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Population genomics of the honeybee , Apis mellifera

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The honeybee, *Apis mellifera*, has a global distribution resulting from ancient expansions out of Africa. The incredible phenotypic diversity observed among the different geographic subspecies of the honeybee is in-part caused by genetic divergence across the genome. We re-sequenced 39 *A. mellifera* honeybee workers from progenitor populations using Illumina Hi-Seq sequencing. Using this large dataset, we identified regions of the honeybee genome with signatures of positive selection associated with local adaptation. We have identified clear signals of selection acting across the honeybee genome, and we used this knowledge to better understand the evolutionary and genetic basis of phenotypic diversity in honeybees.