A worldwide survey of genome sequence variation reveals the evolutionary history of the honeybee Apis mellifera

The honeybee Apis mellifera is a species of huge ecological and economic importance and yet little is known about global patterns of genetic variation, which hold information about its evolutionary history and its adaptation to climate, pathogens and cultivation by humans. I will present an analysis of genetic variation on a whole genome scale of 140 honeybees, representing a worldwide sampling of 13 localities. We used coalescent approaches to determine the nature and timing of main events on population history. The analysis reveals a strong influence of selection in shaping patterns of variation across the genome: levels of variation are reduced near genes, with a magnitude dependent on methylation and expression patterns. We also identify regions of the genome with large population differentiation between different geographical regions indicating they contain mutations important for functional adaptation. Our results illuminate the origins and evolution of honeybees and the genetic adaptations that allow them to survive over their large geographical range.