Chromosomal footprint of a human-induced adaptive introgression and its structural variation in sea-squirts

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Résumé

Adaptive introgression (i.e., the incorporation of beneficial alleles through introgressive hybridization) has gained increasing attention in recent years because of its possible pivotal role in species responses to global change, as well as its potential applications in agriculture or conservation, such as evolutionary rescue through introgression. While cases of introgression, particularly of genes conferring resistance to pesticides or pollution, are accumulating, the marine environment remains relatively underexplored in this regard, leaving many questions unanswered. Key among these are inquiries into the specific molecular variations that confer selective advantage and the chromosomal footprint resulting from the increased frequency of favorable mutations and subsequent gene flow. Two ascidian species, *Ciona intestinalis* and *C. robusta*, with a divergence history spanning 3 million years, have recently come into contact following the human-mediated introduction of the North Pacific *C. robusta* into the native range of its North Atlantic congener *C. intestinalis*. The two congeners inhabit human-altered environments, namely ports. Previous studies have identified a genomic island where segments of *C. robusta* ancestry have introgressed into *C. intestinalis*. Although not observed in all populations, several pieces of evidence pointed to adaptive introgression. Using a combination of long-read and linked-read sequencing methods, we examined a candidate tandem repeat of a P450 gene, likely involved in detoxification processes, located at the core of this introgression island, as well as the chromosomal landscape of ancestry within its flanking regions. This approach enabled us to refine our understanding of the adaptive molecular variation. It also allowed us to characterize tracts of *C. robusta* ancestry, in the flanking regions of the introgression island, that are due to gene flow from introgressed to non-introgressed *C. intestinalis* populations. These findings are consistent with the expectations of a local selective sweep model.

Mots-Clés: Anthropogenic hybridization, selective sweep, local adaptation, tandem repeat, marine species introduction

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