



Seminar/Talk

The genetic basis of adaptation: constrained, flexible, or somewhere in between?

Samuel Yeaman

University of Calgary

Host: Nick Barton

Genome-Wide Association Studies have revealed that hundreds or thousands of loci commonly drive standing variation in adaptive traits, which implies extreme evolutionary potential with many different genotypic ways to evolve a given phenotype. But in nature, we often find the same gene contributing to adaptation in distantly related species, implying that adaptation tends to work with a much smaller set of truly useful genotypes. What is the reason for this discrepancy, and what does it tell us about the flexibility of the evolutionary process? This presentation will explore this question and discuss projects in my lab studying: 1) the genomic basis of local adaptation to climate in a range of plants, 2) theoretical predictions about how genetics affects the repeatability of adaptation, 3) a comparative genomic test of whether local adaptation favours the evolution of genomic rearrangements (in stickleback). Taken together, this research shows that we know slightly more than nothing about the basis of adaptation, but have an abundance of tools that may help us rectify this.

Wednesday, September 22, 2021 12:15pm - 02:00pm

I22 Lakeside View (I22.O1.006)



This invitation is valid as a ticket for the ISTA Shuttle from and to Heiligenstadt Station.

Please find a schedule of the ISTA Shuttle on our webpage:

<https://ista.ac.at/en/campus/how-to-get-here/> The ISTA Shuttle bus is marked ISTA Shuttle (#142) and has the Institute Logo printed on the side.