Graduate School Event

Thesis Defense: The genomic architecture of local adaptation in introduced populations

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Rapid local adaptation to new environments is critical for species persistence, especially in introduced populations. The evolutionary success of these populations is fundamentally dictated by the organization of genetic variation—the genomic architecture—in the face of severe demographic constraints, such as the founder effects and genetic bottlenecks that frequently accompany colonization. A central question in evolutionary biology is whether rapid adaptation relies on major-effect loci, such as chromosomal inversions, or on many small-effect loci dispersed across the genome. Furthermore, the genomic architecture strongly influences the extent to which evolutionary outcomes are predictable. Using introduced populations of the marine snail, Littorina saxatilis, as a model, this thesis investigates how genetic variation and genomic structure drive adaptation following introduction. We employed a comparative genomics approach on experimentally and accidentally introduced populations to dissect the specific genomic features that underpin divergence in newly colonized environments.In Chapter 2, we tested the predictability of local adaptation through an uncommon 30-year transplant experiment in nature. By distinguishing allele and chromosomal inversion frequency changes from neutral expectations, we found that evolutionary change was highly predictable at the macro-scale (phenotypes and chromosomal inversions), but less robust at the level of individual collinear loci. This result demonstrates that evolution can be predictable when a population possesses sufficient standing genetic variation (SGV), with chromosomal inversions acting as key integrated units that facilitate a rapid response to selection. Building on this, Chapter 3 applied whole-genome sequencing to three accidentally introduced populations (Venice, San Francisco, and Redwood City) to investigate their likely source and genomic patterns of divergence. We identified genomic regions of remarkable divergence potentially associated with local adaptation, and likely fuelled by SGV, while explicitly acknowledging the difficulty in disentangling these selection signals from the genome-wide effects of demographic processes. Furthermore, we found that the divergence patterns relied extensively on the collinear genome in these introduced populations, and less clearly on the chromosomal inversions. This observation contrasts with local adaptation observed in the experimental system that relied on both collinear loci and highly selected chromosomal inversions, highlighting how demographic history and genomic architecture influence the detectable signature of local adaptation.A major limitation to conducting large-scale comparative evolutionary studies is the lack of data standardization, which prevents the integration of

community knowledge and high-resolution environmental and genetic data. Chapter 4 addresses this by developing a community database for the Littorina system. This platform implements standardized protocols for the integration of diverse phenotypic and environmental data from multiple Littorina species. Likewise, the platform also centralizes the availability of associated genomic data through links to external repositories. This database represents a crucial tool to test complex, large-scale evolutionary hypotheses.Collectively, this thesis strongly reinforces the fundamental importance of SGV as the raw material for successful local adaptation, a conclusion supported by evidence in both experimental and accidental introductions. Furthermore, this work highlights the critical role of the genomic architecture—specifically chromosomal inversions—in driving the predictability and effectiveness of adaptive responses. Our findings underscore how the interplay between SGV and genomic architecture dictates the trajectory and detectability of evolution in colonizing populations, while simultaneously providing a necessary tool to advance comparative evolutionary genomics in non-model organisms.

Friday, December 5, 2025 01:00pm - 02:00pm

Office Bldg West / Ground floor / Heinzel Seminar Room (I21.EG.101) and Zoom

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