Risk of disease outbreaks in aquaculture when selecting against mortality in the presence of genetically correlated underlying epidemiological traits

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Abstract

Infectious disease outbreaks represent a significant threat to the sustainability of the aquaculture industry. Consequently, selection for disease resistance has become a key objective in aquaculture breeding programs. Disease resistance is typically recorded as mortality in challenge tests performed on sibs of selection candidates. Thus, selection for disease resistance aims to minimize mortality rates. However, to enhance commercial success, it is crucial to address not only mortality rates but also mitigate infectious disease transmission (i.e., the incidence and severity of outbreaks). Both mortality and transmission depend on three underlying (not readily observable) epidemiological traits: susceptibility, infectivity, and infection-induced mortality. This study aimed to evaluate the effect of applying genomic selection against mortality on disease transmission in a simulated fish population, after exposure to an infectious pathogen in a challenge test. Selection was applied for 10 discrete generations. The disease was assumed to be produced by a virus with a fast transmission rate, such as the infectious salmon anemia virus. Mortality was measured as dead/alive status or time to death. Phenotypes were obtained by assuming a stochastic compartmental Susceptible-Infected-Removed epidemiological model with genetic variation assumed in the three epidemiological traits. Different scenarios varying in the genetic correlations between the underlying traits were considered. Additionally, two challenge test designs were simulated: few large groups and many small groups. All families were equally represented in all groups. For dead/alive status phenotypes, the test stopped when 50% of the fish were dead at 15 days post-challenge. For time to death phenotypes, the test stopped when mortality naturally levels off (with 80% of the fish dead) at 60 days post-challenge. The basic reproductive ratio (R_0) was used to evaluate disease transmission. In scenarios with dead/alive status phenotypes, R_0 values greatly depended on the correlation between the underlying traits. In contrast, in all scenarios with time to death phenotypes, selection always led to a reduction in R_0 reaching in most cases values below one, meaning that the infection is unlikely to propagate. Thus, genomic selection against mortality measured as time to death can simultaneously reduce mortality and disease transmission.

Keywords: disease resistance; infectious disease transmission; genomic selection, salmon breeding programs, SIR epidemiological model