Cologne Evolution Colloquium

CRC 1310   Predictability in Evolution

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The power and promise of single mutations in evolution

Some of the most well-known examples of adaptive evolution involve single mutations with large beneficial effects. However, predicting the evolutionary impact and fate of a new mutation remains difficult. To simplify this problem, we often bin mutations into categories that are expected to have distinct fitness impacts (e.g. synonymous vs. non-synonymous; coding vs. non-coding). However, there is little empirical evidence for differential fitness effects of mutational types across the genome, because prior work has largely focused on the distribution of fitness effects (DFE) for beneficial mutations in single genes. Thus, the general importance of mutation type relative to other factors such as genetic background and environment remains unclear. In this talk, I will describe our efforts to address this problem using bacterial strains, each with a single mutation in its genome that either occurred under strong selection or under genetic drift. Briefly, I suggest that the power and promise of new mutations depends more on the genetic background on which they occur, and very little on the mutational category to which they belong.

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