Ant genomes

The genomes of three ant species were reported recently in the *Proceedings of the National Academy of Sciences of the United States of America*. Yannick Wurm and colleagues now report the draft genome of the fire ant (*Solenopsis invicta*), a major pest that causes crop and livestock loss (*Proc. Natl. Acad. Sci. USA* published online, doi:10.1073/pnas.1009690108, 31 January 2011). Odorant receptors are important for chemical communication, which is a trait that likely contributes to complex social behavior in ants. The authors identified more than 400 putative olfactory receptors, which is the most reported so far in insects. Jurgen Gadau and colleagues report the draft genome of the red harvester ant (*Pogonomyrmex barbatus*), which has a unique system of genetically controlled queen-worker caste determination (*Proc. Natl. Acad. Sci. USA* published online, doi:10.1073/pnas.1007901108, 31 January 2011). The authors manually annotated candidate gene families that may be involved in this process, including insulin/TOR-signaling genes, yellow/major royal jelly genes, biogenic amine receptors and hexamerin storage proteins. Finally, Neil Tsutsui and colleagues report the draft genome of the Argentine ant (*Linepithema humile*), a widely distributed invasive species that outcompetes and eliminates native ants (*Proc. Natl. Acad. Sci. USA* published online, doi:10.1073/pnas.1008617108, 31 January 2011). The authors discovered 231,248 SNPs that should be useful for future analyses of migration patterns of this invasive ant. *PC*