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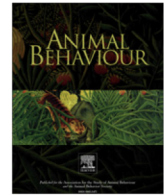


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Heritability and genetic correlations of escape behaviours in juvenile scallop *Argopecten purpuratus*

Katherina Brokordt^{a,b,*}, William Farías^{a,b}, Jean Paul Lhorente^c, Federico Winkler^{a,b}

^aCEAZA (Centre for Advanced Studies in Arid Zones), Universidad Católica del Norte, Coquimbo, Chile

^bMarine Biology Department, Marine Science Faculty, Universidad Católica del Norte, Coquimbo, Chile

^cAquainnovo, Polpaico 037, Puerto Montt, Chile

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Escape behaviours are generally considered adaptive because of their obvious effects on fitness. However, little is known about the genetic basis of escape responses. The estimation of the magnitude of hereditary factors affecting variation in escape responses indicates their potential to evolve by natural selection. Scallops are exceptional among bivalve molluscs because they possess an excellent swimming capacity, which helps them to escape predators. In this study we estimated the narrow-sense heritability (h^2), phenotypic variance components and phenotypic and genetic correlations of several escape response traits (i.e. reaction time, number of claps (rapid valve closures and openings), and the duration and intensity of the clapping response) in juvenile *Argopecten purpuratus* scallops. We stimulated scallop escape responses using their natural predator, the sea star *Meyenaster gelatinosus*. Genetic estimates for escape response traits were determined by the animal model. Most studied traits showed substantial amounts of additive genetic variance controlling their phenotypic variation ($CV_A = 18.43–100.2$), were repeatable (at least over a short period, $R = 0.36–0.42$), and had significant heritabilities ($h^2 = 0.36–0.57$). Indeed, it can be inferred that most of the analysed escape response traits of *A. purpuratus* could evolve through natural selection. Moreover, significant genetic correlations between some escape response traits were observed, suggesting that selection acting on one escape trait will affect that of another, facilitating their coevolution.

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