

SELECTION RESPONSE FOR RESISTANCE TO BACTERIAL DISEASES IN NILE TILAPIA

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Bacterial disease resistance has been studied in the Spring Genetics Nile tilapia breeding program population. Siblings from families produced in the bio-secure breeding nucleus have been challenged with *S. iniae*, *S. agalactiae 1b* and *Francisella*. The objectives of this study were first, to confirm additive genetic variation exists for *S. iniae*, *S. agalactiae 1b* and *Francisella* survival. Second, to determine the genetic correlation between survival for different bacterial diseases. Third, to compare the survival of families produced through positive assortative mating between parents with high and low estimated breeding values (EBV) for each trait. Fourth, to estimate the response to selection for bacterial diseases by genetic trend analysis.

Using a multivariate animal linear model with data from all generations, a significant additive genetic component was found for all traits with heritability (h^2) estimates of 0.21 ± 0.03 for *S. agalactiae*, 0.45 ± 0.06 for *S. iniae* and 0.30 ± 0.05 for *Francisella*. There was a negative and unfavourable genetic relationship between *S. agalactiae* and *S. iniae* survival ($r_g = -0.29 \pm 0.13$). Apart from that, there were no statistically significant relationships between any traits. Assortative mating groups with high breeding values always had higher survival than the groups of low breeding values, and this difference was on average 58%_units (range from 38-78 %_units). For *S. agalactiae* an increase of 20%_units occurred in six generations and for *Francisella* 4%_units in three generations of multitrait selection with ~29% of relative weight per disease resistance traits. Likewise For *S. iniae* an increase of 11%_units was achieved after two generations of selection. These results highlight the efficacy of concurrent selection to improve resistance to multiple bacterial diseases in a commercial tilapia breeding programme.

The work reported here has been followed up with extensive genomic work to further increase the efficacy of selection for improved disease resistance.