



Prospects for using comparative genomics to elucidate the evolution of eusociality

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The evolution of obligate eusociality is an ancient phenotypic innovation that represents a major evolutionary transition in biological complexity. Initial comparative genomic and transcriptomic studies have promised unprecedented insight into this and many other phenotypic innovations. However, critical evaluation of these promises is warranted, in particular now that sequence data are no longer limiting. I will discuss limitations in statistically-supported inferences about the genomic basis of phenotypic innovations from comparative genomics alone based on limited numbers of phylogenetically independent events that occurred millions of years ago, and limitations with the common approach of focusing on lineages considered to be “primitive” or “transitional”. I will highlight the most promising questions and approaches for these lineages as well as lineages that show the major phenotypic innovation of interest, obligate eusociality. Finally, I will discuss how comparative genomic approaches can be complemented with other approaches, and I will describe specific predictions regarding the types of genetic changes that underlie the evolution of eusociality.