Sociogenomics

Ryan Ruboyianes

Sociogenomics

An integrative discipline in behavioral biology that combines
mechanistic and evolutionary analyses of behavior.

(E. O. Wilson inspired)

"Behavioral ecologists study adaptations, which ultimately are the product of natural selection that functions on genes. Neuroscientists study neuroanatomical, neurochemical, neurodevelopmental, neuroendocrinological, neuroethological and neurophysiological mechanisms of behavior, built by proteins that are encoded by genes. This synthesis requires using genomics to integrate mechanistic and evolutionary perspectives. It should also include phylogenetic analysis, especially because of the broad array of taxa that must be used to study the molecular basis of social life."

Robinson, et al. 2005

Genomics – beyond ATGC

• genome: the sum of an organism's entire haploid genetic complement and the molecular basis of cellular development.

• transcriptome: an organismal set of transcriptional RNA that reflects the profile of active gene expression.

• proteome: an organism's entire complement of proteins, including modifications. Varies greatly with time and stress.

• epigenetics: non-genetic mechanisms affecting the expression of phenotypes or individual genes. Not necessarily heritable.

Predicting social organization:
Apis Mellifera

Model organism for sociogenomic study:

• Eusocial

• Division of labor

• Caste differentiation

Since the publishing of the honeybee genome in 2006, comparison is possible with other well-studied model organisms.
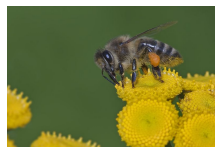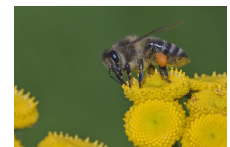

Andreas Trepte, www.photo-natur.de

Predicting social organization:
Apis Mellifera

Genomic features of interest:

• Haplodiplody

• Gene loci with behavioral association

• High degree of chromosome recombination

• Epigenetic caste determining factors

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Model Organism v. Model Organism

Genomic sequencing data has provided a wealth of information related to genes and their effect on behavior.

One method of associating genomic qualities with behavior is by comparing two species with a well established common ancestor.

Drosophila melanogaster and *Apis mellifera* have sharply contrasting life histories and degrees of social behavior.

Mr.checker

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Model Organism v. Model Organism: Foraging behavior

The *for* gene determines foraging behavior in *D. melanogaster*. This gene is responsible for coding an enzyme responsible for regulating neuron pathways in the brain. Allelic variation produces two types, sitters and rovers.

A. mellifera exhibit pheromone-mediated age polyethism in foraging. The needs of the colony determine when young workers leave the hive.

"The foraging gene therefore supports the idea that changes in gene regulation are associated with behavioral evolution." Robinson, et al. 2005

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Model Organism v. Model Organism: Foraging behavior

Amfor, an ortholog of the *D. melanogaster* foraging gene, regulates foraging age in honeybees.

The activity of a bee relates to the expression of this gene. Higher levels of *Amfor* mRNA are found in the brain of foragers than in bees that remain in the hive.

Experimentally increasing the coded enzyme, a kinase, induces young bees to precocious foraging in workers.

ortholog: homologous gene separated by speciation

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More orthologs

Complementary sex determiner:

The *csd* gene is a single locus with two primary alleles that determines sex in honeybees. Heterozygotes become female. Hemizygotes, with only one set of chromosomes, become male. The *transformer* gene, a single locus that determines sex in *D. melanogaster*, codes a very similar protein.
Beye, et al. 2003

Major royal jelly protein:

The *MJRP* gene is responsible for the production of royal jelly by workers. All bee larvae are fed royal jelly for the first few days of development. After, only queen larvae continue to be fed royal jelly. The coding region of this gene is nested within the *yellow protein* genes. These are common across arthropods. For honeybees, the gene likely gained new function with evolution. It now fills the role of helping to regulate social behavior through caste differentiation.

Drapeau, et al. 2006

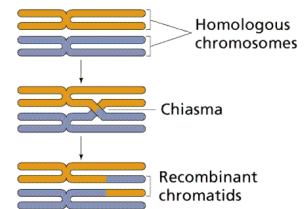## Sociogenomic Evolution: Hymenoptera
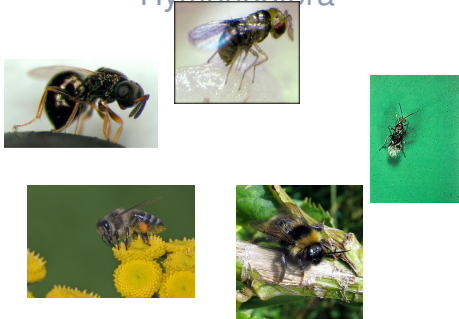
Images from commons.wikimedia.org

Apis Mellifera

Recombination

A chromosomal exchange process occurring during meiosis. For our purposes, recombination will refer simply to the joining of homologous chromosomes at a site called a chiasma.

Mixing of alleles is the evolutionary benefit of this activity.

Homologous chromosomes

Chiasma

Recombinant chromatids

Beye, et al. 2006

Slide 1

Sociogenomic Evolution: Hymenoptera

The organization of genomes within hymenoptera varies somewhat in correlation to the social behaviors of individual species. Parasitic hymenoptera tend to have less chromosomes and lower recombination frequency than eusocial species.

	Nasonia vitripennis × N. giraulti	Trichogramma brassicae	Bracon hebetor	Bombus terrestris	Apis mellifera
Relative map size	829 cM/80 markers	1330 cM/84 markers	1156 cM/79 markers	1091 cM/80 markers	2020 cM/80 markers
Chromosome number	5	5	10	18	16
Relative average marker distance (cM)	8.4	17.7	17.0	13.5	29.7
Life history traits	Parasitic	Parasitic	Parasitic	Primitively eusocial	Highly eusocial
Mating system	Regularly inbred	–	Outbreed	Outbreed/monandrous	Outbreed/polyandrous
Sex determination	Not single locus	Not single locus	Single locus	Single locus	Single locus
Parasite load	–	–	–	High	High
Colony size (n = workers)	Solitary	Solitary	Solitary	Small colonies (200)	Large colonies (30,000–40,000)
Division of labor	–	–	–	Weakly developed	Strongly developed

Gadau 1999

Slide 2

Recombination maps

Intra-chromosomal distance (cM) between gene loci and separation to different chromosomes determines gene linkage.

Recombination of gene loci is mediated by this distance and gene separation. If recombination sites are random, then closer genes recombine less often.

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Gadau 1999

Slide 3

Apis Mellifera

Recombination

Apis mellifera experience 5.7 chiasmata per chromosome for every meiotic event.

This contrasts with other eukaryotes, with an average of 1.6 per chromosome per meiosis.

This activity is not ubiquitous among hymenoptera and likely evolved independently in eusocial species.

Which came first, eusociality or unique chromosomal activity?

Homologous chromosomes

Chiasma

Recombinant chromatids

Beye, et al. 2006

Slide 4
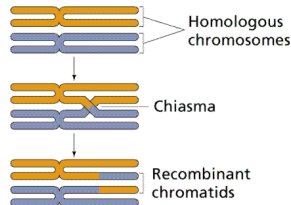
Apis Mellifera

Sociogenomic Evolution: Hymenoptera

Bombus terrestris: primitive eusociality with small colony size. Monandrous outbreeding.

Apis mellifera: Highly eusocial with large colony size. Polyandrous outbreeding.

Problem: there is a poor relationship between number of chromosomes and recombination frequency. Map distance doesn't tell the whole story.
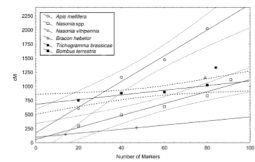
Polyandrous breeding

Gadau 1999

Slide 5

Recombination and Kin Selection

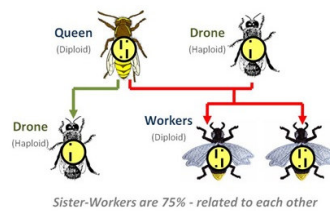Focusing on the two social species of the group lends more insights into genomic function.

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B. terrestris are monandrous, but outbreeding with a small colony and average recombination rate.

A. mellifera are polyandrous, colony size is many times larger. Assuming that mutation occurs at a fixed rate, it may be neccesary to recombine more to as evolutionary pressure builds to maintain consistent coefficients of relatedness across the colony.

Gadau 1999

Slide 6

Hypothesis: "more genotype diversity results in more complex and stable division of labor"

Queen (Diploid)   Drone (Haploid)

Drone (Haploid)   Workers (Diploid)

Sister-Workers are 75% - related to each other

natureblognetwork.com

Gadau 1999

Slide 1

Apis Mellifera

Caste Determination

Nourishment determines whether a honeybee female will be a queen or worker.

An epigenetic mechanism might be responsible for determination, both morphological forms arise from the same genome.

Genetic evidence indicates that the differential feeding of royal jelly to queen larvae increases their respiratory capability through differential expression of respiration critical genes.

- COX-1 mtDNA: encodes an oxidase critical to mitochondrial electron transport chain
- cyt c nDNA: encodes and electron carrying protein for synthesis of ATP
- AmIF-2$_{mit}$ mRNA: ortholog of mitochondrial transcription initiator

Corona, et al. 1999

Slide 2

*Apis Mellifera*

Caste Determination

Elevated expression of mitochondrial protein coding genes in queen larvae:

The ratio of mtDNA and nDNA remains nearly the same for queens and workers. Biogenesis of organelles occurs to the same extent.

*translation rate = [mRNA][ribosomes]

The energy demand of queen larvae is met through increased organelle activity.

There is no change in the genome of the larvae. Their genetic sequences remain as similar to their sisters' (r = 0.75) as before.

Corona, et al. 1999

Slide 3
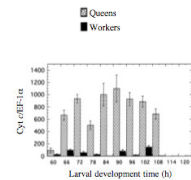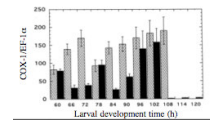
Comparing other species

Camponotus floridanus

April Nobile, commons.wikimedia.org

Harpegnathos saltator

L. Shyamal, commons.wikimedia.org

Bonasio, et al. 2010

Slide 4

Comparing other species

Camponotus floridanus

- Large colony size
- Strict reproductive caste
- Differentiation in worker caste
- Colony dies when queen dies
- Developed division of labor

Harpegnathos saltator

- Limited caste dimorphism
- Limited social organization
- Some workers can reproduce
- Fertile workers replace queen
- Low complexity division of labor

Bonasio, et al. 2010

Slide 5

Discussion

Genomic analysis of *H. saltator* and *C. floridanus* indicate that they likely possess mechanistic pathways similar to *A. mellifera*.

- Cellular aging in castes differs dramatically → Up-regulation of telomerases and histone methyltrasnferase.
- Division of labor mediated by gene expression → Caste-specsific expression of "smelling" genes.
- Morphological differentiation within worker castes. → Differential expression of genes involved in human muscle development.

Bonasio, et al. 2010