**S13 Table. Statistical analysis of the variation in toxin gene composition across evolution treatments and time1.**

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| --- | --- | --- | --- | --- |
| **Comparison** | **Factor** | **df** | ***χ2*** | ***P*** |
| Coevolution vs. Adaptation | Treatment | 5 | < 0.01 | >0.99 |
|  | Transfer | 5 | 10.9 | 0.0544 |
|  | Treatment \* Transfer | 5 | 48.3 | **< 0.0001** |
| Coevolution vs. Control | Treatment | 5 | 96.3 | **< 0.0001** |
|  | Transfer | 5 | 7.1 | 0.2129 |
|  | Treatment \* Transfer | 5 | 54.5 | **< 0.0001** |
| Adaptation vs. Control | Treatment | 4 | < 0.01 | > 0.99 |
|  | Transfer | 4 | 69.6 | **< 0.0001** |
|  | Treatment \* Transfer | 4 | 2.55 | 0.6358 |

1 The defined nominal logistic models included evolution treatment, transfer, and the interactions between the two as fixed factors and replicate nested within treatment as random factor. The specified models provided a better fit to the data than the corresponding minimal model (*P* < 0.0001). The table shows the effect tests for the fixed factors. Significant probabilities after FDR correction are given in bold. The data is shown in S4 Data.