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### “The genomic footprint of polygenic adaptation: From sweeps to small frequency shifts”

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Assume that a phenotype adapts rapidly to a novel environment. How does process unfold on the level of the underlying genotype? In molecular population genetics, the scenario of "selective sweeps" has long dominated the literature: adaptation occurs when selection drives beneficial alleles at several loci from a very low to very high frequency. Recently, however, an alternative view (derived from quantitative genetics and supported by GWAS data) has gained traction: Rapid phenotypic adaptation may also result from subtle frequency shifts at very many underlying loci. Theory shows that both adaptive scenarios are possible, but it remains unclear under which conditions each type should be expected.

I will present analytical work and computer simulations to address these questions in model of polygenic adaptation. The results show that the genome-wide mutation rate is the decisive factor to determine the expected pattern, while selection strength or presence/absence of standing genetic variation is largely inconsequential. We identify three parameter regimes corresponding to distinct genomic patterns of phenotypic adaptation. For small mutation rates, we find single selective sweeps. For intermediate rates we observe a pattern of heterogeneous partial sweeps at a small number of loci. Only for very high mutation rates, adaptation occurs via subtle frequency shifts at many loci.

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