**S4 Table. Comparison between evolved and ancestral pathogen phenotypes1**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Trait** | **Treatment** | **Transfer2** | ***F*** | **df** | ***P*** |
| Killing ability | Coevolution | 12 | 0.50 | 1,16 | 0.4858 |
|  |  | 20 | 0.79 | 1,16 | 0.3869 |
|  |  | 28 | 8.53 | 1,16 | **0.0100** |
|  | Adaptation | 12 | 4.41 | 1,16 | 0.0517 |
|  |  | 20 | 0.46 | 1,11 | 0.5086 |
|  |  | 28 | 2.10 | 1,11 | 0.1748 |
|  | Control | 12 | 215.88 | 1,15 | **<0.0001** |
|  |  | 20 | 1715.68 | 1,15 | **<0.0001** |
|  |  | 28 | 1542.75 | 1,14 | **<0.0001** |
| Pathogen  | Coevolution | 12 | 1.02 | 1,14 | 0.3200 |
| impact |  | 20 | 1.26 | 1,14 | 0.2700 |
| on host pop. |  | 28 | 2.94 | 1,14 | 0.1081 |
| growth | Adaptation | 12 | 3.20 | 1,14 | 0.0949 |
|  |  | 20 | 1.64 | 1,10 | 0.2287 |
|  |  | 28 | 0.79 | 1,8 | 0.3975 |
|  | Control | 12 | 21.89 | 1,14 | **0.0004** |
|  |  | 20 | 95.13 | 1,10 | **<0.0001** |
|  |  | 28 | 18.70 | 1,14 | **0.0007** |
| Pathogen  | Coevolution | 12 | 4.89 | 1,14 | 0.0440 |
| impact |  | 20 | 4.19 | 1,13 | 0.0612 |
| on host body |  | 28 | 11.84 | 1,15 | **0.0036** |
| size | Adaptation | 12 | 0.00 | 1,14 | 0.9623 |
|  |  | 20 | 0.27 | 1,10 | 0.6138 |
|  |  | 28 | 0.08 | 1,10 | 0.7792 |
|  | Control | 12 | 46.68 | 1,15 | **<0.0001** |
|  |  | 20 | 111.18 | 1,11 | **<0.0001** |
|  |  | 28 | 103.81 | 1,13 | **<0.0001** |
| Pathogen  | Coevolution | 12 | 2.79 | 1,14 | 0.1168 |
| infection load3 |  | 20 | 1.83 | 1,14 | 0.1967 |
|  |  | 28 | 3.95 | 1,15 | 0.0653 |
|  | Adaptation | 12 | 4.10 | 1,13 | 0.0638 |
|  |  | 20 | 3.40 | 1,8 | 0.1023 |
|  |  | 28 | 5.18 | 1,8 | 0.0523 |
|  | Control | 12 | 3.42 | 1,15 | 0.0842 |
|  |  | 20 | 2.26 | 1,11 | 0.1607 |
|  |  | 28 | 3.2 | 1,13 | 0.0966 |

1 Comparison between evolved (pathogen coevolution, pathogen one-sided adaptation and pathogen control) and ancestral pathogens both exposed to ancestral hosts using an analysis of variance. Degrees of freedom (df) are given for the comparison and the error (before and after comma, respectively). Significant values after FDR adjustment are in bold. The data is shown in S1 Data.

2 Time point is given as host transfer number.

3 Infection load is adjusted by body size.