**Differences in alpha diversity between main genera**

**Species richness:**

ANOVA found the main effect of psyllid genus on microbial ASV richness to be significant (F(2, 174) = 12.16, p < .001) and can be considered as medium (partial omega squared = 0.11). A post hoc Tukey test indicated that both the Psylla and Trioza genera had significantly lower ASV richness than Ctenarytaina (p < .001), while there was no significant difference in microbial ASV richness between Trioza and Psylla.

Unrarefied:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **comparison** | estimate | conf.low | conf.high | adj.p.value |
| Psylla-Ctenarytaina | -23.833735 | -38.011281 | -9.6561893 | 0.00030343 |
| Trioza-Ctenarytaina | -13.091963 | -21.034836 | -5.14909 | 0.00040726 |
| Trioza-Psylla | 10.7417722 | -3.490605 | 24.9741493 | 0.17789899 |

Rarefied:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| comparison | estimate | conf.low | conf.high | adj.p.value |
| Psylla-Ctenarytaina | -9.4232932 | -17.901745 | -0.944841 | 0.0252762 |
| Trioza-Ctenarytaina | -9.1439683 | -13.893963 | -4.3939736 | 2.97E-05 |
| Trioza-Psylla | 0.27932489 | -8.2319176 | 8.79056734 | 0.99668728 |

Without Gammaproteobacteria:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| comparison | estimate | conf.low | conf.high | adj.p.value |
| Psylla-Ctenarytaina | -14.275502 | -24.347535 | -4.2034687 | 2.83E-03 |
| Trioza-Ctenarytaina | -7.2890041 | -12.931792 | -1.6462165 | 0.00734441 |
| Trioza-Psylla | 6.98649789 | -3.1244889 | 17.0974846 | 0.23436457 |

**Shannon diversity**

ANOVA found the main effect of psyllid genus on microbial Shannon diversity to be significant (F(2, 174) = 7.79, p < .001) and can be considered as medium (partial omega squared = 0.07). A post hoc Tukey test indicated that both the Psylla and Trioza genera had significantly lower Shannon diversity than Ctenarytaina (p < .05), while there was no significant difference in microbial Shannon diversity between Trioza and Psylla.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| comparison | estimate | conf.low | conf.high | adj.p.value |
| Psylla-Ctenarytaina | -0.4317089 | -0.8450283 | -0.0183896 | 0.03837304 |
| Trioza-Ctenarytaina | -0.3563431 | -0.5879025 | -0.1247838 | 0.0010505 |
| Trioza-Psylla | 0.07536579 | -0.3395521 | 0.49028365 | 0.9034349 |

Rarefied

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| comparison | estimate | conf.low | conf.high | adj.p.value |
| Psylla-Ctenarytaina | -0.429772 | -0.8417108 | -0.0178332 | 0.03865354 |
| Trioza-Ctenarytaina | -0.3443314 | -0.5751173 | -0.1135454 | 0.00155199 |
| Trioza-Psylla | 0.08544063 | -0.3280914 | 0.49897263 | 0.87690627 |

Without Gammaproteobacteria

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| comparison | estimate | conf.low | conf.high | adj.p.value |
| Psylla-Ctenarytaina | -0.429772 | -0.8417108 | -0.0178332 | 0.03865354 |
| Trioza-Ctenarytaina | -0.3443314 | -0.5751173 | -0.1135454 | 0.00155199 |
| Trioza-Psylla | 0.08544063 | -0.3280914 | 0.49897263 | 0.87690627 |

**Phylogenetic diversity**

ANOVA found the main effect of psyllid genus on microbial phylogenetic diversity to be significant (F(2, 174) = 13.17, p < .001) and can be considered as medium (partial omega squared = 0.12). A post hoc Tukey test indicated that both the Psylla and Trioza genera had significantly lower phylogenetic diversity than Ctenarytaina (p < .001), while there was no significant difference in microbial phylogenetic diversity between Trioza and Psylla.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| comparison | estimate | conf.low | conf.high | adj.p.value |
| Psylla-Ctenarytaina | -2.896E+10 | -4.495E+10 | -1.298E+10 | 8.95E-05 |
| Trioza-Ctenarytaina | -1.473E+10 | -2.368E+10 | -5.772E+09 | 0.00042083 |
| Trioza-Psylla | 1.4239E+10 | -1.805E+09 | 3.0283E+10 | 0.09319637 |

Rarefied

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| comparison | estimate | conf.low | conf.high | adj.p.value |
| Psylla-Ctenarytaina | -1.304E+10 | -2.477E+10 | -1.314E+09 | 0.02518197 |
| Trioza-Ctenarytaina | -1.277E+10 | -1.934E+10 | -6.199E+09 | 2.47E-05 |
| Trioza-Psylla | 272420321 | -1.15E+10 | 1.2046E+10 | 0.99835204 |

Without Gammaproteobacteria

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| comparison | estimate | conf.low | conf.high | adj.p.value |
| Psylla-Ctenarytaina | -2.399E+10 | -3.794E+10 | -1.004E+10 | 0.00021313 |
| Trioza-Ctenarytaina | -1.132E+10 | -1.916E+10 | -3.482E+09 | 2.29E-03 |
| Trioza-Psylla | 1.2668E+10 | -1.348E+09 | 2.6684E+10 | 0.08549326 |

**Differences in alpha diversity between main genera, taking into account AUS/NZ split in Ctenarytaina**

**Species richness:**

ANOVA found the main effect of genus/geo on microbial ASV richness to be significant (F(3, 173) = 9.67, p < .001) and can be considered as medium (partial omega squared = 0.13). A post hoc Tukey test indicated that the genus Psylla had significantly lower ASV richness than Ctenarytaina\_AUS and Ctenarytaina\_NZ (p < .05, and p < .001). The genus Trioza had significantly lower ASV richness than Ctenarytaina\_NZ (p < .05) however no significant difference with Ctenarytaina\_AUS. No significant difference for ASV richness was found between Trioza and Psylla or Ctenarytaina\_NZ and Ctenarytaina\_AUS.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| comparison | estimate | conf.low | conf.high | adj.p.value |
| Ctenarytaina\_NZ-Ctenarytaina\_AUS | 9.58538012 | -2.5204739 | 21.6912342 | 0.17255088 |
| Psylla-Ctenarytaina\_AUS | -18.636842 | -35.392248 | -1.8814363 | 0.0226537 |
| Trioza-Ctenarytaina\_AUS | -7.89507 | -18.742879 | 2.95273905 | 0.23696461 |
| Psylla-Ctenarytaina\_NZ | -28.222222 | -44.604647 | -11.839797 | 8.31E-05 |
| Trioza-Ctenarytaina\_NZ | -17.48045 | -27.742768 | -7.2181317 | 0.00010225 |
| Trioza-Psylla | 10.7417722 | -4.7342447 | 26.217789 | 0.27657559 |

Rarefied

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| comparison | estimate | conf.low | conf.high | adj.p.value |
| Ctenarytaina\_NZ-Ctenarytaina\_AUS | 4.99707602 | -2.2636248 | 12.2577768 | 0.28384806 |
| Psylla-Ctenarytaina\_AUS | -6.7140351 | -16.763387 | 3.33531685 | 0.30970958 |
| Trioza-Ctenarytaina\_AUS | -6.4347102 | -12.940876 | 0.07145575 | 0.05378272 |
| Psylla-Ctenarytaina\_NZ | -11.711111 | -21.536761 | -1.8854612 | 0.0123036 |
| Trioza-Ctenarytaina\_NZ | -11.431786 | -17.586794 | -5.2767787 | 1.86E-05 |
| Trioza-Psylla | 0.27932489 | -9.0026909 | 9.56134064 | 0.99982877 |

Without Gammaproteobacteria

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| comparison | estimate | conf.low | conf.high | adj.p.value |
| Ctenarytaina\_NZ-Ctenarytaina\_AUS | 10.3678363 | 1.90693517 | 18.8287373 | 0.00940581 |
| Psylla-Ctenarytaina\_AUS | -8.654386 | -20.364905 | 3.05613279 | 0.22464395 |
| Trioza-Ctenarytaina\_AUS | -1.6678881 | -9.249529 | 5.91375289 | 0.94068112 |
| Psylla-Ctenarytaina\_NZ | -19.022222 | -30.472061 | -7.5723836 | 0.00015958 |
| Trioza-Ctenarytaina\_NZ | -12.035724 | -19.20816 | -4.8632886 | 1.34E-04 |
| Trioza-Psylla | 6.98649789 | -3.8298433 | 17.8028391 | 0.33970285 |

**Shannon diversity**

ANOVA found the main effect of genus/geo on microbial Shannon diversity to be significant (F(3, 173) = 5.21, p = 0.002) and can be considered as medium (partial omega squared = 0.07). A post hoc Tukey test indicated that the genus Psylla had significantly lower Shannon diversity than Ctenarytaina\_AUS and Ctenarytaina\_NZ (p < .05, and p < .001). The genus Trioza had significantly lower Shannon diversity than Ctenarytaina\_NZ (p < .05) however no significant difference with Ctenarytaina\_AUS. No significant difference for Shannon diversity was found between Trioza and Psylla or Ctenarytaina\_NZ and Ctenarytaina\_AUS.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| comparison | estimate | conf.low | conf.high | adj.p.value |
| Ctenarytaina\_NZ-Ctenarytaina\_AUS | 9.58538012 | -2.5204739 | 21.6912342 | 0.17255088 |
| Psylla-Ctenarytaina\_AUS | -18.636842 | -35.392248 | -1.8814363 | 0.0226537 |
| Trioza-Ctenarytaina\_AUS | -7.89507 | -18.742879 | 2.95273905 | 0.23696461 |
| Psylla-Ctenarytaina\_NZ | -28.222222 | -44.604647 | -11.839797 | 8.31E-05 |
| Trioza-Ctenarytaina\_NZ | -17.48045 | -27.742768 | -7.22E+00 | 0.00010225 |
| Trioza-Psylla | 10.7417722 | -4.7342447 | 26.217789 | 0.27657559 |

Rarefied

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| comparison | estimate | conf.low | conf.high | adj.p.value |
| Ctenarytaina\_NZ-Ctenarytaina\_AUS | 4.99707602 | -2.2636248 | 12.2577768 | 0.28384806 |
| Psylla-Ctenarytaina\_AUS | -6.7140351 | -16.763387 | 3.33531685 | 0.30970958 |
| Trioza-Ctenarytaina\_AUS | -6.4347102 | -12.940876 | 0.07145575 | 0.05378272 |
| Psylla-Ctenarytaina\_NZ | -11.711111 | -21.536761 | -1.8854612 | 0.0123036 |
| Trioza-Ctenarytaina\_NZ | -11.431786 | -17.586794 | -5.2767787 | 1.86E-05 |
| Trioza-Psylla | 0.27932489 | -9.0026909 | 9.56134064 | 0.99982877 |

Without Gammaproteobacteria

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| comparison | estimate | conf.low | conf.high | adj.p.value |
| Ctenarytaina\_NZ-Ctenarytaina\_AUS | 10.3678363 | 1.90693517 | 18.8287373 | 0.00940581 |
| Psylla-Ctenarytaina\_AUS | -8.654386 | -20.364905 | 3.05613279 | 0.22464395 |
| Trioza-Ctenarytaina\_AUS | -1.6678881 | -9.249529 | 5.91375289 | 0.94068112 |
| Psylla-Ctenarytaina\_NZ | -19.022222 | -30.472061 | -7.5723836 | 0.00015958 |
| Trioza-Ctenarytaina\_NZ | -12.035724 | -19.20816 | -4.8632886 | 0.00013383 |
| Trioza-Psylla | 6.98649789 | -3.8298433 | 17.8028391 | 3.40E-01 |

**Phylogenetic diversity**

ANOVA found the main effect of genus/geo on microbial phylogenetic diversity to be significant (F(3, 173) = 9.67, p < .001) and can be considered as medium (partial omega squared = 0.13). A post hoc Tukey test indicated that the genus Psylla had significantly lower phylogenetic diversity than Ctenarytaina\_AUS and Ctenarytaina\_NZ (p < .05, and p < .001). The genus Trioza had significantly lower phylogenetic diversity than Ctenarytaina\_NZ (p < .05) however no significant difference with Ctenarytaina\_AUS. Ctenarytaina\_NZ had a significant but slightly higher phylogenetic diversity than Ctenarytaina\_AUS (p < 0.05) and no significant difference was found between the genera Trioza and Psylla.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| comparison | estimate | conf.low | conf.high | adj.p.value |
| Ctenarytaina\_NZ-Ctenarytaina\_AUS | 1.3841E+10 | 300926179 | 2.7381E+10 | 0.0430322 |
| Psylla-Ctenarytaina\_AUS | -2.146E+10 | -4.02E+10 | -2.72E+09 | 0.0176914 |
| Trioza-Ctenarytaina\_AUS | -7.222E+09 | -1.935E+10 | 4911336967 | 0.41356417 |
| Psylla-Ctenarytaina\_NZ | -3.53E+10 | -5.362E+10 | -1.698E+10 | 8.37E-06 |
| Trioza-Ctenarytaina\_NZ | -2.106E+10 | -3.254E+10 | -9.584E+09 | 2.40E-05 |
| Trioza-Psylla | 1.4239E+10 | -3.07E+09 | 3.1548E+10 | 0.14648745 |

Rarefied

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| comparison | estimate | conf.low | conf.high | adj.p.value |
| Ctenarytaina\_NZ-Ctenarytaina\_AUS | 1.2574E+10 | 2746015439 | 2.2402E+10 | 0.00601264 |
| Psylla-Ctenarytaina\_AUS | -6.225E+09 | -1.983E+10 | 7377641518 | 0.63574716 |
| Trioza-Ctenarytaina\_AUS | -5.953E+09 | -1.476E+10 | 2853969398 | 0.29949363 |
| Psylla-Ctenarytaina\_NZ | -1.88E+10 | -3.21E+10 | -5.499E+09 | 0.0018403 |
| Trioza-Ctenarytaina\_NZ | -1.853E+10 | -2.686E+10 | -1.02E+10 | 2.16E-07 |
| Trioza-Psylla | 272420321 | -1.229E+10 | 1.2837E+10 | 0.99993588 |

Without Gammaproteobacteria

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| comparison | estimate | conf.low | conf.high | adj.p.value |
| Ctenarytaina\_NZ-Ctenarytaina\_AUS | 1.3292E+10 | 1528168345 | 2.5056E+10 | 0.01986236 |
| Psylla-Ctenarytaina\_AUS | -1.678E+10 | -3.307E+10 | -501275970 | 0.04058011 |
| Trioza-Ctenarytaina\_AUS | -4.115E+09 | -1.468E+10 | 6447895947 | 0.74337185 |
| Psylla-Ctenarytaina\_NZ | -3.008E+10 | -4.6E+10 | -1.416E+10 | 1.30E-05 |
| Trioza-Ctenarytaina\_NZ | -1.741E+10 | -2.74E+10 | -7.412E+09 | 6.79E-05 |
| Trioza-Psylla | 1.2668E+10 | -2.386E+09 | 2.7722E+10 | 1.32E-01 |

**Differences in Beta diversity between main genera for all microbial taxa**

Adonis tests found the main effect of psyllid genus on Aitchison distance between samples to be significant (R2 = 0.06, p = 0.001). Pairwise adonis tests then found

Ctenarytaina to have significantly different composition to Trioza (R2 = 0.13, p = 0.001) and Psylla (R2 = 0.10, p = 0.001) but no significant difference in composition found between Trioza and Psylla (R2 = 0.01567, p >0.05)

**Differences in alpha diversity between main genera for all microbial taxa, taking into account AUS/NZ split in Ctenarytaina**

Adonis tests found the main effect of genus/geo on Aitchison distance between samples to be significant (R2 = 0.09, p = 0.001). Pairwise adonis tests then found that

Ctenarytaina\_AUS\_vs\_Trioza to be significant (R2 = 0.10, p = 0.001), Ctenarytaina\_AUS\_vs\_Psylla to be significant (R2 = 0.19, p = 0.002), Trioza\_vs\_Ctenarytaina\_NZ to be significant (R2 = 0.17, p = 0.001),

Ctenarytaina\_NZ\_vs\_Psylla to be significant (R2 = 0.17, p = 0.001),

Ctenarytaina\_AUS\_vs\_Ctenarytaina\_NZ to be significant (R2 = 0.06, p = 0.004),

But no significant differences between Trioza and Psylla (R2 = 0.01567, p > 0.05)