**Table S1. Per-generation changes in mean, genetic variance, environmental variance and mutational heritability after approximately 1,500 generations of mutation accumulation under normal and salt-stress environments.**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Fitness component | Treatment | N, # lines | Number of MA lines different in mean from the ancestor  (greater, lesser) | Per-generation change in Mean  (Δ*M*) | Mutational Variance  (*V*m = Δ*V*G/*t*) | Per-generation change in Environmental Variance (Δ*V*E/*t*) | Mutational Heritability  (*h*2m) |
| Diploid growth rate | Normal-MA | 416, 42 | 0,5 | **−7.73×10-6**  (0.02) | **6.72×10-7**  (<0.0001) | 1.95×10-7  (0.14) | **0.000538**  (<0.0001) |
|  | Salt-MA | 366, 42 | 0,3 | **−1.06×10-5**  (< 0.0001) | **2.63×10-7**  (<0.0001) | **4.57×10-7**  (0.0086) | **0.000158**  (0.0018) |
|  | Normal- vs. Salt-MA |  |  | (0.50) | (0.16) | (0.22) | (0.071) |
|  |  |  |  |  |  |  |  |
| Sporulation efficiency | Normal-MA | 206, 42 | 0,4 | **−1.13×10-5**  (0.035) | **1.60×10-6**  (0.0004) | 2.62×10-7  (0.21) | **0.000726**  (0.0008) |
|  | Salt-MA | 196, 45 | 2,6 | −1.13×10-5  (0.17) | **3.78×10-6**  (<0.0001) | **6.84×10-7**  (0.0044) | **0.00132**  (<0.0001) |
|  | Normal- vs. Salt-MA |  |  | (0.99) | (0.11) | (0.13) | (0.30) |
|  |  |  |  |  |  |  |  |
| Haploid viability | Normal-MA | 89, 17 | 0,0 | −1.85×10-4  (0.32) | **0.000516**  (0.0016) | −0.000347  (0.18) | **0.000343**  (0.0016) |
|  | Salt-MA | 107, 21 | 0,0 | **−3.23×10-4**  (0.04) | **0.000523**  (<0.0001) | **−0.000866**  (<0.0001) | **0.000723**  (<0.0001) |
|  | Normal- vs. Salt-MA |  |  | (0.30) | (0.98) | (0.023) | (0.23) |
|  |  |  |  |  |  |  |  |
| Haploid growth rate | Normal-MA | 350, 16 | 0,3 | **−1.09×10-5**  (<0.001) | **7.62×10-7**  (0.003) | −3.88×10-8  (0.86) | **0.000444**  (0.003) |
|  | Salt-MA | 358, 18 | 1,4 | **−2.61×10-5**  (0.0014) | **5.94×10-6**  (<0.001) | **2.46×10-6**  (0.006) | **0.00119**  (<0.001) |
|  | Normal- vs. Salt-MA |  |  | (0.11) | (0.004) | (0.006) | (0.19) |

Tests of differences in MA lines from ancestor and between treatments were obtained by bootstrapping among lines (*P*-values in parentheses).