.0000	21	0.0000	0.0000
ASV_8058	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_8060	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_8089	Mediterranean California	asexual	Isosphaeraceae	0.0000	21	0.0000	0.0000
ASV_8458	Mediterranean California	asexual	Burkholderiaceae	0.0000	21	0.0000	0.0000
ASV_8486	Mediterranean California	asexual	Entotheonellaceae	0.0000	21	0.0000	0.0000
ASV_8496	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_8560	Mediterranean California	asexual	Endomicrobiaceae	0.0000	21	0.0000	0.0000
ASV_8588	Mediterranean California	asexual	Paenibacillaceae	0.0000	21	0.0000	0.0000
ASV_8715	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_8883	Mediterranean California	asexual	Nitrosomonadaceae	0.0000	21	0.0000	0.0000
ASV_8903	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_9043	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_9092	Mediterranean California	asexual	Rs-E47 termite group	0.0000	21	0.0000	0.0000
ASV_9242	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_9364	Mediterranean California	asexual	Micrococcales Incertae	0.0000	21	0.0000	0.0000
ASV_9379	Mediterranean California	asexual	Pasteurellaceae	0.0000	21	0.0000	0.0000
ASV_9469	Mediterranean California	asexual	Herpetosiphonaceae	0.0000	21	0.0000	0.0000

ASV_9797	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_9810	Mediterranean California	asexual	Trueperaceae	0.0000	21	0.0000	0.0000
ASV_9813	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_9879	Mediterranean California	asexual	NA	0.0000	21	0.0000	0.0000
ASV_4	South Central Semiarid Prairi	asexual	Micrococcacea	37.5766	1	NA	NA
ASV_1	South Central Semiarid Prairi	asexual	Dietziaceae	14.7264	1	NA	NA
ASV_7	South Central Semiarid Prairi	asexual	Lachnospiraceae	13.7480	1	NA	NA
ASV_8	South Central Semiarid Prairi	asexual	Brevibacteriaceae	6.2437	1	NA	NA
ASV_12	South Central Semiarid Prairi	asexual	Dermabacteraceae	6.1894	1	NA	NA
ASV_11	South Central Semiarid Prairi	asexual	Oscillospiraceae	2.5706	1	NA	NA
ASV_6	South Central Semiarid Prairi	asexual	Corynebacteriaceae	2.3563	1	NA	NA
ASV_19	South Central Semiarid Prairi	asexual	Nocardiaceae	2.3514	1	NA	NA
ASV_24	South Central Semiarid Prairi	asexual	Micrococcaceae	1.5340	1	NA	NA
ASV_22	South Central Semiarid Prairi	asexual	Ruminococcaceae	1.3381	1	NA	NA
ASV_69	South Central Semiarid Prairi	asexual	Geodermatophilaceae	1.1917	1	NA	NA
ASV_162	South Central Semiarid Prairi	asexual	Sphingomonadaceae	1.1820	1	NA	NA
ASV_3	South Central Semiarid Prairi	asexual	Helicobacteraceae	1.1045	1	NA	NA
ASV_21	South Central Semiarid Prairi	asexual	Intrasporangiaceae	0.9280	1	NA	NA
ASV_20	South Central Semiarid Prairi	asexual	Nocardioidaceae	0.8659	1	NA	NA
ASV_97	South Central Semiarid Prairi	asexual	Beijerinckiaceae	0.6157	1	NA	NA
ASV_117	South Central Semiarid Prairi	asexual	Marinifilaceae	0.5740	1	NA	NA
ASV_345	South Central Semiarid Prairi	asexual	Dermacoccaceae	0.5294	1	NA	NA
ASV_49	South Central Semiarid Prairi	asexual	Microbacteriaceae	0.4751	1	NA	NA
ASV_18	South Central Semiarid Prairi	asexual	Rhodobacteraceae	0.3568	1	NA	NA
ASV_32	South Central Semiarid Prairi	asexual	Bacteroidaceae	0.3355	1	NA	NA
ASV_405	South Central Semiarid Prairi	asexual	NA	0.3355	1	NA	NA
ASV_309	South Central Semiarid Prairi	asexual	Family XI	0.3103	1	NA	NA
ASV_250	South Central Semiarid Prairi	asexual	Butyricicoccaceae	0.2463	1	NA	NA
ASV_1285	South Central Semiarid Prairi	asexual	NA	0.2444	1	NA	NA
ASV_867	South Central Semiarid Prairi	asexual	Gaiellaceae	0.1998	1	NA	NA
ASV_139	South Central Semiarid Prairi	asexual	Acetobacteraceae	0.1901	1	NA	NA
ASV_121	South Central Semiarid Prairi	asexual	NA	0.1833	1	NA	NA

ASV_1686	South Central Semiarid Prairi	asexual	Anaeromyxobacteracea	0.1726	1	NA	NA
ASV_153	South Central Semiarid Prairi	asexual	Pseudonocardiaceae	0.1474	1	NA	NA
ASV_2104	South Central Semiarid Prairi	asexual	NA	0.1241	1	NA	NA
ASV_1150	South Central Semiarid Prairi	asexual	NA	0.1222	1	NA	NA
ASV_815	South Central Semiarid Prairi	asexual	NA	0.1135	1	NA	NA
ASV_214	South Central Semiarid Prairi	asexual	Eggerthellaceae	0.1047	1	NA	NA
ASV_729	South Central Semiarid Prairi	asexual	Longimicrobiaceae	0.0950	1	NA	NA
ASV_538	South Central Semiarid Prairi	asexual	Caulobacteraceae	0.0756	1	NA	NA
ASV_660	South Central Semiarid Prairi	asexual	Moraxellaceae	0.0718	1	NA	NA
ASV_10	South Central Semiarid Prairi	asexual	Clostridiaceae	0.0698	1	NA	NA
ASV_2708	South Central Semiarid Prairi	asexual	Bifidobacteriaceae	0.0659	1	NA	NA
ASV_994	South Central Semiarid Prairi	asexual	NA	0.0572	1	NA	NA
ASV_282	South Central Semiarid Prairi	asexual	Thermoactinomycetace	0.0388	1	NA	NA
ASV_73	South Central Semiarid Prairi	asexual	Cellulomonadaceae	0.0368	1	NA	NA
ASV_1080	South Central Semiarid Prairi	asexual	NA	0.0349	1	NA	NA
ASV_4894	South Central Semiarid Prairi	asexual	NA	0.0310	1	NA	NA
ASV_468	South Central Semiarid Prairi	asexual	Weeksellaceae	0.0252	1	NA	NA
ASV_142	South Central Semiarid Prairi	asexual	Streptomycetaceae	0.0223	1	NA	NA
ASV_681	South Central Semiarid Prairi	asexual	Sporichthyaceae	0.0155	1	NA	NA
ASV_283	South Central Semiarid Prairi	asexual	Micromonosporaceae	0.0145	1	NA	NA
ASV_3766	South Central Semiarid Prairi	asexual	NA	0.0145	1	NA	NA
ASV_420	South Central Semiarid Prairi	asexual	Enterobacteriaceae	0.0126	1	NA	NA
ASV_439	South Central Semiarid Prairi	asexual	Polyangiaceae	0.0078	1	NA	NA
ASV_1974	South Central Semiarid Prairi	asexual	NA	0.0048	1	NA	NA
ASV_4700	South Central Semiarid Prairi	asexual	Reyranellaceae	0.0039	1	NA	NA
ASV_9813	South Central Semiarid Prairi	asexual	NA	0.0039	1	NA	NA
ASV_1110	South Central Semiarid Prairi	asexual	Mycobacteriaceae	0.0029	1	NA	NA
ASV_23	South Central Semiarid Prairi	asexual	Diplorickettsiaceae	0.0029	1	NA	NA
ASV_38	South Central Semiarid Prairi	asexual	Tannerellaceae	0.0029	1	NA	NA
ASV_552	South Central Semiarid Prairi	asexual	Propionibacteriaceae	0.0019	1	NA	NA
ASV_10092	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_10319	South Central Semiarid Prairi	asexual	Neisseriaceae	0.0000	1	NA	NA

ASV_10336	South Central Semiarid Prairi	asexual	Xanthomonadaceae	0.0000	1	NA	NA
ASV_10434	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_10439	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_10617	South Central Semiarid Prairi	asexual	Aerococcaceae	0.0000	1	NA	NA
ASV_10922	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_1096	South Central Semiarid Prairi	asexual	UCG-010	0.0000	1	NA	NA
ASV_1107	South Central Semiarid Prairi	asexual	Muribaculaceae	0.0000	1	NA	NA
ASV_11196	South Central Semiarid Prairi	asexual	Vulgatibacteraceae	0.0000	1	NA	NA
ASV_11270	South Central Semiarid Prairi	asexual	Caedibacteraceae	0.0000	1	NA	NA
ASV_11284	South Central Semiarid Prairi	asexual	Salisediminibacteriacea	0.0000	1	NA	NA
ASV_11365	South Central Semiarid Prairi	asexual	SM2D12	0.0000	1	NA	NA
ASV_11493	South Central Semiarid Prairi	asexual	Leptolyngbyaceae	0.0000	1	NA	NA
ASV_11494	South Central Semiarid Prairi	asexual	Magnetospiraceae	0.0000	1	NA	NA
ASV_11504	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_11538	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_11541	South Central Semiarid Prairi	asexual	Crocinitomicaceae	0.0000	1	NA	NA
ASV_11608	South Central Semiarid Prairi	asexual	FFCH9454	0.0000	1	NA	NA
ASV_1162	South Central Semiarid Prairi	asexual	Puniceispirillales Incerta	0.0000	1	NA	NA
ASV_11668	South Central Semiarid Prairi	asexual	Desulfobulbaceae	0.0000	1	NA	NA
ASV_11680	South Central Semiarid Prairi	asexual	Atopobiaceae	0.0000	1	NA	NA
ASV_11787	South Central Semiarid Prairi	asexual	Parachlamydiaceae	0.0000	1	NA	NA
ASV_11833	South Central Semiarid Prairi	asexual	Blrii41	0.0000	1	NA	NA
ASV_11913	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_11956	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_1201	South Central Semiarid Prairi	asexual	Sphingobacteriaceae	0.0000	1	NA	NA
ASV_12171	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_12229	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_12365	South Central Semiarid Prairi	asexual	Elusimicrobiaceae	0.0000	1	NA	NA
ASV_12449	South Central Semiarid Prairi	asexual	Steroidobacteraceae	0.0000	1	NA	NA
ASV_12453	South Central Semiarid Prairi	asexual	B1-7BS	0.0000	1	NA	NA
ASV_1246	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_12467	South Central Semiarid Prairi	asexual	Coxiellaceae	0.0000	1	NA	NA

ASV_12517	South Central Semiarid Prairi	asexual	Aquaspirillaceae	0.0000	1	NA	NA
ASV_12532	South Central Semiarid Prairi	asexual	Bacteriovoracaceae	0.0000	1	NA	NA
ASV_12595	South Central Semiarid Prairi	asexual	Demequinaceae	0.0000	1	NA	NA
ASV_126	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_12650	South Central Semiarid Prairi	asexual	Morganellaceae	0.0000	1	NA	NA
ASV_12655	South Central Semiarid Prairi	asexual	Sporolactobacillaceae	0.0000	1	NA	NA
ASV_1275	South Central Semiarid Prairi	asexual	Actinomycetaceae	0.0000	1	NA	NA
ASV_12858	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_12860	South Central Semiarid Prairi	asexual	Tepidisphaeraceae	0.0000	1	NA	NA
ASV_129	South Central Semiarid Prairi	asexual	Peptostreptococcaceae	0.0000	1	NA	NA
ASV_12984	South Central Semiarid Prairi	asexual	Acidimicrobiaceae	0.0000	1	NA	NA
ASV_13067	South Central Semiarid Prairi	asexual	AKAU3644	0.0000	1	NA	NA
ASV_1308	South Central Semiarid Prairi	asexual	Desulfotomaculaceae	0.0000	1	NA	NA
ASV_13082	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_13085	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_13217	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_1325	South Central Semiarid Prairi	asexual	Acidobacteriaceae (Sub	0.0000	1	NA	NA
ASV_13265	South Central Semiarid Prairi	asexual	Veillonellaceae	0.0000	1	NA	NA
ASV_13268	South Central Semiarid Prairi	asexual	Aeromonadaceae	0.0000	1	NA	NA
ASV_13269	South Central Semiarid Prairi	asexual	Prolixibacteraceae	0.0000	1	NA	NA
ASV_13301	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_13305	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_13328	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_13329	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_13344	South Central Semiarid Prairi	asexual	vadinHA21	0.0000	1	NA	NA
ASV_1340	South Central Semiarid Prairi	asexual	Microtrichaceae	0.0000	1	NA	NA
ASV_13507	South Central Semiarid Prairi	asexual	Mycoplasmataceae	0.0000	1	NA	NA
ASV_13511	South Central Semiarid Prairi	asexual	Methylophagaceae	0.0000	1	NA	NA
ASV_13581	South Central Semiarid Prairi	asexual	Terasakiellaceae	0.0000	1	NA	NA
ASV_13598	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_13609	South Central Semiarid Prairi	asexual	Stappiaceae	0.0000	1	NA	NA
ASV_13614	South Central Semiarid Prairi	asexual	Wohlfahrtiimonadaceae	0.0000	1	NA	NA

ASV_13670	South Central Semiarid Prairi	asexual	Phycisphaeraceae	0.0000	1	NA	NA
ASV_13739	South Central Semiarid Prairi	asexual	Koribacteraceae	0.0000	1	NA	NA
ASV_13753	South Central Semiarid Prairi	asexual	Yersiniaceae	0.0000	1	NA	NA
ASV_13789	South Central Semiarid Prairi	asexual	Zavarziniaceae	0.0000	1	NA	NA
ASV_13922	South Central Semiarid Prairi	asexual	Thermoanaerobaculace	0.0000	1	NA	NA
ASV_13957	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_13965	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_14007	South Central Semiarid Prairi	asexual	Rhodanobacteraceae	0.0000	1	NA	NA
ASV_14037	South Central Semiarid Prairi	asexual	Magnetospirillaceae	0.0000	1	NA	NA
ASV_14123	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_14142	South Central Semiarid Prairi	asexual	Syntrophomonadaceae	0.0000	1	NA	NA
ASV_14155	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_14225	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_14349	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_1445	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_14535	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_14744	South Central Semiarid Prairi	asexual	Alcaligenaceae	0.0000	1	NA	NA
ASV_14757	South Central Semiarid Prairi	asexual	Gemmataceae	0.0000	1	NA	NA
ASV_1501	South Central Semiarid Prairi	asexual	Sanguibacteraceae	0.0000	1	NA	NA
ASV_152	South Central Semiarid Prairi	asexual	3M1PL1-52 termite grou	0.0000	1	NA	NA
ASV_1554	South Central Semiarid Prairi	asexual	Cryptosporangiaceae	0.0000	1	NA	NA
ASV_1563	South Central Semiarid Prairi	asexual	Erysipelatoclostridiacea	0.0000	1	NA	NA
ASV_1571	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_1575	South Central Semiarid Prairi	asexual	Defluviitaleaceae	0.0000	1	NA	NA
ASV_1605	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_161	South Central Semiarid Prairi	asexual	Bacillaceae	0.0000	1	NA	NA
ASV_163	South Central Semiarid Prairi	asexual	Monoglobaceae	0.0000	1	NA	NA
ASV_166	South Central Semiarid Prairi	asexual	Tsukamurellaceae	0.0000	1	NA	NA
ASV_1664	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_1694	South Central Semiarid Prairi	asexual	Marinococcaceae	0.0000	1	NA	NA
ASV_1715	South Central Semiarid Prairi	asexual	Eubacteriaceae	0.0000	1	NA	NA
ASV_1813	South Central Semiarid Prairi	asexual	D05-2	0.0000	1	NA	NA

ASV_1864	South Central Semiarid Prairi	asexual	Anaerofustaceae	0.0000	1	NA	NA
ASV_1904	South Central Semiarid Prairi	asexual	Cytophagaceae	0.0000	1	NA	NA
ASV_1996	South Central Semiarid Prairi	asexual	Thermincolaceae	0.0000	1	NA	NA
ASV_2133	South Central Semiarid Prairi	asexual	Nitrospiraceae	0.0000	1	NA	NA
ASV_2146	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_2156	South Central Semiarid Prairi	asexual	Hyphomicrobiaceae	0.0000	1	NA	NA
ASV_2172	South Central Semiarid Prairi	asexual	Hungateiclostridiaceae	0.0000	1	NA	NA
ASV_2211	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_2306	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_2367	South Central Semiarid Prairi	asexual	Abditibacteriaceae	0.0000	1	NA	NA
ASV_2445	South Central Semiarid Prairi	asexual	Streptosporangiales Inc	0.0000	1	NA	NA
ASV_2450	South Central Semiarid Prairi	asexual	Prevotellaceae	0.0000	1	NA	NA
ASV_2482	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_2494	South Central Semiarid Prairi	asexual	Thermicanaceae	0.0000	1	NA	NA
ASV_2506	South Central Semiarid Prairi	asexual	Acidothermaceae	0.0000	1	NA	NA
ASV_2522	South Central Semiarid Prairi	asexual	Beutenbergiaceae	0.0000	1	NA	NA
ASV_2550	South Central Semiarid Prairi	asexual	Spirosomaceae	0.0000	1	NA	NA
ASV_2554	South Central Semiarid Prairi	asexual	Fusobacteriaceae	0.0000	1	NA	NA
ASV_259	South Central Semiarid Prairi	asexual	Enterococcaceae	0.0000	1	NA	NA
ASV_2606	South Central Semiarid Prairi	asexual	Euzebyaceae	0.0000	1	NA	NA
ASV_2624	South Central Semiarid Prairi	asexual	Unknown Family	0.0000	1	NA	NA
ASV_2687	South Central Semiarid Prairi	asexual	Unknown Family	0.0000	1	NA	NA
ASV_2726	South Central Semiarid Prairi	asexual	Bdellovibrionaceae	0.0000	1	NA	NA
ASV_2819	South Central Semiarid Prairi	asexual	Micropepsaceae	0.0000	1	NA	NA
ASV_2892	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_29	South Central Semiarid Prairi	asexual	[Eubacterium] coprostar	0.0000	1	NA	NA
ASV_2959	South Central Semiarid Prairi	asexual	Phaselicystidaceae	0.0000	1	NA	NA
ASV_2986	South Central Semiarid Prairi	asexual	Actinospicaceae	0.0000	1	NA	NA
ASV_2996	South Central Semiarid Prairi	asexual	Nitrosococcaceae	0.0000	1	NA	NA
ASV_3064	South Central Semiarid Prairi	asexual	Paludibacteraceae	0.0000	1	NA	NA
ASV_3114	South Central Semiarid Prairi	asexual	Solibacteraceae	0.0000	1	NA	NA
ASV_3144	South Central Semiarid Prairi	asexual	Roseiflexaceae	0.0000	1	NA	NA

ASV_3155	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_317	South Central Semiarid Prairi	asexual	Hafniaceae	0.0000	1	NA	NA
ASV_3179	South Central Semiarid Prairi	asexual	Sulfurospirillaceae	0.0000	1	NA	NA
ASV_3356	South Central Semiarid Prairi	asexual	Caldalkalibacillaceae	0.0000	1	NA	NA
ASV_3376	South Central Semiarid Prairi	asexual	Sandaracinaceae	0.0000	1	NA	NA
ASV_3410	South Central Semiarid Prairi	asexual	Selenomonadaceae	0.0000	1	NA	NA
ASV_3419	South Central Semiarid Prairi	asexual	Dysgonomonadaceae	0.0000	1	NA	NA
ASV_3442	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_3453	South Central Semiarid Prairi	asexual	Streptococcaceae	0.0000	1	NA	NA
ASV_3457	South Central Semiarid Prairi	asexual	Sedimentibacteraceae	0.0000	1	NA	NA
ASV_347	South Central Semiarid Prairi	asexual	Azospirillaceae	0.0000	1	NA	NA
ASV_3501	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_3510	South Central Semiarid Prairi	asexual	A0839	0.0000	1	NA	NA
ASV_3519	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_3549	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_362	South Central Semiarid Prairi	asexual	Thermomonosporaceae	0.0000	1	NA	NA
ASV_3627	South Central Semiarid Prairi	asexual	Ethanoligenenaceae	0.0000	1	NA	NA
ASV_3660	South Central Semiarid Prairi	asexual	Paracaedibacteraceae	0.0000	1	NA	NA
ASV_3726	South Central Semiarid Prairi	asexual	Rhodothermaceae	0.0000	1	NA	NA
ASV_3769	South Central Semiarid Prairi	asexual	Williamwhitmaniaceae	0.0000	1	NA	NA
ASV_3781	South Central Semiarid Prairi	asexual	Coleofasciculaceae	0.0000	1	NA	NA
ASV_3972	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_4022	South Central Semiarid Prairi	asexual	Pseudomonadaceae	0.0000	1	NA	NA
ASV_404	South Central Semiarid Prairi	asexual	Kineosporiaceae	0.0000	1	NA	NA
ASV_4085	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_4086	South Central Semiarid Prairi	asexual	Nostocaceae	0.0000	1	NA	NA
ASV_410	South Central Semiarid Prairi	asexual	Ilumatobacteraceae	0.0000	1	NA	NA
ASV_4124	South Central Semiarid Prairi	asexual	Leptotrichiaceae	0.0000	1	NA	NA
ASV_417	South Central Semiarid Prairi	asexual	Streptosporangiaceae	0.0000	1	NA	NA
ASV_4184	South Central Semiarid Prairi	asexual	Methyloligellaceae	0.0000	1	NA	NA
ASV_4224	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_4227	South Central Semiarid Prairi	asexual	Halomonadaceae	0.0000	1	NA	NA

ASV_4236	South Central Semiarid Prairi	asexual	Fibrobacteraceae	0.0000	1	NA	NA
ASV_4284	South Central Semiarid Prairi	asexual	Ardenticatenaceae	0.0000	1	NA	NA
ASV_4291	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_4297	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_4341	South Central Semiarid Prairi	asexual	Simkaniaceae	0.0000	1	NA	NA
ASV_4399	South Central Semiarid Prairi	asexual	Anaplasmataceae	0.0000	1	NA	NA
ASV_44	South Central Semiarid Prairi	asexual	Rikenellaceae	0.0000	1	NA	NA
ASV_442	South Central Semiarid Prairi	asexual	Rhizobiaceae	0.0000	1	NA	NA
ASV_4558	South Central Semiarid Prairi	asexual	Myxococcaceae	0.0000	1	NA	NA
ASV_456	South Central Semiarid Prairi	asexual	Promicromonosporacea	0.0000	1	NA	NA
ASV_4602	South Central Semiarid Prairi	asexual	Lactobacillaceae	0.0000	1	NA	NA
ASV_4645	South Central Semiarid Prairi	asexual	Dongiaceae	0.0000	1	NA	NA
ASV_4655	South Central Semiarid Prairi	asexual	Iamiaceae	0.0000	1	NA	NA
ASV_4673	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_474	South Central Semiarid Prairi	asexual	Chitinophagaceae	0.0000	1	NA	NA
ASV_4747	South Central Semiarid Prairi	asexual	Solirubrobacteraceae	0.0000	1	NA	NA
ASV_4785	South Central Semiarid Prairi	asexual	Oxobacteraceae	0.0000	1	NA	NA
ASV_481	South Central Semiarid Prairi	asexual	Oxalobacteraceae	0.0000	1	NA	NA
ASV_483	South Central Semiarid Prairi	asexual	Hymenobacteraceae	0.0000	1	NA	NA
ASV_4929	South Central Semiarid Prairi	asexual	Erysipelotrichaceae	0.0000	1	NA	NA
ASV_493	South Central Semiarid Prairi	asexual	Frankiaceae	0.0000	1	NA	NA
ASV_4934	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_5057	South Central Semiarid Prairi	asexual	Nitriliruptoraceae	0.0000	1	NA	NA
ASV_5059	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_5102	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_512	South Central Semiarid Prairi	asexual	Geminicoccaceae	0.0000	1	NA	NA
ASV_5152	South Central Semiarid Prairi	asexual	Rickettsiaceae	0.0000	1	NA	NA
ASV_5154	South Central Semiarid Prairi	asexual	KF-JG30-B3	0.0000	1	NA	NA
ASV_5177	South Central Semiarid Prairi	asexual	Candidatus Jidaibacter	0.0000	1	NA	NA
ASV_5248	South Central Semiarid Prairi	asexual	Phormidiaceae	0.0000	1	NA	NA
ASV_5250	South Central Semiarid Prairi	asexual	WD2101 soil group	0.0000	1	NA	NA
ASV_5301	South Central Semiarid Prairi	asexual	Glycomycetaceae	0.0000	1	NA	NA

ASV_5314	South Central Semiarid Prairi	asexual	Marinilabiliaceae	0.0000	1	NA	NA
ASV_5351	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_5389	South Central Semiarid Prairi	asexual	Desulfotomaculales Ince	0.0000	1	NA	NA
ASV_5396	South Central Semiarid Prairi	asexual	Caloramatoraceae	0.0000	1	NA	NA
ASV_5486	South Central Semiarid Prairi	asexual	Microscillaceae	0.0000	1	NA	NA
ASV_5504	South Central Semiarid Prairi	asexual	Alicyclobacillaceae	0.0000	1	NA	NA
ASV_5527	South Central Semiarid Prairi	asexual	Comamonadaceae	0.0000	1	NA	NA
ASV_5553	South Central Semiarid Prairi	asexual	Rhizobiales Incertae Sec	0.0000	1	NA	NA
ASV_5631	South Central Semiarid Prairi	asexual	Sporomusaceae	0.0000	1	NA	NA
ASV_5638	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_5681	South Central Semiarid Prairi	asexual	Rhodospirillaceae	0.0000	1	NA	NA
ASV_57	South Central Semiarid Prairi	asexual	Devosiaceae	0.0000	1	NA	NA
ASV_571	South Central Semiarid Prairi	asexual	Flavobacteriaceae	0.0000	1	NA	NA
ASV_5823	South Central Semiarid Prairi	asexual	Competibacteraceae	0.0000	1	NA	NA
ASV_586	South Central Semiarid Prairi	asexual	Saccharimonadaceae	0.0000	1	NA	NA
ASV_5887	South Central Semiarid Prairi	asexual	Budviciaceae	0.0000	1	NA	NA
ASV_5915	South Central Semiarid Prairi	asexual	env.OPS 17	0.0000	1	NA	NA
ASV_5924	South Central Semiarid Prairi	asexual	Exiguobacteraceae	0.0000	1	NA	NA
ASV_604	South Central Semiarid Prairi	asexual	Hydrogenoanaerobacte	0.0000	1	NA	NA
ASV_6091	South Central Semiarid Prairi	asexual	JG30-KF-CM45	0.0000	1	NA	NA
ASV_6102	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_6172	South Central Semiarid Prairi	asexual	Inquilinaceae	0.0000	1	NA	NA
ASV_621	South Central Semiarid Prairi	asexual	NA	0.0000	1	NA	NA
ASV_624	South Central Semiarid Prairi	asexual	Bryobacteraceae	0.0000	1	NA	NA

ASV_6308	Tamaulipas - Texas Semiarid	asexual	Barnesiellaceae	0.0000	3	0.0000	0.0000
ASV_6395	Tamaulipas - Texas Semiarid	asexual	Campylobacteraceae	0.0000	3	0.0000	0.0000
ASV_6397	Tamaulipas - Texas Semiarid	asexual	NA	0.0000	3	0.0000	0.0000
ASV_6560	Tamaulipas - Texas Semiarid	asexual	Rubrobacteriaceae	0.0000	3	0.0000	0.0000
ASV_6583	Tamaulipas - Texas Semiarid	asexual	NA	0.0000	3	0.0000	0.0000
ASV_6643	Tamaulipas - Texas Semiarid	asexual	Gemellaceae	0.0000	3	0.0000	0.0000

ASV_6732	Tamaulipas - Texas Semiarid	asexual	Hyphomonadaceae	0.0000	3	0.0000	0.0000
ASV_6794	Tamaulipas - Texas Semiarid	asexual	Carnobacteriaceae	0.0000	3	0.0000	0.0000
ASV_681	Tamaulipas - Texas Semiarid	asexual	Sporichthyaceae	0.0000	3	0.0000	0.0000
ASV_685	Tamaulipas - Texas Semiarid	asexual	NA	0.0000	3	0.0000	0.0000
ASV_6978	Tamaulipas - Texas Semiarid	asexual	Defluviicoccaceae	0.0000	3	0.0000	0.0000
ASV_7023	Tamaulipas - Texas Semiarid	asexual	NA	0.0000	3	0.0000	0.0000
ASV_7025	Tamaulipas - Texas Semiarid	asexual	Cyclobacteriaceae	0.0000	3	0.0000	0.0000
ASV_7083	Tamaulipas - Texas Semiarid	asexual	Synergistaceae	0.0000	3	0.0000	0.0000
ASV_7107	Tamaulipas - Texas Semiarid	asexual	Bogoriellaceae	0.0000	3	0.0000	0.0000
ASV_711	Tamaulipas - Texas Semiarid	asexual	Pleomorphomonadacea	0.0000	3	0.0000	0.0000
ASV_7111	Tamaulipas - Texas Semiarid	asexual	Family III	0.0000	3	0.0000	0.0000
ASV_7146	Tamaulipas - Texas Semiarid	asexual	Planococcaceae	0.0000	3	0.0000	0.0000
ASV_7358	Tamaulipas - Texas Semiarid	asexual	Methylophilaceae	0.0000	3	0.0000	0.0000
ASV_7459	Tamaulipas - Texas Semiarid	asexual	NA	0.0000	3	0.0000	0.0000
ASV_7464	Tamaulipas - Texas Semiarid	asexual	Blastocatellaceae	0.0000	3	0.0000	0.0000
ASV_7490	Tamaulipas - Texas Semiarid	asexual	COB P4-1 termite grou	0.0000	3	0.0000	0.0000
ASV_753	Tamaulipas - Texas Semiarid	asexual	[Clostridium] methylpen	0.0000	3	0.0000	0.0000
ASV_7533	Tamaulipas - Texas Semiarid	asexual	Saprospiraceae	0.0000	3	0.0000	0.0000
ASV_758	Tamaulipas - Texas Semiarid	asexual	Coriobacteriales Incerta	0.0000	3	0.0000	0.0000
ASV_7766	Tamaulipas - Texas Semiarid	asexual	AKYH767	0.0000	3	0.0000	0.0000
ASV_7838	Tamaulipas - Texas Semiarid	asexual	Sulfuricellaceae	0.0000	3	0.0000	0.0000
ASV_7869	Tamaulipas - Texas Semiarid	asexual	Silvanigrellaceae	0.0000	3	0.0000	0.0000
ASV_7906	Tamaulipas - Texas Semiarid	asexual	LWQ8	0.0000	3	0.0000	0.0000
ASV_795	Tamaulipas - Texas Semiarid	asexual	Labraceae	0.0000	3	0.0000	0.0000
ASV_7964	Tamaulipas - Texas Semiarid	asexual	AKYG1722	0.0000	3	0.0000	0.0000
ASV_7971	Tamaulipas - Texas Semiarid	asexual	Vicinamibacteraceae	0.0000	3	0.0000	0.0000
ASV_8058	Tamaulipas - Texas Semiarid	asexual	NA	0.0000	3	0.0000	0.0000
ASV_8060	Tamaulipas - Texas Semiarid	asexual	NA	0.0000	3	0.0000	0.0000
ASV_8089	Tamaulipas - Texas Semiarid	asexual	Isosphaeraceae	0.0000	3	0.0000	0.0000
ASV_838	Tamaulipas - Texas Semiarid	asexual	Erwiniaceae	0.0000	3	0.0000	0.0000
ASV_8455	Tamaulipas - Texas Semiarid	asexual	NA	0.0000	3	0.0000	0.0000
ASV_8458	Tamaulipas - Texas Semiarid	asexual	Burkholderiaceae	0.0000	3	0.0000	0.0000

ASV_8486	Tamaulipas - Texas Semiarid	asexual	Entotheonellaceae	0.0000	3	0.0000	0.0000
ASV_8496	Tamaulipas - Texas Semiarid	asexual	NA	0.0000	3	0.0000	0.0000
ASV_8560	Tamaulipas - Texas Semiarid	asexual	Endomicrobiaceae	0.0000	3	0.0000	0.0000
ASV_8572	Tamaulipas - Texas Semiarid	asexual	Nocardiopsaceae	0.0000	3	0.0000	0.0000
ASV_8588	Tamaulipas - Texas Semiarid	asexual	Paenibacillaceae	0.0000	3	0.0000	0.0000
ASV_8715	Tamaulipas - Texas Semiarid	asexual	NA	0.0000	3	0.0000	0.0000
ASV_8883	Tamaulipas - Texas Semiarid	asexual	Nitrosomonadaceae	0.0000	3	0.0000	0.0000
ASV_8903	Tamaulipas - Texas Semiarid	asexual	NA	0.0000	3	0.0000	0.0000
ASV_9043	Tamaulipas - Texas Semiarid	asexual	NA	0.0000	3	0.0000	0.0000
ASV_9092	Tamaulipas - Texas Semiarid	asexual	Rs-E47 termite group	0.0000	3	0.0000	0.0000
ASV_912	Tamaulipas - Texas Semiarid	asexual	NA	0.0000	3	0.0000	0.0000
ASV_9144	Tamaulipas - Texas Semiarid	asexual	NA	0.0000	3	0.0000	0.0000
ASV_9161	Tamaulipas - Texas Semiarid	asexual	Legionellaceae	0.0000	3	0.0000	0.0000
ASV_9242	Tamaulipas - Texas Semiarid	asexual	NA	0.0000	3	0.0000	0.0000
ASV_9364	Tamaulipas - Texas Semiarid	asexual	Micrococcales Incertae	0.0000	3	0.0000	0.0000
ASV_9379	Tamaulipas - Texas Semiarid	asexual	Pasteurellaceae	0.0000	3	0.0000	0.0000
ASV_9469	Tamaulipas - Texas Semiarid	asexual	Herpetosiphonaceae	0.0000	3	0.0000	0.0000
ASV_9488	Tamaulipas - Texas Semiarid	asexual	NA	0.0000	3	0.0000	0.0000
ASV_9515	Tamaulipas - Texas Semiarid	asexual	Rhodomicrobiaceae	0.0000	3	0.0000	0.0000
ASV_9517	Tamaulipas - Texas Semiarid	asexual	Chloroflexaceae	0.0000	3	0.0000	0.0000
ASV_96	Tamaulipas - Texas Semiarid	asexual	Christensenellaceae	0.0000	3	0.0000	0.0000
ASV_9672	Tamaulipas - Texas Semiarid	asexual	Methylopilaceae	0.0000	3	0.0000	0.0000
ASV_9715	Tamaulipas - Texas Semiarid	asexual	Desulfitobacteriaceae	0.0000	3	0.0000	0.0000
ASV_98	Tamaulipas - Texas Semiarid	asexual	Desulfovibrionaceae	0.0000	3	0.0000	0.0000
ASV_9810	Tamaulipas - Texas Semiarid	asexual	Trueperaceae	0.0000	3	0.0000	0.0000
ASV_9813	Tamaulipas - Texas Semiarid	asexual	NA	0.0000	3	0.0000	0.0000
ASV_9818	Tamaulipas - Texas Semiarid	asexual	67-14	0.0000	3	0.0000	0.0000
ASV_9871	Tamaulipas - Texas Semiarid	asexual	Nannocystaceae	0.0000	3	0.0000	0.0000
ASV_9879	Tamaulipas - Texas Semiarid	asexual	NA	0.0000	3	0.0000	0.0000
ASV_9931	Tamaulipas - Texas Semiarid	asexual	Caldilineaceae	0.0000	3	0.0000	0.0000
ASV_994	Tamaulipas - Texas Semiarid	asexual	NA	0.0000	3	0.0000	0.0000
ASV_1	Warm North American Deser	asexual	Dietziaceae	36.1225	35	43.7552	7.3960

ASV_4	Warm North American Deser	asexual	Micrococcacea	16.3695	35	31.3132	5.2929
ASV_7	Warm North American Deser	asexual	Lachnospiraceae	10.2614	35	17.2919	2.9229
ASV_10	Warm North American Deser	asexual	Clostridiaceae	2.7614	35	12.9418	2.1876
ASV_69	Warm North American Deser	asexual	Geodermatophilaceae	2.3198	35	3.4899	0.5899
ASV_21	Warm North American Deser	asexual	Intrasporangiaceae	2.0099	35	10.9764	1.8554
ASV_24	Warm North American Deser	asexual	Micrococcaceae	1.9731	35	4.4594	0.7538
ASV_20	Warm North American Deser	asexual	Nocardioidaceae	1.9492	35	3.3002	0.5578
ASV_11	Warm North American Deser	asexual	Oscillospiraceae	1.9284	35	4.3876	0.7416
ASV_97	Warm North American Deser	asexual	Beijerinckiaceae	1.6008	35	2.8353	0.4793
ASV_162	Warm North American Deser	asexual	Sphingomonadaceae	1.4734	35	2.7535	0.4654
ASV_32	Warm North American Deser	asexual	Bacteroidaceae	1.4511	35	3.3458	0.5655
ASV_22	Warm North American Deser	asexual	Ruminococcaceae	1.4167	35	3.5050	0.5925
ASV_6	Warm North American Deser	asexual	Corynebacteriaceae	1.3594	35	4.5955	0.7768
ASV_18	Warm North American Deser	asexual	Rhodobacteraceae	1.0357	35	2.8026	0.4737
ASV_420	Warm North American Deser	asexual	Enterobacteriaceae	0.9849	35	1.9376	0.3275
ASV_49	Warm North American Deser	asexual	Microbacteriaceae	0.8742	35	1.9697	0.3329
ASV_12	Warm North American Deser	asexual	Dermabacteraceae	0.8002	35	3.9578	0.6690
ASV_19	Warm North American Deser	asexual	Nocardiaceae	0.7615	35	2.8065	0.4744
ASV_38	Warm North American Deser	asexual	Tannerellaceae	0.6940	35	2.2170	0.3747
ASV_98	Warm North American Deser	asexual	Desulfovibrionaceae	0.6544	35	1.8026	0.3047
ASV_309	Warm North American Deser	asexual	Family XI	0.5612	35	2.1336	0.3606
ASV_139	Warm North American Deser	asexual	Acetobacteraceae	0.5541	35	1.0510	0.1777
ASV_142	Warm North American Deser	asexual	Streptomycetaceae	0.5073	35	1.3561	0.2292
ASV_86	Warm North American Deser	asexual	Anaerovoracaceae	0.4835	35	1.3584	0.2296
ASV_166	Warm North American Deser	asexual	Tsukamurellaceae	0.4810	35	2.6446	0.4470
ASV_117	Warm North American Deser	asexual	Marinifilaceae	0.4282	35	1.1774	0.1990
ASV_283	Warm North American Deser	asexual	Micromonosporaceae	0.4103	35	0.9849	0.1665
ASV_161	Warm North American Deser	asexual	Bacillaceae	0.3904	35	1.3527	0.2286
ASV_153	Warm North American Deser	asexual	Pseudonocardiaceae	0.3612	35	0.6077	0.1027
ASV_29	Warm North American Deser	asexual	[Eubacterium] coprosta	0.3050	35	1.1592	0.1959
ASV_73	Warm North American Deser	asexual	Cellulomonadaceae	0.3016	35	0.5478	0.0926
ASV_121	Warm North American Deser	asexual	NA	0.2919	35	0.5545	0.0937

ASV_250	Warm North American Deser	asexual	Butyricicoccaceae	0.2760	35	0.6928	0.1171
ASV_214	Warm North American Deser	asexual	Eggerthellaceae	0.2617	35	0.9185	0.1553
ASV_44	Warm North American Deser	asexual	Rikenellaceae	0.2492	35	0.6761	0.1143
ASV_404	Warm North American Deser	asexual	Kineosporiaceae	0.2462	35	0.5330	0.0901
ASV_483	Warm North American Deser	asexual	Hymenobacteraceae	0.2421	35	0.5903	0.0998
ASV_474	Warm North American Deser	asexual	Chitinophagaceae	0.2415	35	0.6582	0.1113
ASV_259	Warm North American Deser	asexual	Enterococcaceae	0.2356	35	0.7911	0.1337
ASV_660	Warm North American Deser	asexual	Moraxellaceae	0.2342	35	0.5230	0.0884
ASV_442	Warm North American Deser	asexual	Rhizobiaceae	0.2266	35	0.3940	0.0666
ASV_345	Warm North American Deser	asexual	Dermacoccaceae	0.2125	35	1.1027	0.1864
ASV_538	Warm North American Deser	asexual	Caulobacteraceae	0.1969	35	0.4294	0.0726
ASV_729	Warm North American Deser	asexual	Longimicrobiaceae	0.1491	35	0.4122	0.0697
ASV_129	Warm North American Deser	asexual	Peptostreptococcaceae	0.1485	35	0.4300	0.0727
ASV_3	Warm North American Deser	asexual	Helicobacteraceae	0.1484	35	0.4648	0.0786
ASV_2494	Warm North American Deser	asexual	Thermicanaceae	0.1281	35	0.6772	0.1145
ASV_807	Warm North American Deser	asexual	Gemmatimonadaceae	0.1255	35	0.2494	0.0422
ASV_282	Warm North American Deser	asexual	Thermoactinomycetace	0.1215	35	0.6765	0.1144
ASV_728	Warm North American Deser	asexual	Xanthobacteraceae	0.1205	35	0.2465	0.0417
ASV_57	Warm North American Deser	asexual	Devosiaceae	0.1191	35	0.2529	0.0428
ASV_347	Warm North American Deser	asexual	Azospirillaceae	0.1090	35	0.3665	0.0620
ASV_1150	Warm North American Deser	asexual	NA	0.1051	35	0.2426	0.0410
ASV_912	Warm North American Deser	asexual	NA	0.0912	35	0.4342	0.0734
ASV_2104	Warm North American Deser	asexual	NA	0.0885	35	0.2068	0.0350
ASV_8	Warm North American Deser	asexual	Brevibacteriaceae	0.0854	35	0.2160	0.0365
ASV_410	Warm North American Deser	asexual	Ilumatobacteraceae	0.0783	35	0.1838	0.0311
ASV_512	Warm North American Deser	asexual	Geminicoccaceae	0.0778	35	0.1886	0.0319
ASV_867	Warm North American Deser	asexual	Gaiellaceae	0.0607	35	0.2220	0.0375
ASV_624	Warm North American Deser	asexual	Bryobacteraceae	0.0600	35	0.1404	0.0237
ASV_468	Warm North American Deser	asexual	Weeksellaceae	0.0554	35	0.2102	0.0355
ASV_362	Warm North American Deser	asexual	Thermomonosporaceae	0.0531	35	0.1153	0.0195
ASV_417	Warm North American Deser	asexual	Streptosporangiaceae	0.0529	35	0.1590	0.0269
ASV_439	Warm North American Deser	asexual	Polyangiaceae	0.0501	35	0.2236	0.0378

ASV_817	Warm North American Deser	asexual	Porphyromonadaceae	0.0464	35	0.1775	0.0300
ASV_815	Warm North American Deser	asexual	NA	0.0431	35	0.1029	0.0174
ASV_681	Warm North American Deser	asexual	Sporichthyaceae	0.0395	35	0.1186	0.0200
ASV_317	Warm North American Deser	asexual	Hafniaceae	0.0380	35	0.2251	0.0380
ASV_96	Warm North American Deser	asexual	Christensenellaceae	0.0358	35	0.0833	0.0141
ASV_5553	Warm North American Deser	asexual	Rhizobiales Incertae Se	0.0357	35	0.1260	0.0213
ASV_1246	Warm North American Deser	asexual	NA	0.0347	35	0.0863	0.0146
ASV_91	Warm North American Deser	asexual	Peptococcaceae	0.0345	35	0.1032	0.0174
ASV_1275	Warm North American Deser	asexual	Actinomycetaceae	0.0342	35	0.1045	0.0177
ASV_2554	Warm North American Deser	asexual	Fusobacteriaceae	0.0341	35	0.1144	0.0193
ASV_4785	Warm North American Deser	asexual	Oxobacteraceae	0.0340	35	0.1806	0.0305
ASV_1110	Warm North American Deser	asexual	Mycobacteriaceae	0.0339	35	0.0800	0.0135
ASV_126	Warm North American Deser	asexual	NA	0.0324	35	0.1342	0.0227
ASV_604	Warm North American Deser	asexual	Hydrogenoanaerobacte	0.0315	35	0.0871	0.0147
ASV_1080	Warm North American Deser	asexual	NA	0.0309	35	0.0899	0.0152
ASV_1664	Warm North American Deser	asexual	NA	0.0299	35	0.1138	0.0192
ASV_6397	Warm North American Deser	asexual	NA	0.0280	35	0.0946	0.0160
ASV_493	Warm North American Deser	asexual	Frankiaceae	0.0274	35	0.1143	0.0193
ASV_3376	Warm North American Deser	asexual	Sandaracinaceae	0.0268	35	0.0925	0.0156
ASV_941	Warm North American Deser	asexual	Staphylococcaceae	0.0259	35	0.0558	0.0094
ASV_571	Warm North American Deser	asexual	Flavobacteriaceae	0.0251	35	0.1244	0.0210
ASV_2550	Warm North American Deser	asexual	Spirosomaceae	0.0250	35	0.0620	0.0105
ASV_456	Warm North American Deser	asexual	Promicromonosporace	0.0250	35	0.1138	0.0192
ASV_994	Warm North American Deser	asexual	NA	0.0233	35	0.0905	0.0153
ASV_2306	Warm North American Deser	asexual	NA	0.0217	35	0.0492	0.0083
ASV_795	Warm North American Deser	asexual	Labraceae	0.0207	35	0.1063	0.0180
ASV_1201	Warm North American Deser	asexual	Sphingobacteriaceae	0.0190	35	0.0509	0.0086
ASV_552	Warm North American Deser	asexual	Propionibacteriaceae	0.0186	35	0.0558	0.0094
ASV_1162	Warm North American Deser	asexual	Puniceispirillales Incert	0.0186	35	0.0573	0.0097
ASV_163	Warm North American Deser	asexual	Monoglobaceae	0.0184	35	0.0641	0.0108
ASV_2445	Warm North American Deser	asexual	Streptosporangiales Inc	0.0182	35	0.0586	0.0099
ASV_2450	Warm North American Deser	asexual	Prevotellaceae	0.0175	35	0.0749	0.0127

ASV_5351	Warm North American Deser	asexual	NA	0.0156	35	0.0792	0.0134
ASV_2606	Warm North American Deser	asexual	Euzebyaceae	0.0146	35	0.0516	0.0087
ASV_1813	Warm North American Deser	asexual	D05-2	0.0142	35	0.0440	0.0074
ASV_838	Warm North American Deser	asexual	Erwiniaceae	0.0139	35	0.0820	0.0139
ASV_1575	Warm North American Deser	asexual	Defluviitaleaceae	0.0136	35	0.0802	0.0136
ASV_1445	Warm North American Deser	asexual	NA	0.0135	35	0.0354	0.0060
ASV_2146	Warm North American Deser	asexual	NA	0.0133	35	0.0479	0.0081
ASV_979	Warm North American Deser	asexual	Nakamurellaceae	0.0132	35	0.0474	0.0080
ASV_3155	Warm North American Deser	asexual	NA	0.0132	35	0.0598	0.0101
ASV_6560	Warm North American Deser	asexual	Rubrobacteriaceae	0.0122	35	0.0644	0.0109
ASV_4086	Warm North American Deser	asexual	Nostocaceae	0.0121	35	0.0443	0.0075
ASV_405	Warm North American Deser	asexual	NA	0.0116	35	0.0350	0.0059
ASV_6794	Warm North American Deser	asexual	Carnobacteriaceae	0.0114	35	0.0677	0.0114
ASV_621	Warm North American Deser	asexual	NA	0.0113	35	0.0374	0.0063
ASV_8588	Warm North American Deser	asexual	Paenibacillaceae	0.0108	35	0.0447	0.0076
ASV_1974	Warm North American Deser	asexual	NA	0.0108	35	0.0301	0.0051
ASV_1715	Warm North American Deser	asexual	Eubacteriaceae	0.0107	35	0.0423	0.0072
ASV_7146	Warm North American Deser	asexual	Planococcaceae	0.0107	35	0.0454	0.0077
ASV_3144	Warm North American Deser	asexual	Roseiflexaceae	0.0106	35	0.0441	0.0074
ASV_1285	Warm North American Deser	asexual	NA	0.0103	35	0.0439	0.0074
ASV_1904	Warm North American Deser	asexual	Cytophagaceae	0.0097	35	0.0334	0.0056
ASV_2482	Warm North American Deser	asexual	NA	0.0097	35	0.0227	0.0038
ASV_2708	Warm North American Deser	asexual	Bifidobacteriaceae	0.0096	35	0.0499	0.0084
ASV_11284	Warm North American Deser	asexual	Salisediminibacteriacea	0.0095	35	0.0564	0.0095
ASV_2726	Warm North American Deser	asexual	Bdellovibrionaceae	0.0094	35	0.0280	0.0047
ASV_2819	Warm North American Deser	asexual	Micropepsaceae	0.0088	35	0.0518	0.0088
ASV_740	Warm North American Deser	asexual	NA	0.0086	35	0.0283	0.0048
ASV_1694	Warm North American Deser	asexual	Marinococcaceae	0.0082	35	0.0487	0.0082
ASV_753	Warm North American Deser	asexual	[Clostridium] methylpen	0.0079	35	0.0266	0.0045
ASV_3442	Warm North American Deser	asexual	NA	0.0076	35	0.0263	0.0045
ASV_11956	Warm North American Deser	asexual	NA	0.0076	35	0.0451	0.0076
ASV_3660	Warm North American Deser	asexual	Paracaedibacteraceae	0.0069	35	0.0407	0.0069

ASV_4655	Warm North American Deser	asexual	Iamiaceae	0.0067	35	0.0181	0.0031
ASV_23	Warm North American Deser	asexual	Diplorickettsiaceae	0.0064	35	0.0238	0.0040
ASV_4291	Warm North American Deser	asexual	NA	0.0063	35	0.0373	0.0063
ASV_4747	Warm North American Deser	asexual	Solirubrobacteraceae	0.0058	35	0.0158	0.0027
ASV_3419	Warm North American Deser	asexual	Dysgonomonadaceae	0.0057	35	0.0339	0.0057
ASV_9364	Warm North American Deser	asexual	Micrococcales Incertae	0.0057	35	0.0339	0.0057
ASV_8572	Warm North American Deser	asexual	Nocardiopsaceae	0.0051	35	0.0303	0.0051
ASV_481	Warm North American Deser	asexual	Oxalobacteraceae	0.0050	35	0.0195	0.0033
ASV_7906	Warm North American Deser	asexual	LWQ8	0.0044	35	0.0186	0.0031
ASV_5504	Warm North American Deser	asexual	Alicyclobacillaceae	0.0043	35	0.0193	0.0033
ASV_2156	Warm North American Deser	asexual	Hyphomicrobiaceae	0.0043	35	0.0190	0.0032
ASV_2367	Warm North American Deser	asexual	Abditibacteriaceae	0.0041	35	0.0171	0.0029
ASV_1563	Warm North American Deser	asexual	Erysipelatoclostridiacea	0.0037	35	0.0160	0.0027
ASV_2506	Warm North American Deser	asexual	Acidothermaceae	0.0036	35	0.0158	0.0027
ASV_1501	Warm North American Deser	asexual	Sanguibacteraceae	0.0035	35	0.0127	0.0022
ASV_1308	Warm North American Deser	asexual	Desulfotomaculaceae	0.0033	35	0.0197	0.0033
ASV_1325	Warm North American Deser	asexual	Acidobacteriaceae (Sub	0.0033	35	0.0194	0.0033
ASV_1340	Warm North American Deser	asexual	Microtrichaceae	0.0032	35	0.0127	0.0021
ASV_9161	Warm North American Deser	asexual	Legionellaceae	0.0030	35	0.0131	0.0022
ASV_1096	Warm North American Deser	asexual	UCG-010	0.0030	35	0.0126	0.0021
ASV_6395	Warm North American Deser	asexual	Campylobacteraceae	0.0030	35	0.0178	0.0030
ASV_1571	Warm North American Deser	asexual	NA	0.0030	35	0.0125	0.0021
ASV_1686	Warm North American Deser	asexual	Anaeromyxobacteracea	0.0030	35	0.0175	0.0030
ASV_8496	Warm North American Deser	asexual	NA	0.0030	35	0.0125	0.0021
ASV_4673	Warm North American Deser	asexual	NA	0.0029	35	0.0119	0.0020
ASV_758	Warm North American Deser	asexual	Coriobacteriales Incerta	0.0029	35	0.0115	0.0019
ASV_3726	Warm North American Deser	asexual	Rhodothermaceae	0.0027	35	0.0096	0.0016
ASV_2133	Warm North American Deser	asexual	Nitrospiraceae	0.0026	35	0.0088	0.0015
ASV_4700	Warm North American Deser	asexual	Reyranellaceae	0.0026	35	0.0115	0.0020
ASV_12229	Warm North American Deser	asexual	NA	0.0024	35	0.0143	0.0024
ASV_11270	Warm North American Deser	asexual	Caedibacteraceae	0.0024	35	0.0142	0.0024
ASV_8486	Warm North American Deser	asexual	Entotheonellaceae	0.0024	35	0.0140	0.0024

ASV_7145	Warm North American Deser	asexual	Haliangiaceae	0.0021	35	0.0064	0.0011
ASV_9488	Warm North American Deser	asexual	NA	0.0021	35	0.0098	0.0017
ASV_2996	Warm North American Deser	asexual	Nitrosococcaceae	0.0021	35	0.0088	0.0015
ASV_3781	Warm North American Deser	asexual	Coleofasciculaceae	0.0021	35	0.0088	0.0015
ASV_2211	Warm North American Deser	asexual	NA	0.0020	35	0.0118	0.0020
ASV_11365	Warm North American Deser	asexual	SM2D12	0.0019	35	0.0113	0.0019
ASV_5250	Warm North American Deser	asexual	WD2101 soil group	0.0019	35	0.0063	0.0011
ASV_1996	Warm North American Deser	asexual	Thermincolaceae	0.0018	35	0.0105	0.0018
ASV_4124	Warm North American Deser	asexual	Leptotrichiaceae	0.0018	35	0.0084	0.0014
ASV_13614	Warm North American Deser	asexual	Wohlfahrtiimonadaceae	0.0017	35	0.0074	0.0012
ASV_2959	Warm North American Deser	asexual	Phaselicystidaceae	0.0017	35	0.0072	0.0012
ASV_8455	Warm North American Deser	asexual	NA	0.0016	35	0.0094	0.0016
ASV_5631	Warm North American Deser	asexual	Sporomusaceae	0.0015	35	0.0090	0.0015
ASV_3453	Warm North American Deser	asexual	Streptococcaceae	0.0015	35	0.0051	0.0009
ASV_13085	Warm North American Deser	asexual	NA	0.0014	35	0.0059	0.0010
ASV_3627	Warm North American Deser	asexual	Ethanoligenenaceae	0.0014	35	0.0047	0.0008
ASV_5396	Warm North American Deser	asexual	Caloramatoraceae	0.0014	35	0.0082	0.0014
ASV_4284	Warm North American Deser	asexual	Ardenticatenaceae	0.0014	35	0.0057	0.0010
ASV_586	Warm North American Deser	asexual	Saccharimonadaceae	0.0014	35	0.0057	0.0010
ASV_8058	Warm North American Deser	asexual	NA	0.0014	35	0.0080	0.0014
ASV_6978	Warm North American Deser	asexual	Defluviicoccaceae	0.0013	35	0.0077	0.0013
ASV_13739	Warm North American Deser	asexual	Koribacteraceae	0.0013	35	0.0076	0.0013
ASV_14037	Warm North American Deser	asexual	Magnetospirillaceae	0.0012	35	0.0071	0.0012
ASV_4558	Warm North American Deser	asexual	Myxococcaceae	0.0011	35	0.0047	0.0008
ASV_1864	Warm North American Deser	asexual	Anaerofustaceae	0.0011	35	0.0048	0.0008
ASV_6091	Warm North American Deser	asexual	JG30-KF-CM45	0.0011	35	0.0049	0.0008
ASV_3501	Warm North American Deser	asexual	NA	0.0011	35	0.0048	0.0008
ASV_3457	Warm North American Deser	asexual	Sedimentibacteraceae	0.0011	35	0.0045	0.0008
ASV_2892	Warm North American Deser	asexual	NA	0.0010	35	0.0061	0.0010
ASV_7464	Warm North American Deser	asexual	Blastocatellaceae	0.0010	35	0.0058	0.0010
ASV_9818	Warm North American Deser	asexual	67-14	0.0010	35	0.0037	0.0006
ASV_2172	Warm North American Deser	asexual	Hungateiclostridiaceae	0.0010	35	0.0040	0.0007

ASV_12650	Warm North American Deser	asexual	Morganellaceae	0.0010	35	0.0056	0.0010
ASV_11913	Warm North American Deser	asexual	NA	0.0009	35	0.0055	0.0009
ASV_14744	Warm North American Deser	asexual	Alcaligenaceae	0.0009	35	0.0040	0.0007
ASV_3114	Warm North American Deser	asexual	Solibacteraceae	0.0009	35	0.0055	0.0009
ASV_10336	Warm North American Deser	asexual	Xanthomonadaceae	0.0009	35	0.0054	0.0009
ASV_4184	Warm North American Deser	asexual	Methyloligellaceae	0.0009	35	0.0038	0.0006
ASV_7971	Warm North American Deser	asexual	Vicinamibacteraceae	0.0009	35	0.0035	0.0006
ASV_3356	Warm North American Deser	asexual	Caldalkalibacillaceae	0.0008	35	0.0049	0.0008
ASV_5924	Warm North American Deser	asexual	Exiguobacteraceae	0.0008	35	0.0049	0.0008
ASV_5486	Warm North American Deser	asexual	Microscillaceae	0.0008	35	0.0048	0.0008
ASV_4236	Warm North American Deser	asexual	Fibrobacteraceae	0.0008	35	0.0035	0.0006
ASV_13082	Warm North American Deser	asexual	NA	0.0008	35	0.0046	0.0008
ASV_12655	Warm North American Deser	asexual	Sporolactobacillaceae	0.0007	35	0.0043	0.0007
ASV_12532	Warm North American Deser	asexual	Bacteriovoracaceae	0.0007	35	0.0039	0.0007
ASV_6570	Warm North American Deser	asexual	Oligoflexaceae	0.0006	35	0.0038	0.0006
ASV_2522	Warm North American Deser	asexual	Beutenbergiaceae	0.0006	35	0.0038	0.0006
ASV_3972	Warm North American Deser	asexual	NA	0.0006	35	0.0037	0.0006
ASV_4085	Warm North American Deser	asexual	NA	0.0006	35	0.0036	0.0006
ASV_4894	Warm North American Deser	asexual	NA	0.0006	35	0.0035	0.0006
ASV_14757	Warm North American Deser	asexual	Gemmataceae	0.0006	35	0.0034	0.0006
ASV_7111	Warm North American Deser	asexual	Family III	0.0005	35	0.0032	0.0005
ASV_12860	Warm North American Deser	asexual	Tepidisphaeraceae	0.0005	35	0.0031	0.0005
ASV_13598	Warm North American Deser	asexual	NA	0.0005	35	0.0029	0.0005
ASV_13609	Warm North American Deser	asexual	Stappiaceae	0.0005	35	0.0029	0.0005
ASV_9871	Warm North American Deser	asexual	Nannocystaceae	0.0005	35	0.0029	0.0005
ASV_4645	Warm North American Deser	asexual	Dongiaceae	0.0005	35	0.0029	0.0005
ASV_5057	Warm North American Deser	asexual	Nitriliruptoraceae	0.0004	35	0.0025	0.0004
ASV_5059	Warm North American Deser	asexual	NA	0.0004	35	0.0025	0.0004
ASV_4297	Warm North American Deser	asexual	NA	0.0004	35	0.0024	0.0004
ASV_7025	Warm North American Deser	asexual	Cyclobacteriaceae	0.0004	35	0.0023	0.0004
ASV_3769	Warm North American Deser	asexual	Williamwhitmaniaceae	0.0004	35	0.0022	0.0004
ASV_1554	Warm North American Deser	asexual	Cryptosporangiaceae	0.0004	35	0.0021	0.0004

ASV_13581	Warm North American Deser	asexual	Terasakiellaceae	0.0004	35	0.0021	0.0004
ASV_14155	Warm North American Deser	asexual	NA	0.0003	35	0.0016	0.0003
ASV_5527	Warm North American Deser	asexual	Comamonadaceae	0.0002	35	0.0014	0.0002
ASV_7358	Warm North American Deser	asexual	Methylophilaceae	0.0002	35	0.0012	0.0002
ASV_8089	Warm North American Deser	asexual	Isosphaeraceae	0.0002	35	0.0010	0.0002
ASV_8715	Warm North American Deser	asexual	NA	0.0001	35	0.0009	0.0001
ASV_9043	Warm North American Deser	asexual	NA	0.0001	35	0.0008	0.0001
ASV_10319	Warm North American Deser	asexual	Neisseriaceae	0.0001	35	0.0005	0.0001
ASV_8458	Warm North American Deser	asexual	Burkholderiaceae	0.0001	35	0.0005	0.0001
ASV_7238	Warm North American Deser	asexual	AKIW781	0.0001	35	0.0004	0.0001
ASV_10092	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_10434	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_10439	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_10617	Warm North American Deser	asexual	Aerococcaceae	0.0000	35	0.0000	0.0000
ASV_10922	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_1107	Warm North American Deser	asexual	Muribaculaceae	0.0000	35	0.0000	0.0000
ASV_11196	Warm North American Deser	asexual	Vulgatibacteraceae	0.0000	35	0.0000	0.0000
ASV_11493	Warm North American Deser	asexual	Leptolyngbyaceae	0.0000	35	0.0000	0.0000
ASV_11494	Warm North American Deser	asexual	Magnetospiraceae	0.0000	35	0.0000	0.0000
ASV_11504	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_11538	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_11541	Warm North American Deser	asexual	Crocinitomicaceae	0.0000	35	0.0000	0.0000
ASV_11608	Warm North American Deser	asexual	FFCH9454	0.0000	35	0.0000	0.0000
ASV_11668	Warm North American Deser	asexual	Desulfobulbaceae	0.0000	35	0.0000	0.0000
ASV_11680	Warm North American Deser	asexual	Atopobiaceae	0.0000	35	0.0000	0.0000
ASV_11787	Warm North American Deser	asexual	Parachlamydiaceae	0.0000	35	0.0000	0.0000
ASV_11833	Warm North American Deser	asexual	Blrii41	0.0000	35	0.0000	0.0000
ASV_12171	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_12365	Warm North American Deser	asexual	Elusimicrobiaceae	0.0000	35	0.0000	0.0000
ASV_12449	Warm North American Deser	asexual	Steroidobacteraceae	0.0000	35	0.0000	0.0000
ASV_12453	Warm North American Deser	asexual	B1-7BS	0.0000	35	0.0000	0.0000
ASV_12467	Warm North American Deser	asexual	Coxiellaceae	0.0000	35	0.0000	0.0000

ASV_12517	Warm North American Deser	asexual	Aquaspirillaceae	0.0000	35	0.0000	0.0000
ASV_12595	Warm North American Deser	asexual	Demequinaceae	0.0000	35	0.0000	0.0000
ASV_12858	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_12984	Warm North American Deser	asexual	Acidimicrobiaceae	0.0000	35	0.0000	0.0000
ASV_13067	Warm North American Deser	asexual	AKAU3644	0.0000	35	0.0000	0.0000
ASV_13217	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_13265	Warm North American Deser	asexual	Veillonellaceae	0.0000	35	0.0000	0.0000
ASV_13268	Warm North American Deser	asexual	Aeromonadaceae	0.0000	35	0.0000	0.0000
ASV_13269	Warm North American Deser	asexual	Prolixibacteraceae	0.0000	35	0.0000	0.0000
ASV_13301	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_13305	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_13328	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_13329	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_13344	Warm North American Deser	asexual	vadinHA21	0.0000	35	0.0000	0.0000
ASV_13507	Warm North American Deser	asexual	Mycoplasmataceae	0.0000	35	0.0000	0.0000
ASV_13511	Warm North American Deser	asexual	Methylophagaceae	0.0000	35	0.0000	0.0000
ASV_13670	Warm North American Deser	asexual	Phycisphaeraceae	0.0000	35	0.0000	0.0000
ASV_13753	Warm North American Deser	asexual	Yersiniaceae	0.0000	35	0.0000	0.0000
ASV_13789	Warm North American Deser	asexual	Zavarziniaceae	0.0000	35	0.0000	0.0000
ASV_13922	Warm North American Deser	asexual	Thermoanaerobaculace	0.0000	35	0.0000	0.0000
ASV_13957	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_13965	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_14007	Warm North American Deser	asexual	Rhodanobacteraceae	0.0000	35	0.0000	0.0000
ASV_14123	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_14142	Warm North American Deser	asexual	Syntrophomonadaceae	0.0000	35	0.0000	0.0000
ASV_14225	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_14349	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_14535	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_152	Warm North American Deser	asexual	3M1PL1-52 termite gro	0.0000	35	0.0000	0.0000
ASV_1605	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_2624	Warm North American Deser	asexual	Unknown Family	0.0000	35	0.0000	0.0000
ASV_2687	Warm North American Deser	asexual	Unknown Family	0.0000	35	0.0000	0.0000

ASV_2986	Warm North American Deser	asexual	Actinospicaceae	0.0000	35	0.0000	0.0000
ASV_3064	Warm North American Deser	asexual	Paludibacteraceae	0.0000	35	0.0000	0.0000
ASV_3179	Warm North American Deser	asexual	Sulfurospirillaceae	0.0000	35	0.0000	0.0000
ASV_3410	Warm North American Deser	asexual	Selenomonadaceae	0.0000	35	0.0000	0.0000
ASV_3510	Warm North American Deser	asexual	A0839	0.0000	35	0.0000	0.0000
ASV_3519	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_3549	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_3766	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_4022	Warm North American Deser	asexual	Pseudomonadaceae	0.0000	35	0.0000	0.0000
ASV_4224	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_4227	Warm North American Deser	asexual	Halomonadaceae	0.0000	35	0.0000	0.0000
ASV_4341	Warm North American Deser	asexual	Simkaniaceae	0.0000	35	0.0000	0.0000
ASV_4399	Warm North American Deser	asexual	Anaplasmataceae	0.0000	35	0.0000	0.0000
ASV_4602	Warm North American Deser	asexual	Lactobacillaceae	0.0000	35	0.0000	0.0000
ASV_4929	Warm North American Deser	asexual	Erysipelotrichaceae	0.0000	35	0.0000	0.0000
ASV_4934	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_5102	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_5152	Warm North American Deser	asexual	Rickettsiaceae	0.0000	35	0.0000	0.0000
ASV_5154	Warm North American Deser	asexual	KF-JG30-B3	0.0000	35	0.0000	0.0000
ASV_5177	Warm North American Deser	asexual	Candidatus Jidaibacter	0.0000	35	0.0000	0.0000
ASV_5248	Warm North American Deser	asexual	Phormidiaceae	0.0000	35	0.0000	0.0000
ASV_5301	Warm North American Deser	asexual	Glycomycetaceae	0.0000	35	0.0000	0.0000
ASV_5314	Warm North American Deser	asexual	Marinilabiliaceae	0.0000	35	0.0000	0.0000
ASV_5389	Warm North American Deser	asexual	Desulfotomaculales Inc	0.0000	35	0.0000	0.0000
ASV_5638	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_5681	Warm North American Deser	asexual	Rhodospirillaceae	0.0000	35	0.0000	0.0000
ASV_5823	Warm North American Deser	asexual	Competibacteraceae	0.0000	35	0.0000	0.0000
ASV_5887	Warm North American Deser	asexual	Budviciaceae	0.0000	35	0.0000	0.0000
ASV_5915	Warm North American Deser	asexual	env.OPS 17	0.0000	35	0.0000	0.0000
ASV_6102	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_6172	Warm North American Deser	asexual	Inquilinaceae	0.0000	35	0.0000	0.0000
ASV_6308	Warm North American Deser	asexual	Barnesiellaceae	0.0000	35	0.0000	0.0000

ASV_6394	Warm North American Deser	asexual	Chroococcidiopsaceae	0.0000	35	0.0000	0.0000
ASV_6583	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_6643	Warm North American Deser	asexual	Gemellaceae	0.0000	35	0.0000	0.0000
ASV_6732	Warm North American Deser	asexual	Hyphomonadaceae	0.0000	35	0.0000	0.0000
ASV_685	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_7023	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_7083	Warm North American Deser	asexual	Synergistaceae	0.0000	35	0.0000	0.0000
ASV_7107	Warm North American Deser	asexual	Bogoriellaceae	0.0000	35	0.0000	0.0000
ASV_711	Warm North American Deser	asexual	Pleomorphomonadacea	0.0000	35	0.0000	0.0000
ASV_7459	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_7490	Warm North American Deser	asexual	COB P4-1 termite grou	0.0000	35	0.0000	0.0000
ASV_7533	Warm North American Deser	asexual	Saprospiraceae	0.0000	35	0.0000	0.0000
ASV_7766	Warm North American Deser	asexual	AKYH767	0.0000	35	0.0000	0.0000
ASV_7838	Warm North American Deser	asexual	Sulfuricellaceae	0.0000	35	0.0000	0.0000
ASV_7869	Warm North American Deser	asexual	Silvanigrellaceae	0.0000	35	0.0000	0.0000
ASV_7964	Warm North American Deser	asexual	AKYG1722	0.0000	35	0.0000	0.0000
ASV_8060	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_8560	Warm North American Deser	asexual	Endomicrobiaceae	0.0000	35	0.0000	0.0000
ASV_8883	Warm North American Deser	asexual	Nitrosomonadaceae	0.0000	35	0.0000	0.0000
ASV_8903	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_9092	Warm North American Deser	asexual	Rs-E47 termite group	0.0000	35	0.0000	0.0000
ASV_9144	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_9242	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_9379	Warm North American Deser	asexual	Pasteurellaceae	0.0000	35	0.0000	0.0000
ASV_9469	Warm North American Deser	asexual	Herpetosiphonaceae	0.0000	35	0.0000	0.0000
ASV_9515	Warm North American Deser	asexual	Rhodomicrobiaceae	0.0000	35	0.0000	0.0000
ASV_9517	Warm North American Deser	asexual	Chloroflexaceae	0.0000	35	0.0000	0.0000
ASV_9672	Warm North American Deser	asexual	Methylopilaceae	0.0000	35	0.0000	0.0000
ASV_9715	Warm North American Deser	asexual	Desulfitobacteriaceae	0.0000	35	0.0000	0.0000
ASV_9797	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_9810	Warm North American Deser	asexual	Trueperaceae	0.0000	35	0.0000	0.0000
ASV_9813	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000

ASV_9879	Warm North American Deser	asexual	NA	0.0000	35	0.0000	0.0000
ASV_9931	Warm North American Deser	asexual	Caldilineaceae	0.0000	35	0.0000	0.0000
ASV_1	Tamaulipas - Texas Semiarid	sexual	Dietziaceae	40.3681	8	27.1715	9.6066
ASV_8	Tamaulipas - Texas Semiarid	sexual	Brevibacteriaceae	15.0514	8	12.4277	4.3938
ASV_12	Tamaulipas - Texas Semiarid	sexual	Dermabacteraceae	11.2961	8	10.2301	3.6169
ASV_6	Tamaulipas - Texas Semiarid	sexual	Corynebacteriaceae	11.0106	8	7.4141	2.6213
ASV_4	Tamaulipas - Texas Semiarid	sexual	Micrococcacea	10.1626	8	7.6597	2.7081
ASV_21	Tamaulipas - Texas Semiarid	sexual	Intrasporangiaceae	4.1243	8	4.7150	1.6670
ASV_97	Tamaulipas - Texas Semiarid	sexual	Beijerinckiaceae	1.3918	8	2.0646	0.7299
ASV_69	Tamaulipas - Texas Semiarid	sexual	Geodermatophilaceae	0.8856	8	1.2481	0.4413
ASV_162	Tamaulipas - Texas Semiarid	sexual	Sphingomonadaceae	0.7449	8	1.0038	0.3549
ASV_7	Tamaulipas - Texas Semiarid	sexual	Lachnospiraceae	0.3730	8	0.7767	0.2746
ASV_18	Tamaulipas - Texas Semiarid	sexual	Rhodobacteraceae	0.3519	8	0.5395	0.1907
ASV_153	Tamaulipas - Texas Semiarid	sexual	Pseudonocardiaceae	0.3478	8	0.5837	0.2064
ASV_20	Tamaulipas - Texas Semiarid	sexual	Nocardioidaceae	0.3418	8	0.3797	0.1342
ASV_24	Tamaulipas - Texas Semiarid	sexual	Micrococcaceae	0.2918	8	0.5972	0.2112
ASV_538	Tamaulipas - Texas Semiarid	sexual	Caulobacteraceae	0.2842	8	0.6721	0.2376
ASV_139	Tamaulipas - Texas Semiarid	sexual	Acetobacteraceae	0.1897	8	0.2768	0.0979
ASV_57	Tamaulipas - Texas Semiarid	sexual	Devosiaceae	0.1785	8	0.4159	0.1470
ASV_552	Tamaulipas - Texas Semiarid	sexual	Propionibacteriaceae	0.1611	8	0.1799	0.0636
ASV_49	Tamaulipas - Texas Semiarid	sexual	Microbacteriaceae	0.1498	8	0.2416	0.0854
ASV_404	Tamaulipas - Texas Semiarid	sexual	Kineosporiaceae	0.1365	8	0.2317	0.0819
ASV_283	Tamaulipas - Texas Semiarid	sexual	Micromonosporaceae	0.1299	8	0.1927	0.0681
ASV_442	Tamaulipas - Texas Semiarid	sexual	Rhizobiaceae	0.1212	8	0.2451	0.0866
ASV_73	Tamaulipas - Texas Semiarid	sexual	Cellulomonadaceae	0.1154	8	0.2481	0.0877
ASV_22	Tamaulipas - Texas Semiarid	sexual	Ruminococcaceae	0.1143	8	0.3045	0.1077
ASV_729	Tamaulipas - Texas Semiarid	sexual	Longimicrobiaceae	0.1116	8	0.2115	0.0748
ASV_483	Tamaulipas - Texas Semiarid	sexual	Hymenobacteraceae	0.1087	8	0.1912	0.0676
ASV_807	Tamaulipas - Texas Semiarid	sexual	Gemmatimonadaceae	0.1003	8	0.1820	0.0643
ASV_121	Tamaulipas - Texas Semiarid	sexual	NA	0.0974	8	0.1836	0.0649
ASV_11	Tamaulipas - Texas Semiarid	sexual	Oscillospiraceae	0.0759	8	0.1476	0.0522
ASV_3	Tamaulipas - Texas Semiarid	sexual	Helicobacteraceae	0.0699	8	0.0967	0.0342

ASV_142	Tamaulipas - Texas Semiarid	sexual	Streptomycetaceae	0.0554	8	0.0996	0.0352
ASV_1201	Tamaulipas - Texas Semiarid	sexual	Sphingobacteriaceae	0.0447	8	0.1006	0.0356
ASV_660	Tamaulipas - Texas Semiarid	sexual	Moraxellaceae	0.0428	8	0.1144	0.0405
ASV_512	Tamaulipas - Texas Semiarid	sexual	Geminicoccaceae	0.0407	8	0.0756	0.0267
ASV_410	Tamaulipas - Texas Semiarid	sexual	Ilumatobacteraceae	0.0383	8	0.0541	0.0191
ASV_815	Tamaulipas - Texas Semiarid	sexual	NA	0.0374	8	0.0612	0.0216
ASV_347	Tamaulipas - Texas Semiarid	sexual	Azospirillaceae	0.0369	8	0.0302	0.0107
ASV_2550	Tamaulipas - Texas Semiarid	sexual	Spirosomaceae	0.0354	8	0.0689	0.0244
ASV_1080	Tamaulipas - Texas Semiarid	sexual	NA	0.0335	8	0.0642	0.0227
ASV_1096	Tamaulipas - Texas Semiarid	sexual	UCG-010	0.0258	8	0.0730	0.0258
ASV_1904	Tamaulipas - Texas Semiarid	sexual	Cytophagaceae	0.0258	8	0.0584	0.0207
ASV_6397	Tamaulipas - Texas Semiarid	sexual	NA	0.0242	8	0.0503	0.0178
ASV_728	Tamaulipas - Texas Semiarid	sexual	Xanthobacteraceae	0.0224	8	0.0492	0.0174
ASV_439	Tamaulipas - Texas Semiarid	sexual	Polyangiaceae	0.0212	8	0.0600	0.0212
ASV_1445	Tamaulipas - Texas Semiarid	sexual	NA	0.0207	8	0.0392	0.0139
ASV_309	Tamaulipas - Texas Semiarid	sexual	Family XI	0.0198	8	0.0367	0.0130
ASV_1974	Tamaulipas - Texas Semiarid	sexual	NA	0.0194	8	0.0405	0.0143
ASV_624	Tamaulipas - Texas Semiarid	sexual	Bryobacteraceae	0.0191	8	0.0330	0.0117
ASV_1285	Tamaulipas - Texas Semiarid	sexual	NA	0.0185	8	0.0524	0.0185
ASV_5486	Tamaulipas - Texas Semiarid	sexual	Microscillaceae	0.0180	8	0.0508	0.0180
ASV_5152	Tamaulipas - Texas Semiarid	sexual	Rickettsiaceae	0.0174	8	0.0492	0.0174
ASV_456	Tamaulipas - Texas Semiarid	sexual	Promicromonosporacea	0.0173	8	0.0407	0.0144
ASV_1150	Tamaulipas - Texas Semiarid	sexual	NA	0.0165	8	0.0241	0.0085
ASV_468	Tamaulipas - Texas Semiarid	sexual	Weeksellaceae	0.0151	8	0.0292	0.0103
ASV_2133	Tamaulipas - Texas Semiarid	sexual	Nitrospiraceae	0.0140	8	0.0397	0.0140
ASV_979	Tamaulipas - Texas Semiarid	sexual	Nakamurellaceae	0.0140	8	0.0397	0.0140
ASV_29	Tamaulipas - Texas Semiarid	sexual	[Eubacterium] coprosta	0.0140	8	0.0281	0.0099
ASV_1246	Tamaulipas - Texas Semiarid	sexual	NA	0.0139	8	0.0326	0.0115
ASV_6394	Tamaulipas - Texas Semiarid	sexual	Chroococcidiopsaceae	0.0135	8	0.0381	0.0135
ASV_5915	Tamaulipas - Texas Semiarid	sexual	env.OPS 17	0.0125	8	0.0238	0.0084
ASV_1162	Tamaulipas - Texas Semiarid	sexual	Puniceispirillales Incerta	0.0124	8	0.0195	0.0069
ASV_740	Tamaulipas - Texas Semiarid	sexual	NA	0.0118	8	0.0333	0.0118

ASV_941	Tamaulipas - Texas Semiarid	sexual	Staphylococcaceae	0.0118	8	0.0241	0.0085
ASV_2445	Tamaulipas - Texas Semiarid	sexual	Streptosporangiales Inc	0.0112	8	0.0232	0.0082
ASV_420	Tamaulipas - Texas Semiarid	sexual	Enterobacteriaceae	0.0108	8	0.0158	0.0056
ASV_5154	Tamaulipas - Texas Semiarid	sexual	KF-JG30-B3	0.0108	8	0.0305	0.0108
ASV_6732	Tamaulipas - Texas Semiarid	sexual	Hyphomonadaceae	0.0107	8	0.0302	0.0107
ASV_10	Tamaulipas - Texas Semiarid	sexual	Clostridiaceae	0.0106	8	0.0206	0.0073
ASV_3781	Tamaulipas - Texas Semiarid	sexual	Coleofasciculaceae	0.0097	8	0.0236	0.0083
ASV_126	Tamaulipas - Texas Semiarid	sexual	NA	0.0095	8	0.0270	0.0095
ASV_91	Tamaulipas - Texas Semiarid	sexual	Peptococcaceae	0.0095	8	0.0270	0.0095
ASV_2554	Tamaulipas - Texas Semiarid	sexual	Fusobacteriaceae	0.0091	8	0.0258	0.0091
ASV_4645	Tamaulipas - Texas Semiarid	sexual	Dongiaceae	0.0090	8	0.0256	0.0090
ASV_1110	Tamaulipas - Texas Semiarid	sexual	Mycobacteriaceae	0.0088	8	0.0174	0.0061
ASV_3376	Tamaulipas - Texas Semiarid	sexual	Sandaracinaceae	0.0088	8	0.0205	0.0072
ASV_362	Tamaulipas - Texas Semiarid	sexual	Thermomonosporacea	0.0085	8	0.0127	0.0045
ASV_2306	Tamaulipas - Texas Semiarid	sexual	NA	0.0084	8	0.0158	0.0056
ASV_2156	Tamaulipas - Texas Semiarid	sexual	Hyphomicrobiaceae	0.0083	8	0.0235	0.0083
ASV_345	Tamaulipas - Texas Semiarid	sexual	Dermacoccaceae	0.0083	8	0.0235	0.0083
ASV_2687	Tamaulipas - Texas Semiarid	sexual	Unknown Family	0.0082	8	0.0165	0.0058
ASV_3510	Tamaulipas - Texas Semiarid	sexual	A0839	0.0079	8	0.0222	0.0079
ASV_4086	Tamaulipas - Texas Semiarid	sexual	Nostocaceae	0.0075	8	0.0211	0.0075
ASV_867	Tamaulipas - Texas Semiarid	sexual	Gaiellaceae	0.0073	8	0.0164	0.0058
ASV_1664	Tamaulipas - Texas Semiarid	sexual	NA	0.0071	8	0.0202	0.0071
ASV_474	Tamaulipas - Texas Semiarid	sexual	Chitinophagaceae	0.0067	8	0.0191	0.0067
ASV_163	Tamaulipas - Texas Semiarid	sexual	Monoglobaceae	0.0067	8	0.0134	0.0047
ASV_9813	Tamaulipas - Texas Semiarid	sexual	NA	0.0066	8	0.0188	0.0066
ASV_3972	Tamaulipas - Texas Semiarid	sexual	NA	0.0058	8	0.0164	0.0058
ASV_96	Tamaulipas - Texas Semiarid	sexual	Christensenellaceae	0.0056	8	0.0159	0.0056
ASV_1813	Tamaulipas - Texas Semiarid	sexual	D05-2	0.0052	8	0.0147	0.0052
ASV_2146	Tamaulipas - Texas Semiarid	sexual	NA	0.0051	8	0.0143	0.0051
ASV_86	Tamaulipas - Texas Semiarid	sexual	Anaerovoracaceae	0.0045	8	0.0127	0.0045
ASV_3660	Tamaulipas - Texas Semiarid	sexual	Paracaedibacteraceae	0.0045	8	0.0126	0.0045
ASV_2726	Tamaulipas - Texas Semiarid	sexual	Bdellovibrionaceae	0.0042	8	0.0083	0.0029

ASV_5504	Tamaulipas - Texas Semiarid	sexual	Alicyclobacillaceae	0.0042	8	0.0117	0.0042
ASV_7238	Tamaulipas - Texas Semiarid	sexual	AKIW781	0.0042	8	0.0117	0.0042
ASV_1275	Tamaulipas - Texas Semiarid	sexual	Actinomycetaceae	0.0039	8	0.0111	0.0039
ASV_8588	Tamaulipas - Texas Semiarid	sexual	Paenibacillaceae	0.0035	8	0.0098	0.0035
ASV_2172	Tamaulipas - Texas Semiarid	sexual	Hungateiclostridiaceae	0.0034	8	0.0095	0.0034
ASV_12532	Tamaulipas - Texas Semiarid	sexual	Bacteriovoracaceae	0.0033	8	0.0094	0.0033
ASV_3144	Tamaulipas - Texas Semiarid	sexual	Roseiflexaceae	0.0033	8	0.0094	0.0033
ASV_4558	Tamaulipas - Texas Semiarid	sexual	Myxococcaceae	0.0033	8	0.0094	0.0033
ASV_5301	Tamaulipas - Texas Semiarid	sexual	Glycomycetaceae	0.0033	8	0.0094	0.0033
ASV_129	Tamaulipas - Texas Semiarid	sexual	Peptostreptococcacea	0.0030	8	0.0084	0.0030
ASV_32	Tamaulipas - Texas Semiarid	sexual	Bacteroidaceae	0.0030	8	0.0084	0.0030
ASV_38	Tamaulipas - Texas Semiarid	sexual	Tannerellaceae	0.0030	8	0.0084	0.0030
ASV_405	Tamaulipas - Texas Semiarid	sexual	NA	0.0030	8	0.0084	0.0030
ASV_98	Tamaulipas - Texas Semiarid	sexual	Desulfovibrionaceae	0.0030	8	0.0084	0.0030
ASV_11270	Tamaulipas - Texas Semiarid	sexual	Caedibacteraceae	0.0028	8	0.0079	0.0028
ASV_1325	Tamaulipas - Texas Semiarid	sexual	Acidobacteriaceae (Su	0.0028	8	0.0079	0.0028
ASV_2624	Tamaulipas - Texas Semiarid	sexual	Unknown Family	0.0025	8	0.0070	0.0025
ASV_3766	Tamaulipas - Texas Semiarid	sexual	NA	0.0025	8	0.0070	0.0025
ASV_2367	Tamaulipas - Texas Semiarid	sexual	Abditibacteriaceae	0.0022	8	0.0064	0.0022
ASV_2482	Tamaulipas - Texas Semiarid	sexual	NA	0.0022	8	0.0064	0.0022
ASV_3064	Tamaulipas - Texas Semiarid	sexual	Paludibacteraceae	0.0022	8	0.0064	0.0022
ASV_5527	Tamaulipas - Texas Semiarid	sexual	Comamonadaceae	0.0022	8	0.0063	0.0022
ASV_817	Tamaulipas - Texas Semiarid	sexual	Porphyromonadaceae	0.0021	8	0.0059	0.0021
ASV_3155	Tamaulipas - Texas Semiarid	sexual	NA	0.0019	8	0.0055	0.0019
ASV_4655	Tamaulipas - Texas Semiarid	sexual	Iamiaceae	0.0017	8	0.0048	0.0017
ASV_6395	Tamaulipas - Texas Semiarid	sexual	Campylobacteraceae	0.0017	8	0.0048	0.0017
ASV_9810	Tamaulipas - Texas Semiarid	sexual	Trueperaceae	0.0017	8	0.0048	0.0017
ASV_2450	Tamaulipas - Texas Semiarid	sexual	Prevotellaceae	0.0017	8	0.0047	0.0017
ASV_3501	Tamaulipas - Texas Semiarid	sexual	NA	0.0015	8	0.0042	0.0015
ASV_3419	Tamaulipas - Texas Semiarid	sexual	Dysgonomonadaceae	0.0011	8	0.0032	0.0011
ASV_4747	Tamaulipas - Texas Semiarid	sexual	Solirubrobacteraceae	0.0011	8	0.0032	0.0011
ASV_4894	Tamaulipas - Texas Semiarid	sexual	NA	0.0011	8	0.0032	0.0011

ASV_5248	Tamaulipas - Texas Semiarid	sexual	Phormidiaceae	0.0011	8	0.0032	0.0011
ASV_7145	Tamaulipas - Texas Semiarid	sexual	Haliangiaceae	0.0011	8	0.0032	0.0011
ASV_10092	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_10319	Tamaulipas - Texas Semiarid	sexual	Neisseriaceae	0.0000	8	0.0000	0.0000
ASV_10336	Tamaulipas - Texas Semiarid	sexual	Xanthomonadaceae	0.0000	8	0.0000	0.0000
ASV_10434	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_10439	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_10617	Tamaulipas - Texas Semiarid	sexual	Aerococcaceae	0.0000	8	0.0000	0.0000
ASV_10922	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_1107	Tamaulipas - Texas Semiarid	sexual	Muribaculaceae	0.0000	8	0.0000	0.0000
ASV_11196	Tamaulipas - Texas Semiarid	sexual	Vulgatibacteraceae	0.0000	8	0.0000	0.0000
ASV_11284	Tamaulipas - Texas Semiarid	sexual	Salisediminibacteriacea	0.0000	8	0.0000	0.0000
ASV_11365	Tamaulipas - Texas Semiarid	sexual	SM2D12	0.0000	8	0.0000	0.0000
ASV_11493	Tamaulipas - Texas Semiarid	sexual	Leptolyngbyaceae	0.0000	8	0.0000	0.0000
ASV_11494	Tamaulipas - Texas Semiarid	sexual	Magnetospiraceae	0.0000	8	0.0000	0.0000
ASV_11504	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_11538	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_11541	Tamaulipas - Texas Semiarid	sexual	Crocinitomicaceae	0.0000	8	0.0000	0.0000
ASV_11608	Tamaulipas - Texas Semiarid	sexual	FFCH9454	0.0000	8	0.0000	0.0000
ASV_11668	Tamaulipas - Texas Semiarid	sexual	Desulfobulbaceae	0.0000	8	0.0000	0.0000
ASV_11680	Tamaulipas - Texas Semiarid	sexual	Atopobiaceae	0.0000	8	0.0000	0.0000
ASV_117	Tamaulipas - Texas Semiarid	sexual	Marinifilaceae	0.0000	8	0.0000	0.0000
ASV_11787	Tamaulipas - Texas Semiarid	sexual	Parachlamydiaceae	0.0000	8	0.0000	0.0000
ASV_11833	Tamaulipas - Texas Semiarid	sexual	BIrii41	0.0000	8	0.0000	0.0000
ASV_11913	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_11956	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_12171	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_12229	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_12365	Tamaulipas - Texas Semiarid	sexual	Elusimicrobiaceae	0.0000	8	0.0000	0.0000
ASV_12449	Tamaulipas - Texas Semiarid	sexual	Steroidobacteraceae	0.0000	8	0.0000	0.0000
ASV_12453	Tamaulipas - Texas Semiarid	sexual	B1-7BS	0.0000	8	0.0000	0.0000
ASV_12467	Tamaulipas - Texas Semiarid	sexual	Coxiellaceae	0.0000	8	0.0000	0.0000

ASV_12517	Tamaulipas - Texas Semiarid	sexual	Aquaspirillaceae	0.0000	8	0.0000	0.0000
ASV_12595	Tamaulipas - Texas Semiarid	sexual	Demequinaceae	0.0000	8	0.0000	0.0000
ASV_12650	Tamaulipas - Texas Semiarid	sexual	Morganellaceae	0.0000	8	0.0000	0.0000
ASV_12655	Tamaulipas - Texas Semiarid	sexual	Sporolactobacillaceae	0.0000	8	0.0000	0.0000
ASV_12858	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_12860	Tamaulipas - Texas Semiarid	sexual	Tepidisphaeraceae	0.0000	8	0.0000	0.0000
ASV_12984	Tamaulipas - Texas Semiarid	sexual	Acidimicrobiaceae	0.0000	8	0.0000	0.0000
ASV_13067	Tamaulipas - Texas Semiarid	sexual	AKAU3644	0.0000	8	0.0000	0.0000
ASV_1308	Tamaulipas - Texas Semiarid	sexual	Desulfotomaculaceae	0.0000	8	0.0000	0.0000
ASV_13082	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_13085	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_13217	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_13265	Tamaulipas - Texas Semiarid	sexual	Veillonellaceae	0.0000	8	0.0000	0.0000
ASV_13268	Tamaulipas - Texas Semiarid	sexual	Aeromonadaceae	0.0000	8	0.0000	0.0000
ASV_13269	Tamaulipas - Texas Semiarid	sexual	Prolixibacteraceae	0.0000	8	0.0000	0.0000
ASV_13301	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_13305	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_13328	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_13329	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_13344	Tamaulipas - Texas Semiarid	sexual	vadinHA21	0.0000	8	0.0000	0.0000
ASV_1340	Tamaulipas - Texas Semiarid	sexual	Microtrichaceae	0.0000	8	0.0000	0.0000
ASV_13507	Tamaulipas - Texas Semiarid	sexual	Mycoplasmataceae	0.0000	8	0.0000	0.0000
ASV_13511	Tamaulipas - Texas Semiarid	sexual	Methylophagaceae	0.0000	8	0.0000	0.0000
ASV_13581	Tamaulipas - Texas Semiarid	sexual	Terasakiellaceae	0.0000	8	0.0000	0.0000
ASV_13598	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_13609	Tamaulipas - Texas Semiarid	sexual	Stappiaceae	0.0000	8	0.0000	0.0000
ASV_13614	Tamaulipas - Texas Semiarid	sexual	Wohlfahrtiimonadaceae	0.0000	8	0.0000	0.0000
ASV_13670	Tamaulipas - Texas Semiarid	sexual	Phycisphaeraceae	0.0000	8	0.0000	0.0000
ASV_13739	Tamaulipas - Texas Semiarid	sexual	Koribacteraceae	0.0000	8	0.0000	0.0000
ASV_13753	Tamaulipas - Texas Semiarid	sexual	Yersiniaceae	0.0000	8	0.0000	0.0000
ASV_13789	Tamaulipas - Texas Semiarid	sexual	Zavarziniaceae	0.0000	8	0.0000	0.0000
ASV_13922	Tamaulipas - Texas Semiarid	sexual	Thermoanaerobaculace	0.0000	8	0.0000	0.0000

ASV_13957	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_13965	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_14007	Tamaulipas - Texas Semiarid	sexual	Rhodanobacteraceae	0.0000	8	0.0000	0.0000
ASV_14037	Tamaulipas - Texas Semiarid	sexual	Magnetospirillaceae	0.0000	8	0.0000	0.0000
ASV_14123	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_14142	Tamaulipas - Texas Semiarid	sexual	Syntrophomonadaceae	0.0000	8	0.0000	0.0000
ASV_14155	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_14225	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_14349	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_14535	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_14744	Tamaulipas - Texas Semiarid	sexual	Alcaligenaceae	0.0000	8	0.0000	0.0000
ASV_14757	Tamaulipas - Texas Semiarid	sexual	Gemmataceae	0.0000	8	0.0000	0.0000
ASV_1501	Tamaulipas - Texas Semiarid	sexual	Sanguibacteraceae	0.0000	8	0.0000	0.0000
ASV_152	Tamaulipas - Texas Semiarid	sexual	3M1PL1-52 termite gro	0.0000	8	0.0000	0.0000
ASV_1554	Tamaulipas - Texas Semiarid	sexual	Cryptosporangiaceae	0.0000	8	0.0000	0.0000
ASV_1563	Tamaulipas - Texas Semiarid	sexual	Erysipelatoclostridiacea	0.0000	8	0.0000	0.0000
ASV_1571	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_1575	Tamaulipas - Texas Semiarid	sexual	Defluviitaleaceae	0.0000	8	0.0000	0.0000
ASV_1605	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_161	Tamaulipas - Texas Semiarid	sexual	Bacillaceae	0.0000	8	0.0000	0.0000
ASV_166	Tamaulipas - Texas Semiarid	sexual	Tsukamurellaceae	0.0000	8	0.0000	0.0000
ASV_1686	Tamaulipas - Texas Semiarid	sexual	Anaeromyxobacteracea	0.0000	8	0.0000	0.0000
ASV_1694	Tamaulipas - Texas Semiarid	sexual	Marinococcaceae	0.0000	8	0.0000	0.0000
ASV_1715	Tamaulipas - Texas Semiarid	sexual	Eubacteriaceae	0.0000	8	0.0000	0.0000
ASV_1864	Tamaulipas - Texas Semiarid	sexual	Anaerofustaceae	0.0000	8	0.0000	0.0000
ASV_19	Tamaulipas - Texas Semiarid	sexual	Nocardiaceae	0.0000	8	0.0000	0.0000
ASV_1996	Tamaulipas - Texas Semiarid	sexual	Thermincolaceae	0.0000	8	0.0000	0.0000
ASV_2104	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_214	Tamaulipas - Texas Semiarid	sexual	Eggerthellaceae	0.0000	8	0.0000	0.0000
ASV_2211	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_23	Tamaulipas - Texas Semiarid	sexual	Diplorickettsiaceae	0.0000	8	0.0000	0.0000
ASV_2494	Tamaulipas - Texas Semiarid	sexual	Thermicanaceae	0.0000	8	0.0000	0.0000

ASV_250	Tamaulipas - Texas Semiarid	sexual	Butyricicoccaceae	0.0000	8	0.0000	0.0000
ASV_2506	Tamaulipas - Texas Semiarid	sexual	Acidothermaceae	0.0000	8	0.0000	0.0000
ASV_2522	Tamaulipas - Texas Semiarid	sexual	Beutenbergiaceae	0.0000	8	0.0000	0.0000
ASV_259	Tamaulipas - Texas Semiarid	sexual	Enterococcaceae	0.0000	8	0.0000	0.0000
ASV_2606	Tamaulipas - Texas Semiarid	sexual	Euzebyaceae	0.0000	8	0.0000	0.0000
ASV_2708	Tamaulipas - Texas Semiarid	sexual	Bifidobacteriaceae	0.0000	8	0.0000	0.0000
ASV_2819	Tamaulipas - Texas Semiarid	sexual	Micropepsaceae	0.0000	8	0.0000	0.0000
ASV_282	Tamaulipas - Texas Semiarid	sexual	Thermoactinomycetace	0.0000	8	0.0000	0.0000
ASV_2892	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_2959	Tamaulipas - Texas Semiarid	sexual	Phaselicystidaceae	0.0000	8	0.0000	0.0000
ASV_2986	Tamaulipas - Texas Semiarid	sexual	Actinospicaceae	0.0000	8	0.0000	0.0000
ASV_2996	Tamaulipas - Texas Semiarid	sexual	Nitrosococcaceae	0.0000	8	0.0000	0.0000
ASV_3114	Tamaulipas - Texas Semiarid	sexual	Solibacteraceae	0.0000	8	0.0000	0.0000
ASV_317	Tamaulipas - Texas Semiarid	sexual	Hafniaceae	0.0000	8	0.0000	0.0000
ASV_3179	Tamaulipas - Texas Semiarid	sexual	Sulfurospirillaceae	0.0000	8	0.0000	0.0000
ASV_3356	Tamaulipas - Texas Semiarid	sexual	Caldalkalibacillaceae	0.0000	8	0.0000	0.0000
ASV_3410	Tamaulipas - Texas Semiarid	sexual	Selenomonadaceae	0.0000	8	0.0000	0.0000
ASV_3442	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_3453	Tamaulipas - Texas Semiarid	sexual	Streptococcaceae	0.0000	8	0.0000	0.0000
ASV_3457	Tamaulipas - Texas Semiarid	sexual	Sedimentibacteraceae	0.0000	8	0.0000	0.0000
ASV_3519	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_3549	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_3627	Tamaulipas - Texas Semiarid	sexual	Ethanoligenenaceae	0.0000	8	0.0000	0.0000
ASV_3726	Tamaulipas - Texas Semiarid	sexual	Rhodothermaceae	0.0000	8	0.0000	0.0000
ASV_3769	Tamaulipas - Texas Semiarid	sexual	Williamwhitmaniaceae	0.0000	8	0.0000	0.0000
ASV_4022	Tamaulipas - Texas Semiarid	sexual	Pseudomonadaceae	0.0000	8	0.0000	0.0000
ASV_4085	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_4124	Tamaulipas - Texas Semiarid	sexual	Leptotrichiaceae	0.0000	8	0.0000	0.0000
ASV_417	Tamaulipas - Texas Semiarid	sexual	Streptosporangiaceae	0.0000	8	0.0000	0.0000
ASV_4184	Tamaulipas - Texas Semiarid	sexual	Methyloligellaceae	0.0000	8	0.0000	0.0000
ASV_4224	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_4227	Tamaulipas - Texas Semiarid	sexual	Halomonadaceae	0.0000	8	0.0000	0.0000

ASV_4236	Tamaulipas - Texas Semiarid	sexual	Fibrobacteraceae	0.0000	8	0.0000	0.0000
ASV_4284	Tamaulipas - Texas Semiarid	sexual	Ardenticatenaceae	0.0000	8	0.0000	0.0000
ASV_4291	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_4297	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_4341	Tamaulipas - Texas Semiarid	sexual	Simkaniaceae	0.0000	8	0.0000	0.0000
ASV_4399	Tamaulipas - Texas Semiarid	sexual	Anaplasmataceae	0.0000	8	0.0000	0.0000
ASV_44	Tamaulipas - Texas Semiarid	sexual	Rikenellaceae	0.0000	8	0.0000	0.0000
ASV_4602	Tamaulipas - Texas Semiarid	sexual	Lactobacillaceae	0.0000	8	0.0000	0.0000
ASV_4673	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_4700	Tamaulipas - Texas Semiarid	sexual	Reyranellaceae	0.0000	8	0.0000	0.0000
ASV_4785	Tamaulipas - Texas Semiarid	sexual	Oxobacteraceae	0.0000	8	0.0000	0.0000
ASV_481	Tamaulipas - Texas Semiarid	sexual	Oxalobacteraceae	0.0000	8	0.0000	0.0000
ASV_4929	Tamaulipas - Texas Semiarid	sexual	Erysipelotrichaceae	0.0000	8	0.0000	0.0000
ASV_493	Tamaulipas - Texas Semiarid	sexual	Frankiaceae	0.0000	8	0.0000	0.0000
ASV_4934	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_5057	Tamaulipas - Texas Semiarid	sexual	Nitriliruptoraceae	0.0000	8	0.0000	0.0000
ASV_5059	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_5102	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_5177	Tamaulipas - Texas Semiarid	sexual	Candidatus Jidaibacter	0.0000	8	0.0000	0.0000
ASV_5250	Tamaulipas - Texas Semiarid	sexual	WD2101 soil group	0.0000	8	0.0000	0.0000
ASV_5314	Tamaulipas - Texas Semiarid	sexual	Marinilabiliaceae	0.0000	8	0.0000	0.0000
ASV_5351	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_5389	Tamaulipas - Texas Semiarid	sexual	Desulfotomaculales Inc	0.0000	8	0.0000	0.0000
ASV_5396	Tamaulipas - Texas Semiarid	sexual	Caloramatoraceae	0.0000	8	0.0000	0.0000
ASV_5553	Tamaulipas - Texas Semiarid	sexual	Rhizobiales Incertae Se	0.0000	8	0.0000	0.0000
ASV_5631	Tamaulipas - Texas Semiarid	sexual	Sporomusaceae	0.0000	8	0.0000	0.0000
ASV_5638	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_5681	Tamaulipas - Texas Semiarid	sexual	Rhodospirillaceae	0.0000	8	0.0000	0.0000
ASV_571	Tamaulipas - Texas Semiarid	sexual	Flavobacteriaceae	0.0000	8	0.0000	0.0000
ASV_5823	Tamaulipas - Texas Semiarid	sexual	Competibacteraceae	0.0000	8	0.0000	0.0000
ASV_586	Tamaulipas - Texas Semiarid	sexual	Saccharimonadaceae	0.0000	8	0.0000	0.0000
ASV_5887	Tamaulipas - Texas Semiarid	sexual	Budviciaceae	0.0000	8	0.0000	0.0000

ASV_5924	Tamaulipas - Texas Semiarid	sexual	Exiguobacteraceae	0.0000	8	0.0000	0.0000
ASV_604	Tamaulipas - Texas Semiarid	sexual	Hydrogenoanaerobacte	0.0000	8	0.0000	0.0000
ASV_6091	Tamaulipas - Texas Semiarid	sexual	JG30-KF-CM45	0.0000	8	0.0000	0.0000
ASV_6102	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_6172	Tamaulipas - Texas Semiarid	sexual	Inquilinaceae	0.0000	8	0.0000	0.0000
ASV_621	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_6308	Tamaulipas - Texas Semiarid	sexual	Barnesiellaceae	0.0000	8	0.0000	0.0000
ASV_6560	Tamaulipas - Texas Semiarid	sexual	Rubrobacteriaceae	0.0000	8	0.0000	0.0000
ASV_6570	Tamaulipas - Texas Semiarid	sexual	Oligoflexaceae	0.0000	8	0.0000	0.0000
ASV_6583	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_6643	Tamaulipas - Texas Semiarid	sexual	Gemellaceae	0.0000	8	0.0000	0.0000
ASV_6794	Tamaulipas - Texas Semiarid	sexual	Carnobacteriaceae	0.0000	8	0.0000	0.0000
ASV_681	Tamaulipas - Texas Semiarid	sexual	Sporichthyaceae	0.0000	8	0.0000	0.0000
ASV_685	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_6978	Tamaulipas - Texas Semiarid	sexual	Defluviicoccaceae	0.0000	8	0.0000	0.0000
ASV_7023	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_7025	Tamaulipas - Texas Semiarid	sexual	Cyclobacteriaceae	0.0000	8	0.0000	0.0000
ASV_7083	Tamaulipas - Texas Semiarid	sexual	Synergistaceae	0.0000	8	0.0000	0.0000
ASV_7107	Tamaulipas - Texas Semiarid	sexual	Bogoriellaceae	0.0000	8	0.0000	0.0000
ASV_711	Tamaulipas - Texas Semiarid	sexual	Pleomorphomonadace	0.0000	8	0.0000	0.0000
ASV_7111	Tamaulipas - Texas Semiarid	sexual	Family III	0.0000	8	0.0000	0.0000
ASV_7146	Tamaulipas - Texas Semiarid	sexual	Planococcaceae	0.0000	8	0.0000	0.0000
ASV_7358	Tamaulipas - Texas Semiarid	sexual	Methylophilaceae	0.0000	8	0.0000	0.0000
ASV_7459	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_7464	Tamaulipas - Texas Semiarid	sexual	Blastocatellaceae	0.0000	8	0.0000	0.0000
ASV_7490	Tamaulipas - Texas Semiarid	sexual	COB P4-1 termite grou	0.0000	8	0.0000	0.0000
ASV_753	Tamaulipas - Texas Semiarid	sexual	[Clostridium] methylpen	0.0000	8	0.0000	0.0000
ASV_7533	Tamaulipas - Texas Semiarid	sexual	Saprospiraceae	0.0000	8	0.0000	0.0000
ASV_758	Tamaulipas - Texas Semiarid	sexual	Coriobacteriales Incerta	0.0000	8	0.0000	0.0000
ASV_7766	Tamaulipas - Texas Semiarid	sexual	AKYH767	0.0000	8	0.0000	0.0000
ASV_7838	Tamaulipas - Texas Semiarid	sexual	Sulfuricellaceae	0.0000	8	0.0000	0.0000
ASV_7869	Tamaulipas - Texas Semiarid	sexual	Silvanigrellaceae	0.0000	8	0.0000	0.0000

ASV_7906	Tamaulipas - Texas Semiarid	sexual	LWQ8	0.0000	8	0.0000	0.0000
ASV_795	Tamaulipas - Texas Semiarid	sexual	Labraceae	0.0000	8	0.0000	0.0000
ASV_7964	Tamaulipas - Texas Semiarid	sexual	AKYG1722	0.0000	8	0.0000	0.0000
ASV_7971	Tamaulipas - Texas Semiarid	sexual	Vicinamibacteraceae	0.0000	8	0.0000	0.0000
ASV_8058	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_8060	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_8089	Tamaulipas - Texas Semiarid	sexual	Isosphaeraceae	0.0000	8	0.0000	0.0000
ASV_838	Tamaulipas - Texas Semiarid	sexual	Erwiniaceae	0.0000	8	0.0000	0.0000
ASV_8455	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_8458	Tamaulipas - Texas Semiarid	sexual	Burkholderiaceae	0.0000	8	0.0000	0.0000
ASV_8486	Tamaulipas - Texas Semiarid	sexual	Entotheonellaceae	0.0000	8	0.0000	0.0000
ASV_8496	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_8560	Tamaulipas - Texas Semiarid	sexual	Endomicrobiaceae	0.0000	8	0.0000	0.0000
ASV_8572	Tamaulipas - Texas Semiarid	sexual	Nocardiopsaceae	0.0000	8	0.0000	0.0000
ASV_8715	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_8883	Tamaulipas - Texas Semiarid	sexual	Nitrosomonadaceae	0.0000	8	0.0000	0.0000
ASV_8903	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_9043	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_9092	Tamaulipas - Texas Semiarid	sexual	Rs-E47 termite group	0.0000	8	0.0000	0.0000
ASV_912	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_9144	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_9161	Tamaulipas - Texas Semiarid	sexual	Legionellaceae	0.0000	8	0.0000	0.0000
ASV_9242	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_9364	Tamaulipas - Texas Semiarid	sexual	Micrococcales Incertae	0.0000	8	0.0000	0.0000
ASV_9379	Tamaulipas - Texas Semiarid	sexual	Pasteurellaceae	0.0000	8	0.0000	0.0000
ASV_9469	Tamaulipas - Texas Semiarid	sexual	Herpetosiphonaceae	0.0000	8	0.0000	0.0000
ASV_9488	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_9515	Tamaulipas - Texas Semiarid	sexual	Rhodomicrobiaceae	0.0000	8	0.0000	0.0000
ASV_9517	Tamaulipas - Texas Semiarid	sexual	Chloroflexaceae	0.0000	8	0.0000	0.0000
ASV_9672	Tamaulipas - Texas Semiarid	sexual	Methylopilaceae	0.0000	8	0.0000	0.0000
ASV_9715	Tamaulipas - Texas Semiarid	sexual	Desulfitobacteriaceae	0.0000	8	0.0000	0.0000
ASV_9797	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000

ASV_9818	Tamaulipas - Texas Semiarid	sexual	67-14	0.0000	8	0.0000	0.0000
ASV_9871	Tamaulipas - Texas Semiarid	sexual	Nannocystaceae	0.0000	8	0.0000	0.0000
ASV_9879	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_9931	Tamaulipas - Texas Semiarid	sexual	Caldilineaceae	0.0000	8	0.0000	0.0000
ASV_994	Tamaulipas - Texas Semiarid	sexual	NA	0.0000	8	0.0000	0.0000
ASV_1	Warm North American Deser	sexual	Dietziaceae	18.8789	99	25.5598	2.5689
ASV_7	Warm North American Deser	sexual	Lachnospiraceae	14.7435	99	20.2433	2.0345
ASV_4	Warm North American Deser	sexual	Micrococcacea	13.8426	99	24.3944	2.4517
ASV_3	Warm North American Deser	sexual	Helicobacteraceae	5.8475	99	17.3821	1.7470
ASV_6	Warm North American Deser	sexual	Corynebacteriaceae	5.6607	99	12.4308	1.2493
ASV_69	Warm North American Deser	sexual	Geodermatophilaceae	4.3784	99	7.4745	0.7512
ASV_97	Warm North American Deser	sexual	Beijerinckiaceae	2.7851	99	4.9208	0.4946
ASV_10	Warm North American Deser	sexual	Clostridiaceae	2.7513	99	11.9634	1.2024
ASV_8	Warm North American Deser	sexual	Brevibacteriaceae	2.4327	99	6.7542	0.6788
ASV_32	Warm North American Deser	sexual	Bacteroidaceae	2.3356	99	5.3729	0.5400
ASV_11	Warm North American Deser	sexual	Oscillospiraceae	1.8418	99	2.8927	0.2907
ASV_162	Warm North American Deser	sexual	Sphingomonadaceae	1.8016	99	2.7222	0.2736
ASV_22	Warm North American Deser	sexual	Ruminococcaceae	1.7440	99	4.2167	0.4238
ASV_20	Warm North American Deser	sexual	Nocardioidaceae	1.5996	99	3.9158	0.3936
ASV_12	Warm North American Deser	sexual	Dermabacteraceae	1.4924	99	5.3112	0.5338
ASV_21	Warm North American Deser	sexual	Intrasporangiaceae	1.2281	99	4.1227	0.4143
ASV_24	Warm North American Deser	sexual	Micrococcaceae	1.2188	99	2.7918	0.2806
ASV_117	Warm North American Deser	sexual	Marinifilaceae	1.0104	99	2.7250	0.2739
ASV_139	Warm North American Deser	sexual	Acetobacteraceae	0.9367	99	1.7087	0.1717
ASV_153	Warm North American Deser	sexual	Pseudonocardiaceae	0.9335	99	2.1170	0.2128
ASV_38	Warm North American Deser	sexual	Tannerellaceae	0.9042	99	2.4185	0.2431
ASV_18	Warm North American Deser	sexual	Rhodobacteraceae	0.8669	99	1.6871	0.1696
ASV_142	Warm North American Deser	sexual	Streptomycetaceae	0.6664	99	2.5457	0.2559
ASV_73	Warm North American Deser	sexual	Cellulomonadaceae	0.6600	99	1.4614	0.1469
ASV_283	Warm North American Deser	sexual	Micromonosporaceae	0.4958	99	1.3559	0.1363
ASV_121	Warm North American Deser	sexual	NA	0.4926	99	1.0711	0.1077
ASV_44	Warm North American Deser	sexual	Rikenellaceae	0.4282	99	1.3453	0.1352

ASV_29	Warm North American Deser	sexual	[Eubacterium] coprosta	0.4149	99	1.0966	0.1102
ASV_126	Warm North American Deser	sexual	NA	0.3159	99	1.0954	0.1101
ASV_49	Warm North American Deser	sexual	Microbacteriaceae	0.2988	99	0.5419	0.0545
ASV_86	Warm North American Deser	sexual	Anaerovoracaceae	0.2782	99	0.5218	0.0524
ASV_404	Warm North American Deser	sexual	Kineosporiaceae	0.2746	99	0.6461	0.0649
ASV_538	Warm North American Deser	sexual	Caulobacteraceae	0.2527	99	0.4927	0.0495
ASV_57	Warm North American Deser	sexual	Devosiaceae	0.2314	99	0.6514	0.0655
ASV_483	Warm North American Deser	sexual	Hymenobacteraceae	0.2243	99	0.5299	0.0533
ASV_420	Warm North American Deser	sexual	Enterobacteriaceae	0.2114	99	0.6712	0.0675
ASV_807	Warm North American Deser	sexual	Gemmatimonadaceae	0.2097	99	0.3544	0.0356
ASV_442	Warm North American Deser	sexual	Rhizobiaceae	0.2094	99	0.5480	0.0551
ASV_729	Warm North American Deser	sexual	Longimicrobiaceae	0.2048	99	0.5453	0.0548
ASV_474	Warm North American Deser	sexual	Chitinophagaceae	0.1975	99	0.4357	0.0438
ASV_309	Warm North American Deser	sexual	Family XI	0.1862	99	0.5248	0.0527
ASV_347	Warm North American Deser	sexual	Azospirillaceae	0.1859	99	0.4015	0.0404
ASV_250	Warm North American Deser	sexual	Butyricicoccaceae	0.1843	99	0.4210	0.0423
ASV_624	Warm North American Deser	sexual	Bryobacteraceae	0.1811	99	0.5629	0.0566
ASV_96	Warm North American Deser	sexual	Christensenellaceae	0.1729	99	0.5470	0.0550
ASV_19	Warm North American Deser	sexual	Nocardiaceae	0.1706	99	0.2650	0.0266
ASV_98	Warm North American Deser	sexual	Desulfovibrionaceae	0.1659	99	0.6814	0.0685
ASV_163	Warm North American Deser	sexual	Monoglobaceae	0.1637	99	0.4508	0.0453
ASV_815	Warm North American Deser	sexual	NA	0.1500	99	0.3104	0.0312
ASV_214	Warm North American Deser	sexual	Eggerthellaceae	0.1321	99	0.2419	0.0243
ASV_129	Warm North American Deser	sexual	Peptostreptococcaceae	0.1286	99	0.5447	0.0547
ASV_512	Warm North American Deser	sexual	Geminicoccaceae	0.1217	99	0.2790	0.0280
ASV_1150	Warm North American Deser	sexual	NA	0.1179	99	0.2778	0.0279
ASV_410	Warm North American Deser	sexual	Ilumatobacteraceae	0.1138	99	0.2591	0.0260
ASV_1080	Warm North American Deser	sexual	NA	0.0997	99	0.2078	0.0209
ASV_91	Warm North American Deser	sexual	Peptococcaceae	0.0880	99	0.3924	0.0394
ASV_362	Warm North American Deser	sexual	Thermomonosporaceae	0.0872	99	0.3263	0.0328
ASV_456	Warm North American Deser	sexual	Promicromonosporacea	0.0764	99	0.3117	0.0313
ASV_161	Warm North American Deser	sexual	Bacillaceae	0.0760	99	0.2031	0.0204

ASV_728	Warm North American Deser	sexual	Xanthobacteraceae	0.0731	99	0.1517	0.0152
ASV_259	Warm North American Deser	sexual	Enterococcaceae	0.0692	99	0.2137	0.0215
ASV_405	Warm North American Deser	sexual	NA	0.0606	99	0.1732	0.0174
ASV_1110	Warm North American Deser	sexual	Mycobacteriaceae	0.0593	99	0.1379	0.0139
ASV_681	Warm North American Deser	sexual	Sporichthyaceae	0.0593	99	0.1489	0.0150
ASV_740	Warm North American Deser	sexual	NA	0.0551	99	0.2965	0.0298
ASV_552	Warm North American Deser	sexual	Propionibacteriaceae	0.0548	99	0.1023	0.0103
ASV_1445	Warm North American Deser	sexual	NA	0.0535	99	0.1274	0.0128
ASV_994	Warm North American Deser	sexual	NA	0.0532	99	0.1477	0.0148
ASV_2550	Warm North American Deser	sexual	Spirosomaceae	0.0472	99	0.1780	0.0179
ASV_493	Warm North American Deser	sexual	Frankiaceae	0.0455	99	0.1789	0.0180
ASV_1285	Warm North American Deser	sexual	NA	0.0438	99	0.1481	0.0149
ASV_660	Warm North American Deser	sexual	Moraxellaceae	0.0424	99	0.0894	0.0090
ASV_2146	Warm North American Deser	sexual	NA	0.0357	99	0.1162	0.0117
ASV_468	Warm North American Deser	sexual	Weeksellaceae	0.0349	99	0.1386	0.0139
ASV_2306	Warm North American Deser	sexual	NA	0.0339	99	0.1107	0.0111
ASV_1201	Warm North American Deser	sexual	Sphingobacteriaceae	0.0331	99	0.1510	0.0152
ASV_1275	Warm North American Deser	sexual	Actinomycetaceae	0.0317	99	0.2312	0.0232
ASV_1813	Warm North American Deser	sexual	D05-2	0.0300	99	0.1045	0.0105
ASV_1096	Warm North American Deser	sexual	UCG-010	0.0300	99	0.2275	0.0229
ASV_345	Warm North American Deser	sexual	Dermacoccaceae	0.0294	99	0.1841	0.0185
ASV_1340	Warm North American Deser	sexual	Microtrichaceae	0.0283	99	0.0959	0.0096
ASV_604	Warm North American Deser	sexual	Hydrogenoanaerobacte	0.0280	99	0.0756	0.0076
ASV_1325	Warm North American Deser	sexual	Acidobacteriaceae (Sub	0.0279	99	0.1549	0.0156
ASV_867	Warm North American Deser	sexual	Gaiellaceae	0.0270	99	0.0748	0.0075
ASV_2445	Warm North American Deser	sexual	Streptosporangiales Inc	0.0267	99	0.0783	0.0079
ASV_2606	Warm North American Deser	sexual	Euzebyaceae	0.0265	99	0.0697	0.0070
ASV_1974	Warm North American Deser	sexual	NA	0.0262	99	0.0772	0.0078
ASV_1246	Warm North American Deser	sexual	NA	0.0258	99	0.0758	0.0076
ASV_3442	Warm North American Deser	sexual	NA	0.0252	99	0.0694	0.0070
ASV_282	Warm North American Deser	sexual	Thermoactinomycetace	0.0244	99	0.1439	0.0145
ASV_979	Warm North American Deser	sexual	Nakamurellaceae	0.0240	99	0.0701	0.0070

ASV_439	Warm North American Deser	sexual	Polyangiaceae	0.0209	99	0.0974	0.0098
ASV_571	Warm North American Deser	sexual	Flavobacteriaceae	0.0206	99	0.0796	0.0080
ASV_817	Warm North American Deser	sexual	Porphyromonadaceae	0.0205	99	0.0606	0.0061
ASV_417	Warm North American Deser	sexual	Streptosporangiaceae	0.0204	99	0.0833	0.0084
ASV_152	Warm North American Deser	sexual	3M1PL1-52 termite grou	0.0193	99	0.1496	0.0150
ASV_2172	Warm North American Deser	sexual	Hungateiclostridiaceae	0.0190	99	0.1746	0.0175
ASV_6397	Warm North American Deser	sexual	NA	0.0188	99	0.0957	0.0096
ASV_758	Warm North American Deser	sexual	Coriobacteriales Incerta	0.0182	99	0.0652	0.0066
ASV_1501	Warm North American Deser	sexual	Sanguibacteraceae	0.0168	99	0.0892	0.0090
ASV_4124	Warm North American Deser	sexual	Leptotrichiaceae	0.0164	99	0.0766	0.0077
ASV_1563	Warm North American Deser	sexual	Erysipelatoclostridiacea	0.0162	99	0.0587	0.0059
ASV_912	Warm North American Deser	sexual	NA	0.0159	99	0.0553	0.0056
ASV_2104	Warm North American Deser	sexual	NA	0.0157	99	0.0628	0.0063
ASV_481	Warm North American Deser	sexual	Oxalobacteraceae	0.0156	99	0.0859	0.0086
ASV_1904	Warm North American Deser	sexual	Cytophagaceae	0.0148	99	0.0441	0.0044
ASV_2450	Warm North American Deser	sexual	Prevotellaceae	0.0147	99	0.0766	0.0077
ASV_1664	Warm North American Deser	sexual	NA	0.0143	99	0.0771	0.0078
ASV_2506	Warm North American Deser	sexual	Acidothermaceae	0.0135	99	0.0739	0.0074
ASV_941	Warm North American Deser	sexual	Staphylococcaceae	0.0130	99	0.0381	0.0038
ASV_2554	Warm North American Deser	sexual	Fusobacteriaceae	0.0129	99	0.0723	0.0073
ASV_3155	Warm North American Deser	sexual	NA	0.0128	99	0.0557	0.0056
ASV_2726	Warm North American Deser	sexual	Bdellovibrionaceae	0.0125	99	0.0458	0.0046
ASV_4655	Warm North American Deser	sexual	Iamiaceae	0.0123	99	0.0530	0.0053
ASV_2367	Warm North American Deser	sexual	Abditibacteriaceae	0.0117	99	0.0769	0.0077
ASV_3453	Warm North American Deser	sexual	Streptococcaceae	0.0113	99	0.0487	0.0049
ASV_4747	Warm North American Deser	sexual	Solirubrobacteraceae	0.0108	99	0.0452	0.0045
ASV_3064	Warm North American Deser	sexual	Paludibacteraceae	0.0105	99	0.0356	0.0036
ASV_1162	Warm North American Deser	sexual	Puniceispirillales Incerta	0.0104	99	0.0375	0.0038
ASV_795	Warm North American Deser	sexual	Labraceae	0.0103	99	0.0437	0.0044
ASV_3376	Warm North American Deser	sexual	Sandaracinaceae	0.0101	99	0.0422	0.0042
ASV_1575	Warm North American Deser	sexual	Defluviitaleaceae	0.0095	99	0.0463	0.0047
ASV_1554	Warm North American Deser	sexual	Cryptosporangiaceae	0.0095	99	0.0701	0.0070

ASV_621	Warm North American Deser	sexual	NA	0.0091	99	0.0507	0.0051
ASV_2687	Warm North American Deser	sexual	Unknown Family	0.0084	99	0.0471	0.0047
ASV_1571	Warm North American Deser	sexual	NA	0.0083	99	0.0473	0.0048
ASV_2211	Warm North American Deser	sexual	NA	0.0078	99	0.0304	0.0031
ASV_1715	Warm North American Deser	sexual	Eubacteriaceae	0.0073	99	0.0642	0.0065
ASV_3726	Warm North American Deser	sexual	Rhodothermaceae	0.0073	99	0.0349	0.0035
ASV_5553	Warm North American Deser	sexual	Rhizobiales Incertae Se	0.0070	99	0.0445	0.0045
ASV_3519	Warm North American Deser	sexual	NA	0.0069	99	0.0324	0.0033
ASV_5351	Warm North American Deser	sexual	NA	0.0067	99	0.0305	0.0031
ASV_7145	Warm North American Deser	sexual	Haliangiaceae	0.0067	99	0.0282	0.0028
ASV_5389	Warm North American Deser	sexual	Desulfotomaculales Inc	0.0066	99	0.0423	0.0043
ASV_4291	Warm North American Deser	sexual	NA	0.0066	99	0.0450	0.0045
ASV_2819	Warm North American Deser	sexual	Micropepsaceae	0.0065	99	0.0577	0.0058
ASV_5314	Warm North American Deser	sexual	Marinilabiliaceae	0.0063	99	0.0524	0.0053
ASV_711	Warm North American Deser	sexual	Pleomorphomonadace	0.0063	99	0.0436	0.0044
ASV_7083	Warm North American Deser	sexual	Synergistaceae	0.0061	99	0.0531	0.0053
ASV_2996	Warm North American Deser	sexual	Nitrosococcaceae	0.0058	99	0.0460	0.0046
ASV_4284	Warm North American Deser	sexual	Ardenticatenaceae	0.0058	99	0.0285	0.0029
ASV_7490	Warm North American Deser	sexual	COB P4-1 termite grou	0.0057	99	0.0235	0.0024
ASV_6570	Warm North American Deser	sexual	Oligoflexaceae	0.0055	99	0.0206	0.0021
ASV_3769	Warm North American Deser	sexual	Williamwhitmaniaceae	0.0055	99	0.0510	0.0051
ASV_5486	Warm North American Deser	sexual	Microscillaceae	0.0055	99	0.0406	0.0041
ASV_3766	Warm North American Deser	sexual	NA	0.0054	99	0.0389	0.0039
ASV_2986	Warm North American Deser	sexual	Actinospicaceae	0.0053	99	0.0398	0.0040
ASV_2133	Warm North American Deser	sexual	Nitrospiraceae	0.0052	99	0.0202	0.0020
ASV_2156	Warm North American Deser	sexual	Hyphomicrobiaceae	0.0050	99	0.0159	0.0016
ASV_4558	Warm North American Deser	sexual	Myxococcaceae	0.0050	99	0.0235	0.0024
ASV_7238	Warm North American Deser	sexual	AKIW781	0.0048	99	0.0325	0.0033
ASV_2482	Warm North American Deser	sexual	NA	0.0044	99	0.0208	0.0021
ASV_4700	Warm North American Deser	sexual	Reyranellaceae	0.0043	99	0.0286	0.0029
ASV_4934	Warm North American Deser	sexual	NA	0.0042	99	0.0325	0.0033
ASV_3627	Warm North American Deser	sexual	Ethanoligenenaceae	0.0040	99	0.0215	0.0022

ASV_4673	Warm North American Deser	sexual	NA	0.0039	99	0.0285	0.0029
ASV_2708	Warm North American Deser	sexual	Bifidobacteriaceae	0.0039	99	0.0209	0.0021
ASV_4341	Warm North American Deser	sexual	Simkaniaceae	0.0039	99	0.0380	0.0038
ASV_3972	Warm North American Deser	sexual	NA	0.0037	99	0.0292	0.0029
ASV_5102	Warm North American Deser	sexual	NA	0.0036	99	0.0209	0.0021
ASV_3549	Warm North American Deser	sexual	NA	0.0035	99	0.0351	0.0035
ASV_3781	Warm North American Deser	sexual	Coleofasciculaceae	0.0034	99	0.0162	0.0016
ASV_5527	Warm North American Deser	sexual	Comamonadaceae	0.0034	99	0.0115	0.0012
ASV_4602	Warm North American Deser	sexual	Lactobacillaceae	0.0030	99	0.0268	0.0027
ASV_7459	Warm North American Deser	sexual	NA	0.0029	99	0.0290	0.0029
ASV_753	Warm North American Deser	sexual	[Clostridium] methylpen	0.0029	99	0.0155	0.0016
ASV_5177	Warm North American Deser	sexual	Candidatus Jidaibacter	0.0028	99	0.0277	0.0028
ASV_2892	Warm North American Deser	sexual	NA	0.0028	99	0.0202	0.0020
ASV_7464	Warm North American Deser	sexual	Blastocatellaceae	0.0025	99	0.0141	0.0014
ASV_8588	Warm North American Deser	sexual	Paenibacillaceae	0.0025	99	0.0137	0.0014
ASV_5504	Warm North American Deser	sexual	Alicyclobacillaceae	0.0025	99	0.0238	0.0024
ASV_3144	Warm North American Deser	sexual	Roseiflexaceae	0.0025	99	0.0154	0.0015
ASV_6172	Warm North American Deser	sexual	Inquilinaceae	0.0024	99	0.0243	0.0024
ASV_9092	Warm North American Deser	sexual	Rs-E47 termite group	0.0024	99	0.0178	0.0018
ASV_2959	Warm North American Deser	sexual	Phaselicystidaceae	0.0024	99	0.0122	0.0012
ASV_586	Warm North American Deser	sexual	Saccharimonadaceae	0.0024	99	0.0164	0.0016
ASV_7971	Warm North American Deser	sexual	Vicinamibacteraceae	0.0023	99	0.0100	0.0010
ASV_5631	Warm North American Deser	sexual	Sporomusaceae	0.0022	99	0.0096	0.0010
ASV_3501	Warm North American Deser	sexual	NA	0.0022	99	0.0135	0.0014
ASV_6732	Warm North American Deser	sexual	Hyphomonadaceae	0.0022	99	0.0101	0.0010
ASV_6091	Warm North American Deser	sexual	JG30-KF-CM45	0.0022	99	0.0112	0.0011
ASV_7107	Warm North American Deser	sexual	Bogoriellaceae	0.0022	99	0.0185	0.0019
ASV_3660	Warm North American Deser	sexual	Paracaedibacteraceae	0.0022	99	0.0213	0.0021
ASV_4224	Warm North American Deser	sexual	NA	0.0022	99	0.0206	0.0021
ASV_3419	Warm North American Deser	sexual	Dysgonomonadaceae	0.0021	99	0.0133	0.0013
ASV_8058	Warm North American Deser	sexual	NA	0.0021	99	0.0192	0.0019
ASV_7025	Warm North American Deser	sexual	Cyclobacteriaceae	0.0020	99	0.0117	0.0012

ASV_685	Warm North American Deser	sexual	NA	0.0020	99	0.0128	0.0013
ASV_6395	Warm North American Deser	sexual	Campylobacteraceae	0.0020	99	0.0163	0.0016
ASV_5301	Warm North American Deser	sexual	Glycomycetaceae	0.0019	99	0.0182	0.0018
ASV_5250	Warm North American Deser	sexual	WD2101 soil group	0.0018	99	0.0081	0.0008
ASV_7023	Warm North American Deser	sexual	NA	0.0017	99	0.0115	0.0012
ASV_9818	Warm North American Deser	sexual	67-14	0.0017	99	0.0076	0.0008
ASV_12532	Warm North American Deser	sexual	Bacteriovoracaceae	0.0016	99	0.0068	0.0007
ASV_4894	Warm North American Deser	sexual	NA	0.0016	99	0.0098	0.0010
ASV_5681	Warm North American Deser	sexual	Rhodospirillaceae	0.0015	99	0.0071	0.0007
ASV_2522	Warm North American Deser	sexual	Beutenbergiaceae	0.0015	99	0.0088	0.0009
ASV_8560	Warm North American Deser	sexual	Endomicrobiaceae	0.0015	99	0.0128	0.0013
ASV_2494	Warm North American Deser	sexual	Thermicanaceae	0.0014	99	0.0138	0.0014
ASV_4086	Warm North American Deser	sexual	Nostocaceae	0.0014	99	0.0078	0.0008
ASV_6978	Warm North American Deser	sexual	Defluviicoccaceae	0.0014	99	0.0085	0.0009
ASV_6308	Warm North American Deser	sexual	Barnesiellaceae	0.0014	99	0.0098	0.0010
ASV_4184	Warm North American Deser	sexual	Methyloligellaceae	0.0014	99	0.0072	0.0007
ASV_9144	Warm North American Deser	sexual	NA	0.0013	99	0.0072	0.0007
ASV_6583	Warm North American Deser	sexual	NA	0.0013	99	0.0128	0.0013
ASV_6102	Warm North American Deser	sexual	NA	0.0012	99	0.0104	0.0010
ASV_23	Warm North American Deser	sexual	Diplorickettsiaceae	0.0012	99	0.0099	0.0010
ASV_8903	Warm North American Deser	sexual	NA	0.0012	99	0.0116	0.0012
ASV_2624	Warm North American Deser	sexual	Unknown Family	0.0011	99	0.0096	0.0010
ASV_3457	Warm North American Deser	sexual	Sedimentibacteraceae	0.0011	99	0.0106	0.0011
ASV_5915	Warm North American Deser	sexual	env.OPS 17	0.0011	99	0.0060	0.0006
ASV_6560	Warm North American Deser	sexual	Rubrobacteriaceae	0.0010	99	0.0058	0.0006
ASV_9517	Warm North American Deser	sexual	Chloroflexaceae	0.0010	99	0.0064	0.0006
ASV_8060	Warm North American Deser	sexual	NA	0.0010	99	0.0076	0.0008
ASV_9871	Warm North American Deser	sexual	Nannocystaceae	0.0010	99	0.0063	0.0006
ASV_1864	Warm North American Deser	sexual	Anaerofustaceae	0.0010	99	0.0095	0.0010
ASV_3510	Warm North American Deser	sexual	A0839	0.0009	99	0.0068	0.0007
ASV_6394	Warm North American Deser	sexual	Chroococcidiopsaceae	0.0009	99	0.0048	0.0005
ASV_4399	Warm North American Deser	sexual	Anaplasmataceae	0.0009	99	0.0084	0.0008

ASV_5059	Warm North American Deser	sexual	NA	0.0009	99	0.0076	0.0008
ASV_11680	Warm North American Deser	sexual	Atopobiaceae	0.0009	99	0.0091	0.0009
ASV_11538	Warm North American Deser	sexual	NA	0.0009	99	0.0058	0.0006
ASV_7869	Warm North American Deser	sexual	Silvanigrellaceae	0.0009	99	0.0090	0.0009
ASV_4227	Warm North American Deser	sexual	Halomonadaceae	0.0009	99	0.0087	0.0009
ASV_8486	Warm North American Deser	sexual	Entotheonellaceae	0.0009	99	0.0059	0.0006
ASV_10336	Warm North American Deser	sexual	Xanthomonadaceae	0.0009	99	0.0054	0.0005
ASV_5823	Warm North American Deser	sexual	Competibacteraceae	0.0008	99	0.0078	0.0008
ASV_10092	Warm North American Deser	sexual	NA	0.0008	99	0.0080	0.0008
ASV_9043	Warm North American Deser	sexual	NA	0.0008	99	0.0054	0.0005
ASV_7906	Warm North American Deser	sexual	LWQ8	0.0008	99	0.0052	0.0005
ASV_9879	Warm North American Deser	sexual	NA	0.0008	99	0.0078	0.0008
ASV_13305	Warm North American Deser	sexual	NA	0.0008	99	0.0037	0.0004
ASV_8883	Warm North American Deser	sexual	Nitrosomonadaceae	0.0007	99	0.0069	0.0007
ASV_838	Warm North American Deser	sexual	Erwiniaceae	0.0007	99	0.0067	0.0007
ASV_9379	Warm North American Deser	sexual	Pasteurellaceae	0.0007	99	0.0068	0.0007
ASV_9242	Warm North American Deser	sexual	NA	0.0007	99	0.0056	0.0006
ASV_8089	Warm North American Deser	sexual	Isosphaeraceae	0.0007	99	0.0068	0.0007
ASV_14142	Warm North American Deser	sexual	Syntrophomonadaceae	0.0007	99	0.0067	0.0007
ASV_5396	Warm North American Deser	sexual	Caloramatoraceae	0.0007	99	0.0067	0.0007
ASV_11270	Warm North American Deser	sexual	Caedibacteraceae	0.0007	99	0.0067	0.0007
ASV_9931	Warm North American Deser	sexual	Caldilineaceae	0.0006	99	0.0041	0.0004
ASV_10617	Warm North American Deser	sexual	Aerococcaceae	0.0006	99	0.0063	0.0006
ASV_5248	Warm North American Deser	sexual	Phormidiaceae	0.0006	99	0.0032	0.0003
ASV_11493	Warm North American Deser	sexual	Leptolyngbyaceae	0.0006	99	0.0044	0.0004
ASV_11668	Warm North American Deser	sexual	Desulfobulbaceae	0.0006	99	0.0039	0.0004
ASV_9469	Warm North American Deser	sexual	Herpetosiphonaceae	0.0006	99	0.0058	0.0006
ASV_9488	Warm North American Deser	sexual	NA	0.0006	99	0.0051	0.0005
ASV_9672	Warm North American Deser	sexual	Methylopilaceae	0.0005	99	0.0049	0.0005
ASV_8572	Warm North American Deser	sexual	Nocardiopsaceae	0.0005	99	0.0037	0.0004
ASV_9813	Warm North American Deser	sexual	NA	0.0005	99	0.0033	0.0003
ASV_4929	Warm North American Deser	sexual	Erysipelotrichaceae	0.0005	99	0.0041	0.0004

ASV_1605	Warm North American Deser	sexual	NA	0.0005	99	0.0051	0.0005
ASV_11608	Warm North American Deser	sexual	FFCH9454	0.0005	99	0.0046	0.0005
ASV_7964	Warm North American Deser	sexual	AKYG1722	0.0004	99	0.0027	0.0003
ASV_11541	Warm North American Deser	sexual	Crocinitomicaceae	0.0004	99	0.0043	0.0004
ASV_11365	Warm North American Deser	sexual	SM2D12	0.0004	99	0.0039	0.0004
ASV_11494	Warm North American Deser	sexual	Magnetospiraceae	0.0004	99	0.0030	0.0003
ASV_317	Warm North American Deser	sexual	Hafniaceae	0.0004	99	0.0031	0.0003
ASV_1107	Warm North American Deser	sexual	Muribaculaceae	0.0004	99	0.0040	0.0004
ASV_13067	Warm North American Deser	sexual	AKAU3644	0.0004	99	0.0039	0.0004
ASV_9515	Warm North American Deser	sexual	Rhodomicrobiaceae	0.0004	99	0.0033	0.0003
ASV_4236	Warm North American Deser	sexual	Fibrobacteraceae	0.0004	99	0.0030	0.0003
ASV_9810	Warm North American Deser	sexual	Trueperaceae	0.0004	99	0.0037	0.0004
ASV_8496	Warm North American Deser	sexual	NA	0.0004	99	0.0028	0.0003
ASV_9797	Warm North American Deser	sexual	NA	0.0004	99	0.0027	0.0003
ASV_11196	Warm North American Deser	sexual	Vulgatibacteraceae	0.0003	99	0.0035	0.0003
ASV_14123	Warm North American Deser	sexual	NA	0.0003	99	0.0033	0.0003
ASV_6643	Warm North American Deser	sexual	Gemellaceae	0.0003	99	0.0025	0.0002
ASV_7146	Warm North American Deser	sexual	Planococcaceae	0.0003	99	0.0032	0.0003
ASV_1686	Warm North American Deser	sexual	Anaeromyxobacterace	0.0003	99	0.0028	0.0003
ASV_8715	Warm North American Deser	sexual	NA	0.0003	99	0.0030	0.0003
ASV_9161	Warm North American Deser	sexual	Legionellaceae	0.0003	99	0.0021	0.0002
ASV_11787	Warm North American Deser	sexual	Parachlamydiaceae	0.0003	99	0.0027	0.0003
ASV_13085	Warm North American Deser	sexual	NA	0.0003	99	0.0019	0.0002
ASV_7533	Warm North American Deser	sexual	Saprospiraceae	0.0003	99	0.0020	0.0002
ASV_10434	Warm North American Deser	sexual	NA	0.0002	99	0.0020	0.0002
ASV_13328	Warm North American Deser	sexual	NA	0.0002	99	0.0017	0.0002
ASV_12467	Warm North American Deser	sexual	Coxiellaceae	0.0002	99	0.0023	0.0002
ASV_7766	Warm North American Deser	sexual	AKYH767	0.0002	99	0.0022	0.0002
ASV_5887	Warm North American Deser	sexual	Budviciaceae	0.0002	99	0.0019	0.0002
ASV_11504	Warm North American Deser	sexual	NA	0.0002	99	0.0013	0.0001
ASV_10439	Warm North American Deser	sexual	NA	0.0002	99	0.0015	0.0002
ASV_14225	Warm North American Deser	sexual	NA	0.0002	99	0.0018	0.0002

ASV_14155	Warm North American Deser	sexual	NA	0.0002	99	0.0018	0.0002
ASV_5638	Warm North American Deser	sexual	NA	0.0002	99	0.0018	0.0002
ASV_3410	Warm North American Deser	sexual	Selenomonadaceae	0.0002	99	0.0018	0.0002
ASV_13301	Warm North American Deser	sexual	NA	0.0002	99	0.0017	0.0002
ASV_14007	Warm North American Deser	sexual	Rhodanobacteraceae	0.0002	99	0.0017	0.0002
ASV_3114	Warm North American Deser	sexual	Solibacteraceae	0.0002	99	0.0015	0.0002
ASV_12365	Warm North American Deser	sexual	Elusimicrobiaceae	0.0002	99	0.0015	0.0002
ASV_13753	Warm North American Deser	sexual	Yersiniaceae	0.0002	99	0.0015	0.0002
ASV_3179	Warm North American Deser	sexual	Sulfurospirillaceae	0.0002	99	0.0015	0.0002
ASV_13329	Warm North American Deser	sexual	NA	0.0001	99	0.0015	0.0001
ASV_5924	Warm North American Deser	sexual	Exiguobacteraceae	0.0001	99	0.0014	0.0001
ASV_13269	Warm North American Deser	sexual	Prolixibacteraceae	0.0001	99	0.0013	0.0001
ASV_4022	Warm North American Deser	sexual	Pseudomonadaceae	0.0001	99	0.0009	0.0001
ASV_12449	Warm North American Deser	sexual	Steroidobacteraceae	0.0001	99	0.0011	0.0001
ASV_8458	Warm North American Deser	sexual	Burkholderiaceae	0.0001	99	0.0008	0.0001
ASV_13217	Warm North American Deser	sexual	NA	0.0001	99	0.0011	0.0001
ASV_7838	Warm North American Deser	sexual	Sulfuricellaceae	0.0001	99	0.0011	0.0001
ASV_13922	Warm North American Deser	sexual	Thermoanaerobaculace	0.0001	99	0.0011	0.0001
ASV_1694	Warm North American Deser	sexual	Marinococcaceae	0.0001	99	0.0010	0.0001
ASV_4645	Warm North American Deser	sexual	Dongiaceae	0.0001	99	0.0010	0.0001
ASV_14349	Warm North American Deser	sexual	NA	0.0001	99	0.0009	0.0001
ASV_8455	Warm North American Deser	sexual	NA	0.0001	99	0.0007	0.0001
ASV_13344	Warm North American Deser	sexual	vadinHA21	0.0000	99	0.0004	0.0000
ASV_10922	Warm North American Deser	sexual	NA	0.0000	99	0.0004	0.0000
ASV_9364	Warm North American Deser	sexual	Micrococcales Incertae	0.0000	99	0.0004	0.0000
ASV_12171	Warm North American Deser	sexual	NA	0.0000	99	0.0002	0.0000
ASV_12858	Warm North American Deser	sexual	NA	0.0000	99	0.0002	0.0000
ASV_12860	Warm North American Deser	sexual	Tepidisphaeraceae	0.0000	99	0.0002	0.0000
ASV_5152	Warm North American Deser	sexual	Rickettsiaceae	0.0000	99	0.0002	0.0000
ASV_13265	Warm North American Deser	sexual	Veillonellaceae	0.0000	99	0.0002	0.0000
ASV_13268	Warm North American Deser	sexual	Aeromonadaceae	0.0000	99	0.0002	0.0000
ASV_12984	Warm North American Deser	sexual	Acidimicrobiaceae	0.0000	99	0.0002	0.0000

ASV_11833	Warm North American Deser	sexual	Blrii41	0.0000	99	0.0002	0.0000
ASV_13789	Warm North American Deser	sexual	Zavarziniaceae	0.0000	99	0.0002	0.0000
ASV_13957	Warm North American Deser	sexual	NA	0.0000	99	0.0001	0.0000
ASV_13965	Warm North American Deser	sexual	NA	0.0000	99	0.0001	0.0000
ASV_14757	Warm North American Deser	sexual	Gemmataceae	0.0000	99	0.0001	0.0000
ASV_12517	Warm North American Deser	sexual	Aquaspirillaceae	0.0000	99	0.0001	0.0000
ASV_12453	Warm North American Deser	sexual	B1-7BS	0.0000	99	0.0001	0.0000
ASV_10319	Warm North American Deser	sexual	Neisseriaceae	0.0000	99	0.0000	0.0000
ASV_11284	Warm North American Deser	sexual	Salisediminibacteriace	0.0000	99	0.0000	0.0000
ASV_11913	Warm North American Deser	sexual	NA	0.0000	99	0.0000	0.0000
ASV_11956	Warm North American Deser	sexual	NA	0.0000	99	0.0000	0.0000
ASV_12229	Warm North American Deser	sexual	NA	0.0000	99	0.0000	0.0000
ASV_12595	Warm North American Deser	sexual	Demequinaceae	0.0000	99	0.0000	0.0000
ASV_12650	Warm North American Deser	sexual	Morganellaceae	0.0000	99	0.0000	0.0000
ASV_12655	Warm North American Deser	sexual	Sporolactobacillaceae	0.0000	99	0.0000	0.0000
ASV_1308	Warm North American Deser	sexual	Desulfotomaculaceae	0.0000	99	0.0000	0.0000
ASV_13082	Warm North American Deser	sexual	NA	0.0000	99	0.0000	0.0000
ASV_13507	Warm North American Deser	sexual	Mycoplasmataceae	0.0000	99	0.0000	0.0000
ASV_13511	Warm North American Deser	sexual	Methylophagaceae	0.0000	99	0.0000	0.0000
ASV_13581	Warm North American Deser	sexual	Terasakiellaceae	0.0000	99	0.0000	0.0000
ASV_13598	Warm North American Deser	sexual	NA	0.0000	99	0.0000	0.0000
ASV_13609	Warm North American Deser	sexual	Stappiaceae	0.0000	99	0.0000	0.0000
ASV_13614	Warm North American Deser	sexual	Wohlfahrtiimonadacea	0.0000	99	0.0000	0.0000
ASV_13670	Warm North American Deser	sexual	Phycisphaeraceae	0.0000	99	0.0000	0.0000
ASV_13739	Warm North American Deser	sexual	Koribacteraceae	0.0000	99	0.0000	0.0000
ASV_14037	Warm North American Deser	sexual	Magnetospirillaceae	0.0000	99	0.0000	0.0000
ASV_14535	Warm North American Deser	sexual	NA	0.0000	99	0.0000	0.0000
ASV_14744	Warm North American Deser	sexual	Alcaligenaceae	0.0000	99	0.0000	0.0000
ASV_166	Warm North American Deser	sexual	Tsukamurellaceae	0.0000	99	0.0000	0.0000
ASV_1996	Warm North American Deser	sexual	Thermincolaceae	0.0000	99	0.0000	0.0000
ASV_3356	Warm North American Deser	sexual	Caldalkalibacillaceae	0.0000	99	0.0000	0.0000
ASV_4085	Warm North American Deser	sexual	NA	0.0000	99	0.0000	0.0000

ASV_4297	Warm North American Deser	sexual	NA	0.0000	99	0.0000	0.0000
ASV_4785	Warm North American Deser	sexual	Oxobacteraceae	0.0000	99	0.0000	0.0000
ASV_5057	Warm North American Deser	sexual	Nitriliruptoraceae	0.0000	99	0.0000	0.0000
ASV_5154	Warm North American Deser	sexual	KF-JG30-B3	0.0000	99	0.0000	0.0000
ASV_6794	Warm North American Deser	sexual	Carnobacteriaceae	0.0000	99	0.0000	0.0000
ASV_7111	Warm North American Deser	sexual	Family III	0.0000	99	0.0000	0.0000
ASV_7358	Warm North American Deser	sexual	Methylophilaceae	0.0000	99	0.0000	0.0000
ASV_9715	Warm North American Deser	sexual	Desulfitobacteriaceae	0.0000	99	0.0000	0.0000

Appendix IV

Alpha diversity metrics per sample used in this study. Rep = Reproduction; Obs = Observed; SI= Shannon Index; PD= Faith's Phylogenetic Diversity

ID	Genus	Species	Rep	Biome	Obs	SI	PD
KLC002	*Aspidoscelis*	*inornatus*	sexual	Warm North American Deserts	11	0.884	3.517
KLC004	*Aspidoscelis*	*inornatus*	sexual	Warm North American Deserts	43	1.131	14.291
KLC005	*Aspidoscelis*	*inornatus*	sexual	Warm North American Deserts	46	1.554	16.464
KLC006	*Aspidoscelis*	*inornatus*	sexual	Warm North American Deserts	33	1.026	10.549
KLC007	*Aspidoscelis*	*tesselatus*	asexual	Warm North American Deserts	81	2.236	24.700
KLC009	*Aspidoscelis*	*tesselatus*	asexual	Warm North American Deserts	46	3.285	14.592
KLC010	*Aspidoscelis*	*tesselatus*	asexual	Warm North American Deserts	34	0.279	10.500
KLC011	*Aspidoscelis*	*tesselatus*	asexual	Warm North American Deserts	15	0.175	4.917
KLC014	*Aspidoscelis*	*tesselatus*	asexual	Warm North American Deserts	42	1.299	12.868
KLC015	*Aspidoscelis*	*tesselatus*	asexual	Warm North American Deserts	44	1.765	13.498
KLC016	*Aspidoscelis*	*marmoratus*	sexual	Warm North American Deserts	39	1.603	14.211
KLC017	*Aspidoscelis*	*inornatus*	sexual	Warm North American Deserts	38	1.601	11.164
KLC018	*Aspidoscelis*	*inornatus*	sexual	Warm North American Deserts	33	0.418	10.930
KLC020	*Aspidoscelis*	*inornatus*	sexual	Warm North American Deserts	41	1.462	13.876
KLC021	*Aspidoscelis*	*inornatus*	sexual	Warm North American Deserts	14	0.922	4.681
KLC022	*Aspidoscelis*	*inornatus*	sexual	Warm North American Deserts	28	1.107	9.788
KLC023	*Aspidoscelis*	*inornatus*	sexual	Warm North American Deserts	17	1.190	4.996

KLC024	*Aspidoscelis*	*inornatus*	sexual	Warm North American Deserts	15	1.413	3.733
KLC025	*Aspidoscelis*	*inornatus*	sexual	Warm North American Deserts	16	0.573	5.431
KLC026	*Aspidoscelis*	*inornatus*	sexual	Warm North American Deserts	44	1.612	14.881
KLC027	*Aspidoscelis*	*marmoratus*	sexual	Warm North American Deserts	21	0.594	5.645
KLC029	*Aspidoscelis*	*gularis*	sexual	Tamaulipas - Texas Semiarid Plains	12	1.520	3.396
KLC031	*Aspidoscelis*	*laredoensis*	asexual	Tamaulipas - Texas Semiarid Plains	36	1.731	9.959
KLC032	*Aspidoscelis*	*gularis*	sexual	Tamaulipas - Texas Semiarid Plains	32	0.504	10.304
KLC033	*Aspidoscelis*	*laredoensis*	asexual	Tamaulipas - Texas Semiarid Plains	76	1.429	26.256
KLC034	*Aspidoscelis*	*gularis*	sexual	Tamaulipas - Texas Semiarid Plains	89	2.401	29.014
KLC035	*Aspidoscelis*	*gularis*	sexual	Tamaulipas - Texas Semiarid Plains	18	1.358	5.252
KLC036	*Aspidoscelis*	*gularis*	sexual	Tamaulipas - Texas Semiarid Plains	64	2.504	21.772
KLC037	*Aspidoscelis*	*gularis*	sexual	Tamaulipas - Texas Semiarid Plains	35	1.659	10.942
KLC038	*Aspidoscelis*	*laredoensis*	asexual	Tamaulipas - Texas Semiarid Plains	27	1.315	8.978
KLC039	*Aspidoscelis*	*gularis*	sexual	Tamaulipas - Texas Semiarid Plains	35	1.622	11.042
KLC040	*Aspidoscelis*	*gularis*	sexual	Tamaulipas - Texas Semiarid Plains	29	1.445	8.407
KLC041	*Aspidoscelis*	*gularis*	sexual	Warm North American Deserts	26	1.074	7.352
KLC042	*Aspidoscelis*	*exsanguis*	asexual	Warm North American Deserts	44	0.290	13.870
KLC043	*Aspidoscelis*	*exsanguis*	asexual	Warm North American Deserts	114	2.617	36.324
KLC044	*Aspidoscelis*	*exsanguis*	asexual	Warm North American Deserts	22	0.539	6.692
KLC046	*Aspidoscelis*	*gularis*	sexual	Warm North American Deserts	60	0.951	19.246
KLC047	*Aspidoscelis*	*exsanguis*	asexual	Warm North American Deserts	72	3.171	22.175
KLC048	*Aspidoscelis*	*gularis*	sexual	Warm North American Deserts	26	1.551	8.687
KLC049	*Aspidoscelis*	*gularis*	sexual	Warm North American Deserts	56	2.098	17.172
KLC050	*Aspidoscelis*	*gularis*	sexual	Warm North American Deserts	32	1.661	10.409
KLC051	*Aspidoscelis*	*gularis*	sexual	Warm North American Deserts	32	2.076	9.012

KLC052	*Aspidoscelis*	*inornatus*	sexual	Warm North American Deserts	130	2.853	41.701
KLC053	*Aspidoscelis*	*inornatus*	sexual	Warm North American Deserts	101	3.179	32.653
KLC054	*Aspidoscelis*	*inornatus*	sexual	Warm North American Deserts	49	1.446	14.513
KLC055	*Aspidoscelis*	*inornatus*	sexual	Warm North American Deserts	96	2.978	31.199
KLC056	*Aspidoscelis*	*inornatus*	sexual	Warm North American Deserts	106	2.897	33.020
KLC057	*Aspidoscelis*	*inornatus*	sexual	Warm North American Deserts	87	2.637	25.763
KLC060	*Aspidoscelis*	*inornatus*	sexual	Warm North American Deserts	136	1.931	43.420
KLC061	*Aspidoscelis*	*inornatus*	sexual	Warm North American Deserts	90	2.992	29.608
KLC062	*Aspidoscelis*	*inornatus*	sexual	Warm North American Deserts	61	1.621	20.087
KLC063	*Aspidoscelis*	*inornatus*	sexual	Warm North American Deserts	42	0.784	14.360
KLC064	*Aspidoscelis*	*exsanguis*	asexual	Warm North American Deserts	8	0.269	2.887
KLC065	*Aspidoscelis*	*exsanguis*	asexual	Warm North American Deserts	21	0.222	7.022
KLC066	*Aspidoscelis*	*tesselatus*	asexual	Warm North American Deserts	24	0.282	7.872
KLC067	*Aspidoscelis*	*exsanguis*	asexual	Warm North American Deserts	34	0.806	10.798
KLC068	*Aspidoscelis*	*exsanguis*	asexual	Warm North American Deserts	34	0.287	10.051
KLC069	*Aspidoscelis*	*exsanguis*	asexual	Warm North American Deserts	62	2.995	20.660
KLC070	*Aspidoscelis*	*exsanguis*	asexual	Warm North American Deserts	54	1.358	16.249
KLC071	*Aspidoscelis*	*exsanguis*	asexual	Warm North American Deserts	40	0.506	13.228
KLC072	*Aspidoscelis*	*exsanguis*	asexual	Warm North American Deserts	91	3.272	32.387
KLC073	*Aspidoscelis*	*exsanguis*	asexual	Warm North American Deserts	65	1.173	22.261
KLC074	*Aspidoscelis*	*inornatus*	sexual	Warm North American Deserts	53	2.707	15.457
KLC075	*Aspidoscelis*	*exsanguis*	asexual	Warm North American Deserts	66	1.360	21.537
KLC076	*Aspidoscelis*	*inornatus*	sexual	Warm North American Deserts	17	0.999	4.775
KLC077	*Aspidoscelis*	*inornatus*	sexual	Warm North American Deserts	84	3.326	25.953
KLC080	*Aspidoscelis*	*septemvittatus*	sexual	Warm North American Deserts	67	2.437	19.909
KLC081	*Aspidoscelis*	*septemvittatus*	sexual	Warm North American Deserts	15	1.513	4.267
KLC082	*Aspidoscelis*	*septemvittatus*	sexual	Warm North American Deserts	49	1.763	14.241
KLC083	*Aspidoscelis*	*septemvittatus*	sexual	Warm North American Deserts	12	0.174	4.336
KLC084	*Aspidoscelis*	*septemvittatus*	sexual	Warm North American Deserts	22	0.508	8.542
KLC085	*Aspidoscelis*	*septemvittatus*	sexual	Warm North American Deserts	27	0.748	8.496
KLC086	*Aspidoscelis*	*septemvittatus*	sexual	Warm North American Deserts	35	0.448	11.329
KLC087	*Aspidoscelis*	*septemvittatus*	sexual	Warm North American Deserts	40	1.667	12.295

KLC088	*Aspidoscelis*	*septemvittatus*	sexual	Warm North American Deserts	36	1.728	12.557
KLC089	*Aspidoscelis*	*septemvittatus*	sexual	Warm North American Deserts	47	0.660	14.268
KLC090	*Aspidoscelis*	*septemvittatus*	sexual	Warm North American Deserts	26	0.241	8.469
KLC091	*Aspidoscelis*	*septemvittatus*	sexual	Warm North American Deserts	37	2.598	11.563
KLC092	*Aspidoscelis*	*septemvittatus*	sexual	Warm North American Deserts	27	0.823	9.369
KLC093	*Aspidoscelis*	*septemvittatus*	sexual	Warm North American Deserts	20	0.512	7.589
KLC094	*Aspidoscelis*	*septemvittatus*	sexual	Warm North American Deserts	37	1.975	12.290
KLC095	*Aspidoscelis*	*inornatus*	sexual	Warm North American Deserts	41	1.899	12.922
KLC096	*Aspidoscelis*	*inornatus*	sexual	Warm North American Deserts	74	2.849	21.596
KLC097	*Aspidoscelis*	*marmoratus*	sexual	Warm North American Deserts	60	2.137	17.976
KLC098	*Aspidoscelis*	*septemvittatus*	sexual	Warm North American Deserts	50	0.884	15.054
KLC099	*Aspidoscelis*	*marmoratus*	sexual	Warm North American Deserts	37	1.142	10.913
KLC100	*Aspidoscelis*	*marmoratus*	sexual	Warm North American Deserts	63	2.953	20.178
KLC101	*Aspidoscelis*	*marmoratus*	sexual	Warm North American Deserts	42	0.530	14.544
KLC102	*Aspidoscelis*	*marmoratus*	sexual	Warm North American Deserts	46	1.552	14.971
KLC103	*Aspidoscelis*	*marmoratus*	sexual	Warm North American Deserts	69	2.928	20.324
KLC104	*Aspidoscelis*	*marmoratus*	sexual	Warm North American Deserts	73	2.699	22.056
KLC105	*Aspidoscelis*	*marmoratus*	sexual	Warm North American Deserts	36	0.332	11.489
KLC106	*Aspidoscelis*	*marmoratus*	sexual	Warm North American Deserts	58	3.152	19.192
KLC107	*Aspidoscelis*	*marmoratus*	sexual	Warm North American Deserts	48	2.982	15.553
KLC108	*Aspidoscelis*	*marmoratus*	sexual	Warm North American Deserts	88	3.177	27.150
KLC109	*Aspidoscelis*	*marmoratus*	sexual	Warm North American Deserts	55	2.880	17.158
KLC112	*Aspidoscelis*	*marmoratus*	sexual	Warm North American Deserts	70	2.713	22.046
KLC116	*Aspidoscelis*	*marmoratus*	sexual	Warm North American Deserts	42	1.040	11.139
KLC117	*Aspidoscelis*	*marmoratus*	sexual	Warm North American Deserts	62	3.161	21.653
KLC118	*Aspidoscelis*	*septemvittatus*	sexual	Warm North American Deserts	34	2.585	9.831
KLC119	*Aspidoscelis*	*septemvittatus*	sexual	Warm North American Deserts	80	3.147	25.585
KLC120	*Aspidoscelis*	*septemvittatus*	sexual	Warm North American Deserts	47	1.938	15.004
KLC121	*Aspidoscelis*	*marmoratus*	sexual	Warm North American Deserts	67	3.191	20.789
KLC122	*Aspidoscelis*	*septemvittatus*	sexual	Warm North American Deserts	36	1.067	12.355
KLC123	*Aspidoscelis*	*septemvittatus*	sexual	Warm North American Deserts	87	3.106	30.552
KLC124	*Aspidoscelis*	*septemvittatus*	sexual	Warm North American Deserts	37	2.384	13.727

KLC125	*Aspidoscelis*	*septemvittatus*	sexual	Warm North American Deserts	72	2.861	22.646
KLC126	*Aspidoscelis*	*inornatus*	sexual	Warm North American Deserts	87	2.224	28.001
KLC127	*Aspidoscelis*	*inornatus*	sexual	Warm North American Deserts	112	3.086	33.225
KLC129	*Aspidoscelis*	*septemvittatus*	sexual	Warm North American Deserts	43	1.345	13.586
KLC130	*Aspidoscelis*	*septemvittatus*	sexual	Warm North American Deserts	109	2.245	34.195
KLC133	*Aspidoscelis*	*marmoratus*	sexual	Warm North American Deserts	52	2.260	17.031
KLC134	*Aspidoscelis*	*inornatus*	sexual	Warm North American Deserts	40	2.302	11.942
KLC135	*Aspidoscelis*	*septemvittatus*	sexual	Warm North American Deserts	43	2.395	12.887
KLC136	*Aspidoscelis*	*septemvittatus*	sexual	Warm North American Deserts	29	2.106	10.387
KLC137	*Aspidoscelis*	*marmoratus*	sexual	Warm North American Deserts	7	0.860	2.793
KLC138	*Aspidoscelis*	*marmoratus*	sexual	Warm North American Deserts	48	2.363	16.453
KLC139	*Aspidoscelis*	*marmoratus*	sexual	Warm North American Deserts	49	2.588	15.883
KLC140	*Aspidoscelis*	*marmoratus*	sexual	Warm North American Deserts	44	2.013	15.191
KLC141	*Aspidoscelis*	*inornatus*	sexual	Warm North American Deserts	49	2.131	16.389
KLC142	*Aspidoscelis*	*marmoratus*	sexual	Warm North American Deserts	30	0.588	10.804
KLC143	*Aspidoscelis*	*septemvittatus*	sexual	Warm North American Deserts	45	2.296	14.130
KLC145	*Aspidoscelis*	*marmoratus*	sexual	Warm North American Deserts	32	1.798	11.214
KLC146	*Aspidoscelis*	*marmoratus*	sexual	Warm North American Deserts	46	1.968	14.059
KLC147	*Aspidoscelis*	*septemvittatus*	sexual	Warm North American Deserts	47	2.095	16.732
KLC148	*Aspidoscelis*	*inornatus*	sexual	Warm North American Deserts	38	1.480	12.749
KLC149	*Aspidoscelis*	*marmoratus*	sexual	Warm North American Deserts	38	2.150	12.379
KLC151	*Aspidoscelis*	*marmoratus*	sexual	Warm North American Deserts	45	2.078	17.357
KLC166	*Aspidoscelis*	*gularis*	sexual	Warm North American Deserts	93	2.664	31.216
KLC167	*Aspidoscelis*	*gularis*	sexual	Warm North American Deserts	37	1.906	12.001
KLC170	*Aspidoscelis*	*neotesselatus*	asexual	South Central Semiarid Prairies	58	2.263	17.392
KLC172	*Aspidoscelis*	*sonorae*	asexual	Mediterranean California	50	2.299	16.250
KLC173	*Aspidoscelis*	*sonorae*	asexual	Mediterranean California	62	1.793	20.991
KLC174	*Aspidoscelis*	*sonorae*	asexual	Mediterranean California	58	2.608	19.221
KLC175	*Aspidoscelis*	*sonorae*	asexual	Mediterranean California	39	2.360	12.628
KLC176	*Aspidoscelis*	*sonorae*	asexual	Mediterranean California	58	2.512	18.074
KLC177	*Aspidoscelis*	*sonorae*	asexual	Mediterranean California	22	0.496	7.585
KLC178	*Aspidoscelis*	*sonorae*	asexual	Mediterranean California	113	3.306	33.345

KLC179	*Aspidoscelis*	*sonorae*	asexual	Mediterranean California	32	0.987	10.771
KLC180	*Aspidoscelis*	*sonorae*	asexual	Mediterranean California	38	0.598	12.629
KLC181	*Aspidoscelis*	*sonorae*	asexual	Mediterranean California	96	1.563	30.094
KLC182	*Aspidoscelis*	*sonorae*	asexual	Mediterranean California	61	2.591	20.841
KLC183	*Aspidoscelis*	*sonorae*	asexual	Mediterranean California	62	2.047	19.132
KLC185	*Aspidoscelis*	*sonorae*	asexual	Mediterranean California	76	1.652	21.880
KLC186	*Aspidoscelis*	*sonorae*	asexual	Mediterranean California	67	1.235	20.910
KLC187	*Aspidoscelis*	*sonorae*	asexual	Mediterranean California	72	2.397	21.874
KLC190	*Aspidoscelis*	*sonorae*	asexual	Mediterranean California	38	2.203	13.139
KLC191	*Aspidoscelis*	*sonorae*	asexual	Mediterranean California	60	1.242	16.613
KLC192	*Aspidoscelis*	*sonorae*	asexual	Mediterranean California	24	1.033	9.394
KLC193	*Aspidoscelis*	*sonorae*	asexual	Mediterranean California	58	1.779	18.251
KLC194	*Aspidoscelis*	*sonorae*	asexual	Mediterranean California	56	2.416	15.708
KLC195	*Aspidoscelis*	*sonorae*	asexual	Mediterranean California	39	1.697	12.760
RLK072	*Aspidoscelis*	*marmoratus*	sexual	Warm North American Deserts	31	0.982	10.711
RLK079	*Aspidoscelis*	*uniparens*	asexual	Warm North American Deserts	36	0.495	11.604
RLK080	*Aspidoscelis*	*exsanguis*	asexual	Warm North American Deserts	34	0.217	10.573
RLK081	*Aspidoscelis*	*exsanguis*	asexual	Warm North American Deserts	12	0.079	3.546
RLK083	*Aspidoscelis*	*uniparens*	asexual	Warm North American Deserts	54	1.250	15.954
RLK084	*Aspidoscelis*	*exsanguis*	asexual	Warm North American Deserts	53	1.467	15.889
RLK085	*Aspidoscelis*	*neomexicanus*	asexual	Warm North American Deserts	27	1.821	10.323
RLK086	*Aspidoscelis*	*neomexicanus*	asexual	Warm North American Deserts	41	2.208	12.958
RLK087	*Aspidoscelis*	*neomexicanus*	asexual	Warm North American Deserts	88	2.501	26.786
RLK089	*Aspidoscelis*	*neomexicanus*	asexual	Warm North American Deserts	38	1.781	12.894
RLK090	*Aspidoscelis*	*neomexicanus*	asexual	Warm North American Deserts	32	0.392	10.482
RLK097	*Aspidoscelis*	*neomexicanus*	asexual	Warm North American Deserts	44	2.010	13.829
RLK099	*Aspidoscelis*	*neomexicanus*	asexual	Warm North American Deserts	65	3.215	20.909
RLK100	*Aspidoscelis*	*neomexicanus*	asexual	Warm North American Deserts	55	2.479	18.243
RLK102	*Aspidoscelis*	*neomexicanus*	asexual	Warm North American Deserts	29	1.041	9.923