members because they are not motivated to interact with them, and have no need to establish a truce.

Although rooks do not reconcile after conflicts, they do perform affiliative interactions, such as bill-twining, with their partners after conflicts. Similar types of events have been observed in great apes, but are largely absent in other species [17]. Primatologists use the term 'consolation' for third-party post-conflict affiliation, and hypothesize that it relieves distress produced by conflict [10]. The occurrence of consolation in chimpanzees, but not in other primates, is sometimes linked to chimpanzees' capacity for empathy and knowledge of others' minds [17]. Interestingly, corvids display striking convergence with chimpanzees in some aspects of their cognition, including their ability to make use of what others know in competitive settings [18].

The significance of this convergence is complicated by the fact that there is no evidence that third-party post-conflict affiliation actually provides consolation. In a new study of captive chimpanzees, Korski and Sterck [19] show that reconciliatory behavior between former opponents reliably reduces victims' distress. But affiliation by individuals who were not involved in the original conflict does not have the same effect, even when it is initiated by favored partners, such as close kin.

Again, it may be important to consider alternative, and perhaps less anthropomorphic, explanations. Seed *et al.* [8] suggest that third party post-conflict affiliation might reinforce bonds with allies. If so, we might predict that pair-bonded primates, like gibbons and titi monkeys, would engage in post-conflict affiliation with their mates after conflicts with outsiders. This prediction could be tested in pair-bonded primates, and in the many species of pair-bonded birds.

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Behavioral Genomics: A, Bee, C, G, T

Honeybees, termites and ants occupy the 'pinnacle of social evolution' with societies of a complexity that rivals our own. The sequencing of the honeybee genome will provide a strong foundation for studying the genetic basis of complex social behavior.

Yannick Wurm, John Wang and Laurent Keller

> *Go to the ant, thou sluggard;*
> *consider her ways, and be wise*
> Proverbs 6:6

This well-known Bible verse appropriately illustrates the long fascination of human beings for the complexity of social insect colonies and the industrious nature of their workers. The major organizing principle of ant, bee and termite societies is reproductive division of labor whereby one or a few individuals, the queens, specialize in reproduction while the others, the workers, participate in cooperative tasks such as building the nest, collecting food, rearing the young and defending the colony. This social organization provides numerous advantages and is the basis for the tremendous ecological success of social insects [1]. The sequencing of the honeybee genome [2] is an exciting step towards uncovering the molecular events underlying the evolution of altruism and complex behaviors.

A genome sequence, like a honeybee queen, is useless if it is not accompanied by the assiduous labor of a large number of cooperative workers. For this reason, an industrious swarm of scientists has collaborated to conduct detailed analyses and comparisons of the honeybee genome with those of model organisms, in particular the fruitfly *Drosophila melanogaster*. These analyses, reported in no fewer than 40 companion papers published in *Science*, *PNAS* and special issues of *Genome Research* and *Insect Molecular Biology*, have revealed many interesting features associated with the unusual social biology of the honeybee.

To date, most of our understanding of behavioral genetics has come from studies in model organisms such as *D. melanogaster* and *C. elegans*. In only a handful of cases, however, have genetic variants been shown to be responsible for behavioral differences observed under natural conditions [3,4]. An interesting feature of the honeybee is that workers change tasks as they age. They typically remain in the nest when young and then switch to dangerous tasks outside the nest only when they are older. This switch can be manipulated by altering colony needs or by treatment with chemicals that cause precocious foraging. Capitalizing on this, Whitfield *et al.* [5] conducted a series of clever experiments to separate the effects of worker age, genotype, environment and experience on gene expression. They found that the transition from hive work to foraging is accompanied by a robust molecular signature with many genes sharing the same expression pattern across the conducted experiments. Examination of these genes revealed shared *cis*-regulatory promoter elements that may be responsible for their co-regulation [6]. This is a big step towards clarifying the regulatory cascades governing the networks of behavioral genes. Future investigations into the neuronal circuitry of bees and its modulation should also be facilitated by the bioinformatic and proteomic identification of 36 prohormones coding for more than 200 neuropeptides [7].

Comparison of the honeybee genome to that of other insects revealed a number of interesting differences. Not a complete surprise was the identification of nine new genes linked to the production of royal jelly, which workers feed to the queen and larvae. These genes apparently evolved from a single progenitor gene which encodes a member of the ancient Yellow protein family [8]. Similarly, the striking expansion of the odorant receptor family in honeybees (170 genes) relative to *D. melanogaster* (62) and the mosquito *Anopheles gambiae* (79) [9] makes sense given the prime role of pheromones in communication and the need for workers to discriminate between diverse floral odors. These discoveries should help elucidate some of the bees' fascinating skills, which include precise memory of space and odors as well as the abstract modeling and linguistic abilities shown by the 'waggle-dance'.

A more surprising finding was that honeybees have only half as many immune defense genes as *D. melanogaster* or *A. gambiae*. Many authors have suggested that colonies of social insects should be under particularly strong pathogenic pressure because numerous highly related individuals live in close quarters. Although not frequently recognized, however, bees spend most of their lives in a protected colony environment, while flies and mosquitoes grow up in rotting food or stagnant water. Moreover, the food provided to bee larvae has already been processed by adults and thus is less likely to contain pathogens. Likewise, the risk of poisoning or infection may be low when foraging nectar and pollen from flowers with which a mutualism has evolved [10]. The close association between bees and plants, and the lack of incentive for plants to produce toxic nectar or pollen may actually also explain the *a priori* surprising finding that honeybees have far fewer gustatory receptors than *D. melanogaster* and *A. gambiae* [9]. Another possible explanation for why bees have fewer immune defense genes is that they display social behaviors such as extensive grooming and 'social fever' that may effectively combat infections [10].

The honeybee genome has provided several interesting revelations concerning the most unusual characteristic of social insects: their ability to produce very different phenotypes from the same genotype as a result of the alternative developmental programs followed by queens and workers. Indeed, in several ant species, queens can differ dramatically in size and morphology from workers, yet almost nothing is known about the epigenetic factors underlying the developmental switch responsible for these differences. Of particular interest was the discovery of 65 microRNAs, including some that show caste-specific expression patterns during development [2]. This raises the exciting possibility that microRNAs are involved in caste determination via differential gene expression between queens and workers.

The finding that the honeybee genome harbors genes encoding a complete set of methyltransferases, the highest known eukaryotic CpG content, and evidence for CpG methylation of protein coding genes is also of great interest, given that methylation of CpGs represses transcription in mammals. Interestingly, in contrast to mammals, in the honeybees DNA methylation was detected predominantly in coding regions. Perhaps methylation plays a role in regulating genes involved in developmental differences between honeybee queens and workers [11]. Finally, it appears that more than 60 genes are duplicated specifically in the honeybee, including two genes for components of the insulin pathway [2]. This pathway regulates growth in other animals [12] and could be the means through which queen bees become bigger than workers [13]. These and/or other duplicated genes may be involved in caste or sex determination and differences, and/or in social interactions.

Comparative analyses revealed some other peculiar genomic features including the fact that the honeybee genome evolves at a much slower rate than the strongly derived genomes of flies and mosquitoes. This is evidenced by sequence identity, intron conservation, and gene loss relative to an ancestor common to insects and vertebrates [2]. The slow evolution of the honeybee genome may be general to hymenopteran insects, whose haplo-diploid sex-determination system might purge deleterious mutations that would be masked in diploid individuals [2]. Alternatively, it could be due to the long generation time of social insects — queens typically can live many years [14] — and/or to the low effective population size resulting from a single individual monopolizing reproduction in the hive.

Interestingly, these characteristics may also be responsible for another idiosyncrasy of the honeybee, the very high average recombination rate of 5.7 recombinations per chromosome [15]. Such a high recombination rates has only been reported in one other species, the ant *Acromyrmex echinator* [16]. High recombination rates might thus be a characteristic of social insects, again perhaps a result of their typically long generation time and small population size. Alternatively, high recombination rates might have been selected as a means to increase genetic diversity among offspring.

Another striking finding was that the honeybee genes controlling circadian rhythm and telomere length are more similar to vertebrates than to *D. melanogaster* or *A. gambiae* [2]. *Drosophila* is considered the paradigm of insect biology. This clearly needs to be changed given the increasing evidence that many of *Drosophila*'s features, such as their early-acting axis specification genes, are highly derived and not characteristic of insects.

The honeybee genome sequence and attendant analyses and experiments open many avenues for future research. In anticipation of a finished genome, the BeeSpace project has begun the dissection of environmental and hereditary influences on brain gene expression in the context of defensive behavior and foraging using thousands of microarrays (G. Robinson, personal communication). Beyond division of labor and cooperation within a colony, it will be exciting to understand the molecular basis of the evolution of within-colony conflicts and their resolution. Functional tests, through ectopic expression or repression of genes involved in both behavior and caste development, will be essential in elucidating how insect societies function.

At a more basic level, the mechanisms by which solitary species became social could be pinpointed by examining either facultatively social species or contrasting pairs of solitary and primitively social species. The independent evolution of social life in bees, ants, wasps and termites also provides a unique opportunity to determine whether the convergent morphological, physiological and behavioral adaptations that have occurred in these taxa are due to modification of the same developmental pathways and gene networks. The recent development of an EST library, microarray and other molecular genetic tools for the fire ant, *Solenopsis invicta* (our group's unpublished data), should pave the way for such sociogenomic comparative studies.

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