

Complementary genomic and epigenomic adaptation to environmental heterogeneity

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Abstract

While adaptation is commonly thought to result from selection on DNA sequence-based variation, recent studies have highlighted an analogous epigenetic component as well. However, the extent to which these adaptive mechanisms to adaptation to environmental heterogeneity are redundant or complementary remains unclear. To address the underlying genetic and epigenetic mechanisms and their relationship underlying environmental adaptation, we screened the genomes and epigenomes of nine global populations of a predominately sessile marine invasive tunicate, *Botryllus schlosseri*. We detected clear population genetic and epigenetic differentiation, which were both significantly influenced by local environments, and the minimum annual sea surface temperature (T_{min}) was simultaneously identified as the top explanatory variable for both types of variation. However, there remain some degree of difference in population structure patterns between two levels, suggesting a certain level of autonomy in epigenetic variation. From the functional perspective, a set of functional genes and biological pathways were shared between two levels, indicating a conjoint contribution of genetic and epigenetic variation to environmental adaptation. Moreover, we also detected genetic- or epigenetic-specific genes/pathways in relation to a wide variety of core processes potentially underlying adaptation to local environmental factors, suggesting the partly independent relationship between two mechanisms. We infer that complementary genetic and epigenetic routes to adaptation are available in this system. Collectively, these mechanisms may facilitate population persistence under environmental changes and sustain successful invasions in novel but contrasting environments.

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