The >15 000 ant species are all highly social and show great variation in colony organization, complexity and behavior. The mechanisms by which such sociality evolved, as well as those underpinning the elaboration of ant societies since their ~140 million year old common ancestor, have long been pondered. Here, we review recent insights generated using various genomic approaches. This includes understanding the molecular mechanisms underlying caste differentiation and the diversity of social structures, studying the impact of eusociality on genomic evolutionary rates, and investigating gene expression changes associated with differences in lifespan between castes. Furthermore, functional studies involving RNAi and CRISPR have recently been successfully applied to ants, opening the door to exciting research that promises to revolutionize the understanding of the evolution and diversification of social living.

Addresses

1 Organismal Biology Department, School of Biological and Chemical Sciences, Queen Mary University of London, Mile End Road, London E1 4NS, United Kingdom
2 Department of Genetics and Genome Biology, University of Leicester, Leicester LE1 7RH, United Kingdom

Corresponding authors: Hammond, Robert L (rh225@leicester.ac.uk), Wurm, Yannick (v.wurm@qmul.ac.uk)

Introduction

Ants show remarkable division of labor whereby males and queens reproduce while other females, the workers, build and defend the nest, rear brood and forage for food [1**]. Since their evolution from a solitary common ancestor ~140 million years ago [2,3**], the ants have radiated into >15 000 extant species. This ecologically dominant family exhibits an extraordinary diversity of social lifestyles, for example: obligatory fungus farming (leaf cutter ants), nomadic predatory lifestyles (army ants), slave-making and social parasitism [4]. Colonies vary greatly, with tens to several million individuals per colony, up to nine morphological worker castes within a species, as well as an array of mechanisms to resolve intra-colony conflicts [5].

While their behaviors, ecology, evolutionary contexts and morphologies have been extensively studied, it has only recently become possible to perform genome-scale analyses in ants [6], with the first seven ant genomes published in 2010 and 2011 [2]. Here, we review publications from the last few years on the genes and genomic processes underlying caste differentiation, the evolution of social organization, intraspecific variation in lifespan, symbiotic relationships, and chemical communication.

How the ants got their genomes

Publications of the first genome projects of humans and traditional laboratory organisms including *Drosophila* and *Caenorhabditis* alerted many biologists, including social insect researchers, to the power of genome knowledge. The development of post-Sanger sequencing technologies [7] (see Glossary) made genome projects accessible to small teams interested in particular species. Within months of the 2009 ‘ant genomics’ meeting at Arizona State University [8], projects to sequence genomes of seven species were under way (Figure 1).

These first seven ant genomes [2] led to a broad range of studies on these species (some examples below), but also paved the way for the sequencing of genomes and ‘reference transcriptomes’ of additional species. As of writing, genomes of 23 ant species and transcriptomes of 26 additional species have been published (Table 1). Other studies have used reduced representation sequencing techniques such as restriction site associated DNA sequencing (RADseq, e.g. [6], see Glossary) or the sequencing of ultraconserved elements (UCEs, e.g. [9], see Glossary) to identify genetic structures or to resolve phylogenies.

The coexistence of distinct female castes

Queen and worker ants are both female and do not differ genetically (with some exceptions [10]). Instead, caste (worker or queen) is irreversibly determined by environmental factors that trigger larvae to develop down either the worker or queen pathway [11]. Comparisons between
queens and workers in multiple species demonstrate that many genes with strong caste-biased patterns of expression in one developmental stage show no such bias in other stages [12]. The differences in whole-body gene expression between castes are highest during the last larval stages [12,13]. Interestingly, genes with high expression plasticity (i.e. with different expression levels in different castes) during larval development in Cardiocamponistylus obscurior also showed increased evolutionary rates [14*]. In adults, highly pleiotropic genes (i.e. under more phenotypic constraints, see Glossary) are consistently less likely to become caste-biased across a wide taxonomic range of ant species [15*]. Such findings support the idea that phenotypic plasticity along with genetic accommodation (see Glossary) are likely to play an essential role in caste differentiation [16,17*].

Contrary to some expectations, genes expressed exclusively in a single caste are rare [18*]. Instead, transcriptome comparisons suggest that groups of genes have correlated expression profiles (i.e. ‘coexpression modules’) with consistent differential expression between adult queens and workers across 15 ant species [15*,19**]. This suggests that caste-specific phenotypes can arise from modifications in gene regulatory networks (GRNs, see Glossary) (e.g. [18*]). However, other studies have found that taxonomically-restricted genes (see Glossary) are overrepresented among worker-biased genes [20]. These seemingly contradictory views are not mutually exclusive [21*] and the divergence between castes can involve differential usage of existing modules of genes as well as differential usage of fast-evolving genes with low connectivity [22,23].

Because workers generally do not reproduce, selection acts only indirectly on worker phenotypes. All else being equal, selection is therefore expected to be less efficient on genes expressed in workers than on genes expressed in queens [24*,25]. In agreement, expression profiling in Monomorium pharaonis reveals relaxed selection on worker-specific genes and faster evolution [26*]. In contrast, a study of 15 species [19**] shows no difference in

Box 1 Glossary

- Gamergate: Some species lack a distinct queen caste, or can have a hierarchy of reproductive workers. Such reproductive workers are called gamergates. Amongst others, this occurs in Harpegnathos and many other ponerine ants.
- Gene regulatory networks (GRNs): Modules of interacting, coexpressed genes. These networks are highly resilient to modifications of individual members of the network.
- Genetic accommodation: A process by which a phenotype initially determined by environmental cues becomes genetically determined and thus, inheritable.
- Genomics: Generally taken to mean genome-scale analyses, that is, using a very large number of genetic markers. Can include transcriptomics and other large-scale analyses.
- RADseq: Method of DNA sequencing based on Restriction site Associated DNA markers, which retrieves a small fraction of the total genome (e.g. the same 0.1% of the genome in all samples) and enables low-cost studies of genetic variation at 1000s of markers across the genome.
- Sanger-sequencing: Low-throughput DNA sequencing method that is still used for some applications such as targeted sequencing of specific genes. However, the majority of sequencing efforts now use higher-throughput ‘post-Sanger’ sequencing methods including Illumina, Pacific Biosciences and Oxford Nanopore. These technologies are more cost-effective for large projects.
- Social polymorphism: Different types of social organization within the same species. In social insects, a well-studied type of social polymorphism involves the number of the number of queens in the colony.
- Trophallaxis: Fluid passed from an individual to another, through the mouth.
- Ultraconserved elements (UCEs): non-coding regions of the genome that have high similarity among distant species. They have recently been used as a manner of increasing the power of phylogenetic studies.
- Taxonomically restricted genes: Genes identified exclusively in specific taxa. Such genes likely evolve through rapid divergence of existing genes, or through recruitment of previously non-coding sequence. They are thought to be associated with novel taxon-specific functions.
- Pleiotropic gene: Gene that affects more than one phenotypic trait. Most genes are likely pleiotropic.

Figure 1

Solenopsis invicta fire ants (smaller) defending a region of the social chromosome supernome against a Pogonomymex rugosus harvester ant worker (larger) symbolizes the amicable competition between early ant genome projects.
### Table 1

**Overview of ant species with published genomic and transcriptomic data.**

<table>
<thead>
<tr>
<th>Subfamily</th>
<th>Species</th>
<th>Draft genome</th>
<th>Transcriptomics</th>
<th>Functional validation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Dolichoderinae</td>
<td>Linepithema humile</td>
<td>[69]</td>
<td>[19**]</td>
<td>[61**]</td>
</tr>
<tr>
<td>Dorylineae</td>
<td>Ooceraea biroi</td>
<td>[70]</td>
<td>[32]</td>
<td></td>
</tr>
<tr>
<td>Formicaceae</td>
<td>Camponotus floridanus</td>
<td>[71]</td>
<td>[63,72]</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Camponotus fellah</td>
<td></td>
<td>[63]</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Camponotus japonicus</td>
<td></td>
<td>[73]</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Camponotus castaneus</td>
<td></td>
<td>[49]</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Formica exsecta</td>
<td></td>
<td>[19**,74]</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Formica selysi</td>
<td>[39]</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Formica aquilonia</td>
<td></td>
<td>[19**]</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Formica cinerea</td>
<td></td>
<td>[19**]</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Formica fusca</td>
<td></td>
<td>[19**]</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Formica truncorum</td>
<td></td>
<td>[19**]</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Formica pratensis</td>
<td></td>
<td>[19**]</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Formica pressilabris</td>
<td></td>
<td>[19**]</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Lasius niger</td>
<td>[75]</td>
<td>[76]</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Lasius tarsius</td>
<td></td>
<td>[19**]</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Lasius neglectus</td>
<td></td>
<td>[19**]</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Nylasenia pubens</td>
<td></td>
<td>[65]</td>
<td></td>
</tr>
<tr>
<td>Myrmicinae</td>
<td>Acromyrmex echinatior</td>
<td>[77]</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Aphaenogaster picea</td>
<td></td>
<td>[78]</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Aphaenogaster carolinensis</td>
<td></td>
<td>[78]</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Atta cephalotes</td>
<td>[79]</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Atta colombica</td>
<td>[47]</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Cardiocondyla obscurior</td>
<td>[80]</td>
<td>[14,81]</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Crematogaster osakensis</td>
<td></td>
<td>[45]</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Cyphomyrmex costatus</td>
<td>[47]</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Monomorium pharaonis</td>
<td>[21*]</td>
<td>[19**,21*,26*]</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Monomorium chinense</td>
<td></td>
<td>[19**]</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Myrmica rubra</td>
<td></td>
<td>[19**]</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Myrmica ruginodis</td>
<td></td>
<td>[19**]</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Myrmica sulcinodis</td>
<td></td>
<td>[19**]</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Pogonomyrmex barbatus</td>
<td>[82]</td>
<td>[18']</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Pogonomyrmex californicus</td>
<td></td>
<td>[40]</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Pogonomyrmex colei</td>
<td></td>
<td>[18']</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Pogonomyrmex rugosus</td>
<td>[18']</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Pseudomyrmex gracilis</td>
<td>[46']</td>
<td>[46']</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Solenopsis invicta</td>
<td>[57]</td>
<td>[19**,57]</td>
<td>[83]</td>
</tr>
<tr>
<td></td>
<td>Temnothorax longispinosus</td>
<td></td>
<td>[48']</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Temnothorax nylanderi</td>
<td></td>
<td>[48']</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Tetramorium bicarinatum</td>
<td></td>
<td>[84]</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Trachymyrmex cornetzi</td>
<td>[47]</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Trachymyrmix septentrionalis</td>
<td>[47]</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Trachymyrmex zepteki</td>
<td>[47]</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Vollenhovia emeryi</td>
<td>[18']</td>
<td>[18']</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Vollenhovia nipponica</td>
<td>[18']</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ponerinae</td>
<td>Diacamma sp.</td>
<td></td>
<td>[28']</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Dinoponera quadriiceps</td>
<td>[33]</td>
<td>[33,85]</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Harpegnathos saltator</td>
<td>[71]</td>
<td>[29]</td>
<td>[62**]</td>
</tr>
</tbody>
</table>

Evolutionary rates between castes, although this could be due to the use RNAseq from whole bodies. Indeed, allometric differences in tissues between castes are known to confound comparisons [27*]. However, although the *M. pharaonis* study used more specific samples (heads, gasters, larvae), these still include multiple tissues [26*]. Importantly, although the relaxed selection observed in *M. pharaonis* might be caused by indirect selection, an alternative is that relaxed selection facilitated the recruitment of genes to caste-biased roles [17*].

Many ant species have lost the queen caste but have both non-reproductive and reproductive workers (gamergates, see Glossary), comparisons between which can illuminate important molecular mechanisms. For example, this has allowed the identification of differentially expressed genes underpinning reproductive hierarchies [28*] and the role of specific proteins [29] in individual behavior.

Other ant species also display within-caste phenotypic plasticity not associated with reproduction, offering the
Genetic social Current Many chance discovered genes proposed diers anders in two species [31]. Methylation patterns have been proposed as a mechanism to explain both between-caste and within-caste diversity [30], but the evidence so far is unclear [32], and suggests that methylation patterns may not be as important as previously thought in controlling ant polyphenism [33].

Genes and genetic architectures underlying social organization
Many species of ants include both single-queen and multiple-queen colonies. It was long thought that such variation is determined by environmental factors [34]. This idea was challenged in the late 1990s with the discovery that a genetic element, marked by alternate alleles of the odorant-binding protein (OBP) gene Gp-9, is responsible for different social organizations of the red fire ant Solenopsis invicta [35] (see Glossary for social polymorphism). Recent genome-wide analyses showed that the two Gp-9 alleles in fact mark alternate variants of a ‘supergene’ carried by a pair of ‘social chromosomes’. Recombination is suppressed between the two variants of the >19 Mb long supergene [36]. Intriguingly, the supergene variant responsible for multiple-queen colonies has much lower genetic diversity than the rest of the genome, consistent with the effect of a selective sweep or recent bottleneck [37]. The two variants of the supergene carry alternate alleles for many of >400 protein-coding genes, including nine additional Gp-9-like OBPs. Six of these OBPs have differences in coding sequence between supergene variants [38]. This work raised a question: is the situation in S. invicta an oddity? In short, no, because a pair of independently evolved social chromosomes, that bear almost no similarity to those in S. invicta, determine social form in the distantly related alpine silver ant, Formica selys [39]. It is currently unknown whether such genetic architecture is required for the coexistence of social forms in other species, or for transitions between species from obligate single-queen colonies to obligate multiple-queen colonies.

Genetic changes underlying social organization can also be identified by comparing populations or species. For example, young Pogonomyrmex californicus queens predisposed to found nests either alone or in groups show fundamental differences in gene expression profiles of heads [40]. Similarly, in socially parasitic species, one can predict that the loss of the worker caste leads to a loss in the genome of potential ‘worker genes’. Instead, comparisons between the genomes of three social parasite species and genomes of non-parasitic host species found almost no differences in gene presence/absence [18*]. This is consistent with the idea that genes used in workers also have roles in other castes.

Investigating intraspecific variation in lifespan
The intraspecific lifespan of ants is extremely variable and in the same colony queens can live for years while workers typically live a few months and males a few weeks, despite sharing the same genome [41,42]. Such disparity is fascinating yet challenges the application of classic theories of aging [43] and we have limited understanding of the mechanisms involved. A transcriptomic analysis of Lasius ants at three time points found that DNA repair genes are more highly expressed in both brain and leg tissues of queens than age-matched workers [44*], pointing at an association between greater lifespan and somatic repair. Because queens are long lived but mate shortly after emergence from the pupae, the long-term storage of viable sperm in the queen’s specialized organ (spermatheca) is another conundrum that is only now being investigated. Recent comparative transcriptomic analysis of spermatheca in virgin and mated Crema
gaster queens identified a number of differentially expressed genes including some associated with oxidizing function [45*].

Genes and mechanisms underlying the evolution of symbiotic relationships
The intricate symbiotic relationships (e.g. mutualism, parasitism) that many ants have with other taxa can now be scrutinized using genomics. For example, analysis of UCEs in 18 Pseudomyrmex species determined that after the ant-acacia plant mutualism evolved in one lineage, a second independent Pseudomyrmex lineage colonized plants that were involved in the first mutualism [9*]. A different study identified protein-coding genes with signatures of adaptive evolution in three ant-plant mutualistic Pseudomyrmex in comparison with four generalist species [46*]. In the attine ants, mutualistic fungus farming is associated with clear large-scale genomic changes including genomic rearrangements, loss of the arginine biosynthesis and positive selection on chitinase pathways, with complementary changes in the fungus [47].

Transcriptomics analyses are also beginning to illuminate the mechanisms by which parasites manipulate ant host behavior. For instance, hundreds of genes are differentially expressed in brains of Temnothorax workers infected with the cestode Anomo
otaenia compared to controls [48*]. Similarly, large-scale changes in gene expression occur in heads of Camponotus carpenter ants when their behavior is manipulated by the Ophiocordyceps fungus. Interestingly, many of the fungal genes up-regulated during manipulated biting behavior are absent from non-parasitic relatives [49].
Whole genome sequencing has also helped reveal new mutualisms. Sequencing of *C. obscurior* queens [50*] revealed a previously unknown intracellular bacterium symbiont, *Westeberhardia*. Analysis of its genome and titer in the host suggest this bacterium may assist cuticle synthesis. Finally, there is also an interest to identify ant microbiomes (e.g. in *Formico* [51]) and, motivated by pest control efforts, transcriptomic analyses have identified viruses of invasive ants (e.g. *S. invicta* [52], *Linepithema humile* [53], *Nylanderia* spp. [54,55], *Anoplolepis gracilipes* [56]).

**Roles of chemical communication genes in colony life**

Ants have a fascinating communication system based on the production and perception of pheromones. In line with this, the first ant genome projects discovered particularly high number of genes involved in chemical communication, with for example more than 400 putative olfactory receptors in the fire ant [57]. Some chemical communication genes likely have highly conserved functions as indicated by conserved sequences and antennal expression of core sets of single-ortholog odorant binding proteins (OBPs) and chemosensory proteins (CSPs) [58,59]. However, among the 330 ± 26 (mean ± standard deviation) odorant and the 80 ±67 gustatory receptors identified in each of eight ant species, >30% were taxon-specific [60]. Frequent gene duplications and losses suggest that many chemical communication genes are involved in adaptive processes in response to changing environments or arms races. This is in line with analyses of a clade of CSPs with high turnover and extensive evidence of adaptive evolution [59]. There is even variation in olfactory genes within species: the multiple-queen form of *S. invicta* includes an OBP absent from singleton colonies [38*].

CRISPR transgenics recently confirmed that the highly conserved *oro* gene, required for proper functioning of other olfactory receptors in *Drosophila*, plays a similar role in ants: ants with broken *oro* lacked antennal glomeruli and their colonies were dysfunctional, highlighting the importance of such chemical communication genes for social organization [61**,62**].

Recent analyses have shown that non-olfactory communication is also important: trophallaxis fluid (see Glossary) is used to transfer compounds including proteins, micro-RNAs and juvenile hormone between colony members [63].

**Concluding remarks**

The continued improvements in low-cost sequencing technologies are making it possible to pursue analyses that would have been difficult to imagine only few years ago. Focusing on individual species, this includes in-depth tissue-specific profiling of RNAs or epigenetic marks [64*], as well as the sequencing of whole genomes of many individuals to enable population genomics approaches [65*]. Large whole genome sequencing initiatives including large number of related species, or one species for many genera — such as in the Global Ant Genomics Alliance [3**] — are already under way. Such datasets will deepen our understanding of the specific mechanisms and evolutionary forces involved in the evolution of complex phenotypes, symbiotic interactions and social behavior. Furthermore, analyses of such data will make it possible to pinpoint key candidate genes. Detailed analyses which involve artificially modifying the activity or sequence of genes have already begun, with several recent studies demonstrating the effectiveness of temporarily switching genes off using RNA interference [66,67] — which can propagate by trophallaxis through the colony — of changing the reproductive status of an adult worker injecting specific neuropeptides [29] or of permanently modifying gene sequences using CRISPR transgenics [68]. Such approaches pave the way for many new breakthroughs bridging our ultimate and proximate understanding of social evolution.

**Conflict of interest statement**

None declared.

**Acknowledgements**

The authors thank Rodrigo Pracana, Karina Zile and Gino Brignoli for comments on earlier drafts of this manuscript. This work was supported by the Biotechnology and Biological Sciences Research Council [grant BB/K004294/1] and the Natural Environment Research Council [grant NE/L00626X/1 and NE/L002485/1] and Conselho Nacional de Desenvolvimento Científico e Tecnológico [grant 24839/2013-5].

**References**

1. Boomsma JJ, Gawne R: Superorganismality and caste differentiation as points of no return: how the major evolutionary transitions were lost in translation. *Biol Rev Camb Philos Soc* 2017 http://dx.doi.org/10.1111/brv.12330. The authors present a historical and theoretical review of superorganismality and eusociality, arguing that precise terminology that aligns with major transitions should be preferred over muddled terms.


This genomic and transcriptomic analysis in *Monomorium pharaonis* identified modules of coexpressed genes associated with age polyphenism that are evolutionarily conserved in other ant species.


Using a theoretical model, the authors hypothesize that due to the effects of indirect selection in workers and under similar selection pressures, selection should be relaxed in worker-biased genes if compared to queen-biased genes.


Genomic and transcriptomic data from the ant *Monomorium pharaonis* reveal that worker-biased genes are under relaxed selection if compared to queen-biased genes.


Empirical gene expression profiling of gasters and individual tissues within gasters of honeybee queens and workers. This study demonstrates that studies from heterogeneous body parts (e.g. whole bodies or gasters) provide misleading results.


This caste differentiation analysis of *Diacamma ant* species is based on transcriptomics (brain and gaster) and correlates nutrient-processing gene expression levels to the formation of social hierarchy.


In the introduced North American population of Solenopsis invicta, the social supergene variant carrying Gp-9b show signatures of a recent selective sweep.


In Lasius niger, expression of genes related to DNA and protein repair is higher in older queens than in other colony individuals.


Gene expression in the spermatheca of Crematogaster osakensis queens correlate with age and mating status.


Seven Pseudomyrmex genomes were compared, finding that rates of molecular evolution are higher in the species that are mutualistic with Acacia in non-mutualists.


Infection of Termothorax nylanderi workers with the cestode Anomotaenia affects gene expression profiles in the brain.


Genome sequencing of Cardiocondyla revealed the presence of a previously unknown bacterial endosymbiont, here described and named Westeberhardia.


54. Valles SM, Oi DH, Becnel JJ, Wetterer JK, LaPolla JS, Firth AE: Isolation and characterization of Nylanderia fulva virus 1, a positive-sense, single-stranded RNA virus infecting the tawny crazy ant, Nylanderia fulva. Virology 2016, 466:244-254.


58. McKenzie SK, Oxley PR, Kronauer DJC: Comparative genomics and transcriptomics in ants provide new insights into the evolution and function of odorant binding and chemosensory proteins. BMC Genomics 2014, 15:718.


CRISPR was used on Oecerea biroi ants to disable orco, a gene needed for odorant receptors to work. The mutant ants lacked antennal glomeruli.


CRISPR was used on Harpegnathos saltator ants to disable the orco gene required for odorant receptors. This similarly had strong developmental and behavioral effects.


64. Glastad KM, Arsenault SV, Vertacnik KL, Geib SM, Kay S, • Danforth BN, Rehan SM, Linnen CR, Kocher SD, Hunt BG: Variation in DNA methylation is not consistently reflected by sociality in hymenoptera. Genome Biol Evol 2017, 9:1687-1698. Analysis of bisulfite sequencing data from nine hymenopteran species finds no clear correlation between methylation and sociality, and highlights that the correlation between presence of CpG dinucleotides in the genome and actual methylation varies between taxa.


Review of non-Drosophila genomics and transcriptomics projects, with emphasis on population genomic analysis of social insects, butterflies and water flea.

Insect genomics


76. Lucas ER, Romiguier J, Keller L: Gene expression is more strongly influenced by age than caste in the ant Lasius niger. Mol Ecol 2017, 26:5058-5073.


