

Draft genome of the red harvester ant *Pogonomyrmex barbatus*

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We report the draft genome sequence of the red harvester ant, *Pogonomyrmex barbatus*. The genome was sequenced using 454 pyrosequencing, and the current assembly and annotation were completed in less than 1 y. Analyses of conserved gene groups (more than 1,200 manually annotated genes to date) suggest a high-quality assembly and annotation comparable to recently sequenced insect genomes using Sanger sequencing. The red harvester ant is a model for studying reproductive division of labor, phenotypic plasticity, and sociogenomics. Although the genome of *P. barbatus* is similar to other sequenced hymenopterans (*Apis mellifera* and *Nasonia vitripennis*) in GC content and compositional organization, and possesses a complete CpG methylation toolkit, its predicted genomic CpG content differs markedly from the other hymenopterans. Gene networks involved in generating key differences between the queen and worker castes (e.g., wings and ovaries) show signatures of increased methylation and suggest that ants and bees may have independently co-opted the same gene regulatory mechanisms for reproductive division of labor. Gene family expansions (e.g., 344 functional odorant receptors) and pseudogene accumulation in chemoreception and P450 genes compared with *A. mellifera* and *N. vitripennis* are consistent with major life-history changes during the adaptive radiation of *Pogonomyrmex* spp., perhaps in parallel with the development of the North American deserts.

chemoreceptor | de novo genome | eusociality | genomic evolution | social insect

The formation of higher-level organization from independently functioning elements has resulted in some of the most significant transitions in biological evolution (1). These include the transition from prokaryotes to eukaryotes and from uni- to multicellular organisms, as well as the formation of complex animal societies with sophisticated division of labor among individuals. In eusocial insects such as ants, distinct morphological castes specialize in either reproduction or labor (2). Currently, very little is known of the genetic basis of caste and reproductive division of labor in these societies, where individuals follow different developmental trajectories, much like distinct cell lines in an organism (3). The resulting phenotypes, queens and workers, can differ greatly in morphology, physiology, and behavior, as well as in order of magnitude differences in life span and reproductive po-

tential (2). Ants, of all social insects, arguably exhibit the highest diversity in social complexity, such as queen number, mating frequency, and the degree of complexity of division of labor (2), and most social traits have independent origins within the ants, making them well suited to comparative genomic analyses.

The sequencing of the honey bee (*Apis mellifera*) genome marked a milestone in sociogenomics (4, 5), facilitating research on the evolution and maintenance of sociality from its molecular building blocks. Since then, genomes of three closely related species of solitary parasitic hymenopterans, *Nasonia* spp., were published and similarities and differences were extensively discussed in the context of the evolution of eusociality (6). However, *A. mellifera* represents only 1 of at least 10 independent evolutionary origins of eusociality within the order Hymenoptera (7–11), and thus it remains unclear whether differences between the honey bee and *Nasonia* spp. truly reflect differences inherent in sociality. With at least six ant genomes on the horizon (12), among other solitary and social insects, sociogenomic comparisons are likely to yield exciting insights into the common molecular basis for the social lifestyle. Ant genomics will also allow us to gain a better understanding of variation in social organization, of elaborate variations of physical and behavioral divisions of labor, of invasion biology, and of the convergent evolution of life histories and diets. It also remains a major question whether there are many evolutionary routes to eusociality, especially at the molecular level,

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or whether we can extract generalities and rules for the molecular evolution of eusociality (3, 4, 13). Although it is likely that much variation in social structure is due to changes in the regulation of conserved pathways, it is undetermined what, if any, role novel genes or pathways have played in the solitary-to-social transition and diversification of social phenotypes (14).

The genus *Pogonomyrmex* contains species that vary greatly in social organization (15), is among the best studied of ant genera (16, 17), is sister to almost all other genera in the diverse subfamily Myrmicinae (8, 11), and contains species of major ecological importance as granivores in both North and South America (18, 19). Colonies can contain over 10,000 workers and a single multiply mated queen that may live for decades. Some *Pogonomyrmex barbatus* populations have a unique system of genetic queen-worker caste determination (Fig. 1) where individuals are essentially hard-wired to develop as either queens or workers, a contrast to environmentally determined diphenism (20–24) (*SI Appendix, Chapter 1*). As a consequence, individuals can be genotyped using genetic markers to determine their caste even before caste differentiation. This unique system of caste determination provides a means of studying the genes and regulatory networks used in caste determination.

Results and Discussion

Genome coverage is 10.5–12 \times on the basis of the estimates of genome size for *Pogonomyrmex* ants as 250–284 Mb (25). The assembly consists of 4,646 scaffolds (mean contig/scaffold: 7.22) spanning 235 Mb (~88%) of the genome that harbor 220 Mb (~83%) of DNA sequence (15 Mb of which are gaps within scaffolds). The N50 scaffold size of the assembly is 793 kb, and the largest scaffold is 3.8 Mb in length; the N50 contig size is 11.6 kb. The transcriptome assembly yielded 7,400 isogroups with a N50 contig size of 1.3 kb.

The MAKER annotation pipeline predicted 16,331 genes and 16,404 transcripts. InterProScan (26) identified additional genes from the in silico prediction programs, which were added to the MAKER predicted genes. The final official gene set, OGS1.1, which was used for computational analyses, consisted of 17,177 genes encoding 17,250 transcripts. Of these, 7,958 (>46%) had complete or partial EST support from the *P. barbatus* transcriptome assembly. The results of the assembly and annotation of the *P. barbatus* genome are well within the range of other insect genomes (Table 1).

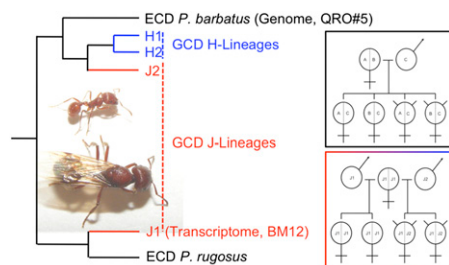


Fig. 1. A pictorial description of the phylogenetic position of the samples used for the genome and transcriptome sequencing, with each put in the context of environmental and genetic caste determination (for a more complete phylogenetic tree, see *SI Appendix, Chapter 1*). The dependent lineages (H1/H2 or J1/J2) obligately co-occur because hybridization between them is necessary to produce workers, although within either J or H, the constituent lineages are reproductively isolated because interlineage hybrids cannot become queens (red/blue box). In the boxes to the right, workers are represented by “horned” female symbols. In all *P. barbatus*, the queen mates multiply; polyandry in genetic caste determining (GCD) colonies is obligate to produce both female castes (queens originate from intralineage matings and workers from interlineage matings). In environmental caste determination (ECD), alleles from any father have an equal chance to be in queens or workers (black box). Photo of gyne and worker *P. barbatus* by C. R. Smith.

More than 1,200 genes have been manually annotated to improve models generated by MAKER (*SI Appendix, Chapter 2*) and were used in gene family-centered analyses (see discussion below and *SI Appendix, Chapters 3, 6–8, 14, and 16–29*). There are two fundamentally different reasons for our choice of gene families: One set comprises highly conserved gene families for quality assessment (e.g., sequencing error, genome completeness), whereas the second set is based on biologically interesting functional groups associated with the evolution and regulation of social behavior or adaptations of *P. barbatus* to a desert seed-harvesting lifestyle.

Quality of Genome Assembly. The core eukaryotic gene-mapping approach (CEGMA) (27) provides a method to rapidly assess genome completeness because it comprises a set of highly conserved, single-copy genes, present in all eukaryotes. In *P. barbatus*, 245 of the 248 (99%) CEGMA genes were found, and 229 of the 248 genes were complete (92%). Cytoplasmic ribosomal protein genes are another highly conserved set of genes that are widely distributed across the physical genome in animals (28, 29). A full complement of 79 proteins was found within the *P. barbatus* genome encoded by 86 genes (*SI Appendix, Chapter 6*). Because ribosomal proteins are highly conserved, their manual annotation also provided an estimate of sequencing errors, such as frameshift-inducing homopolymers (a potential problem inherent to pyrosequencing) (30). Six erroneous frameshifts were found in ribosomal protein genes (only one homopolymer); extrapolating from the number of nucleotides encoding the ribosomal genes suggests that 1 in 7,200 coding nucleotide positions (0.014%) may be affected by frameshifts. Analyses of other highly conserved gene families, including the oxidative phosphorylation (31) pathway and the *Hox* gene cluster (32, 33), also suggest high coverage and good genome assembly (*SI Appendix, Chapters 7 and 8*). Interestingly, the mitochondrial genome did not auto-assemble into scaffolds greater than 2 kb, but 71% of the mitochondrial genome could be manually assembled with the longest contig containing 5,835 bp (*SI Appendix, Chapter 9, Dataset S1*). The largest missing fragment of the mitochondrial genome is typically very high in AT content (96% in *A. mellifera ligustica*) (34) and may not have been sequenced due to PCR biases.

In silico-predicted gene models gain significant support through EST sequences. Another way to confirm predicted gene models is a proteomics approach, which has the additional benefit that it demonstrates that a gene is not only transcribed but also translated. A proteomic analysis of the poison gland and antennae confirmed 165 gene and protein models with at least two peptides (*SI Appendix, Chapter 10*). It also resulted in the identification of proteins likely associated with nest defense (poison gland) and chemoreception (antenna).

Chromosomal coverage in the current draft assembly was assessed by the identification of telomeres. Most insects outside of the Diptera have telomeres consisting of TTAGG repeats. On the basis of the karyotype data ($n = 16$), we expected 32 telomeres in *P. barbatus* (35). We searched the assembled genome and mate pair reads for TTAGG repeats and extended these where possible (6). In total, 27 of the expected 32 telomeres (88%) were found (*SI Appendix, Chapter 11*). These telomeres are even simpler than those of *A. mellifera* (36). Whereas most other insect telomeres commonly include retrotransposon insertions, these seem to be absent from the telomeres of *P. barbatus*.

Genome-Wide Analyses. The mean GC content of the *P. barbatus* genome is 36.5% and the mean ratio of observed-to-expected CpG [CpG(o/e)] is 1.57, both of which are within the ranges reported for other Hymenoptera (5, 6). We define compositional domains as the sequence stretches of variable lengths that differ widely in their GC compositions. A comparison of GC compositional-domain lengths among insects shows that *P. barbatus* and *A. mellifera* have similar compositional domain-length distributions (*SI Appendix, Chapter 4*). Among the compared insect genomes, the hyme-

Table 1. Comparison of metrics for recently sequenced insect genomes

Species	Order/name	Fold coverage	N50 scaffold (kb)	No. of genes	Gene set	Source
<i>Pogonomyrmex barbatus</i>	Hymenoptera (red harvester ant)	12	793	17,177	OGS1.1	This study
<i>Nasonia vitripennis</i>	Hymenoptera (jewel wasp)	6.8	709	18,822	OGS1.2	(6)
<i>Apis mellifera</i>	Hymenoptera (honey bee)	7.5	362	10,156/21,001	OGS1/OGS2	(5)
<i>Acyrtosiphon pisum</i>	Sternorrhyncha (pea aphid)	6.2	88.5	34,604	OGS1	(37)
<i>Tribolium castaneum</i>	Coleoptera (red flower beetle)	7.3	990	16,404	Consensus set	(38)

noptera have the smallest proportion (0.1–0.5%) of long compositional domains (>100 kb) as well as the widest range in GC compositional domains. Similar to the other sequenced hymenopteran genomes, but in contrast to other insect orders, genes in *P. barbatus* occur in the more GC-poor regions of the genome. Although the mean CpG(o/e) values of hymenopteran genomes are among the highest observed, species-specific patterns of CpG (o/e) within each genome are not consistent between the hymenopterans studied (Fig. 2). The distribution of CpG(o/e) in *P. barbatus* exons is similar to that in insects without CpG methylation (although with greater variance) (39) and suggests little germline methylation despite the presence of a complete methylation toolkit (see below and *SI Appendix, Chapter 24*). We used an indirect method [single nucleotide polymorphisms (SNP) frequency: CpG – TpG] and a direct method [methylation-sensitive amplified fragment length polymorphism (AFLP) assay; *SI Appendix, Chapter 4*] to determine the presence and frequency of active CpG methylation in *P. barbatus*. We found that CpG/TpG (and vice versa) SNPs constitute 84% of all CpG-to-NpG polymorphisms. This is an indirect measure of CpG methylation because it has been shown that a methylated cytosine in a CpG has a higher probability to mutate into thymine (*SI Appendix, Chapter 30*). The more direct measure of CpG methylation comes from an AFLP analysis that used methylation-sensitive and -insensitive restriction enzymes. In a comparison of 209 individuals from every female and developmental caste, 33% of all AFLP fragments showed a signature of methylation (*SI Appendix, Chapter 4*). These findings suggest a role of DNA methylation in genome regulation, but additional data are necessary to confirm these predictions and discern the biological role of DNA methylation in *P. barbatus*.

Gene ontology analyses detected significant enrichments in genes associated with sensory perception of smell, cognition, and neurological processes (*SI Appendix, Chapter 5*). These enrichments may reflect the heavy reliance on chemical communication in ants. Consistent with this and detailed analyses of chemosensory and cytochrome P450 gene families (see below), a gene orthology analysis including *Drosophila melanogaster*, *A. mellifera*, and *Nasonia vitripennis* found expansions of genes involved in responses to chemical stimuli and electron transport. The orthology analysis also found a small fraction of genes (3.2% of those in the analysis) common to both social insects studied (*SI Appendix, Chapter 5*); these genes may be important in processes related to the evolution or maintenance of sociality.

Repetitive DNA. Previous results for the *A. mellifera* (5) and *N. vitripennis* (6) genomes illustrate two extreme cases of genomic repeat composition for Hymenoptera: *A. mellifera* is devoid of all except a few *mariner* (40) and rDNA-specific R2 (41) transposable elements whereas *N. vitripennis* has an unusual abundance of repetitive DNA (6). The *P. barbatus* genome assembly contains 18.6 Mb (8% of genome) of interspersed elements (*SI Appendix, Chapter 12*). A total of 9,324 retroviral element fragments and 13,068 DNA transposons were identified; however, the majority of interspersed elements (55,373, 8.8 Mb, 3.75% of genome) could not be classified into a specific transposable element family. Gypsy/DIR1 and L2/CR1/Rex elements were the most abundant transposable elements; however, we discovered most families of

known insect retrotransposable elements. Nearly 1% (269 loci/1 Mb) of the scaffolded genome is microsatellite DNA (*SI Appendix, Chapter 13*), greater than in most insects (42), which are valuable markers for mapping and population genetic studies.

Chemoreceptor Gene Family Expansions. One special focus of the manual annotation was the proteins involved in chemoreception, which plays an important role in colony communication, a cor-

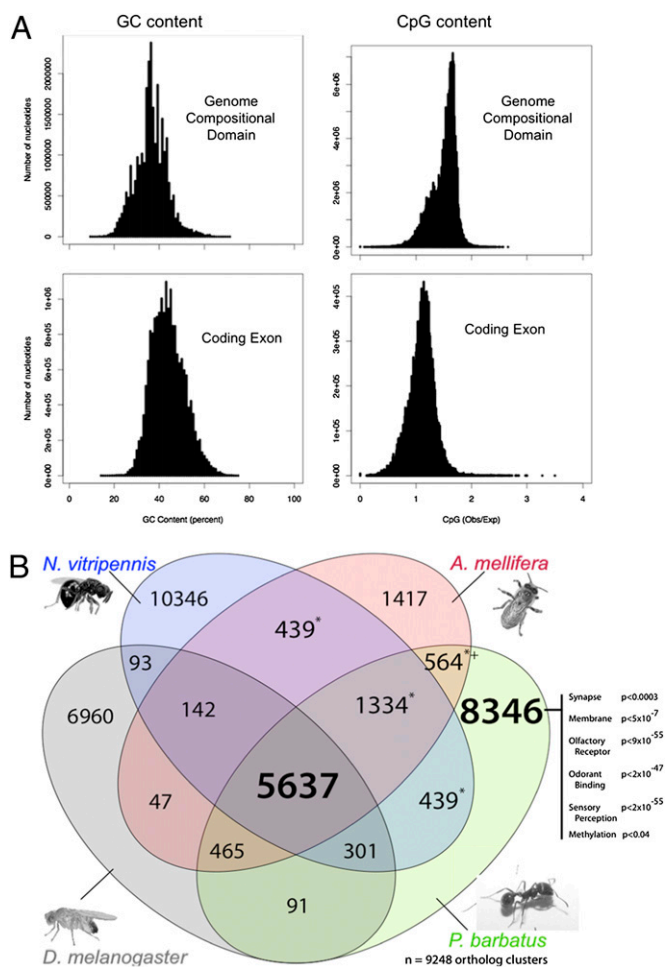


Fig. 2. Genome-wide analyses of nucleotide and relative gene content. (A) Synopsis of GC and CpG(o/e) content of the *P. barbatus* genome. (Upper panels) Comparison of genome regions with the same GC composition. (Lower panels) Comparison of the same features for exons. These distributions are similar to those found in other hymenopterans, except that *P. barbatus* shows no evidence of bimodality in CpG(o/e) for either exons (like *A. mellifera*) or introns (like *N. vitripennis*) (for comparisons, see *SI Appendix, Chapter 4*). (B) A Venn diagram displaying overlap in orthologous genes in three hymenopteran and one dipteran insect (for a detailed description of the method, see *SI Appendix, Chapter 5*). A subset of gene ontology terms significantly enriched in *P. barbatus* are displayed at the right. (*) Hymenoptera-specific genes; (**) social Hymenoptera-specific genes.

nerstone of social living. Below we report insights derived from four gene families involved in chemoreception: the ionotropic receptors (IRs), gustatory receptors (Gr), odorant receptors (Ors), and cytochrome P450s.

The IR family in *P. barbatus* consists of 24 genes, compared with 10 in *A. mellifera* and 10 in *N. vitripennis* (43). Phylogenetic analysis and sequence comparison of IRs identified putative orthologs of conserved IRs that are present in other insect genomes and that are expressed in insect antennae (e.g., IR25a, IR8a, IR93a, IR76b) (44), but a number of ant-specific divergent IRs display no obvious orthology to other hymenopteran or insect receptors (*SI Appendix, Chapter 14*). Some of these IRs may fulfill contact chemosensory functions by analogy to the gustatory neuron expression of species-specific IRs in *D. melanogaster* (43).

The *P. barbatus* Gr family contains 73 genes compared with just 11 in *A. mellifera* and 58 in *N. vitripennis*. Phylogenetic analysis of the Gr proteins (*SI Appendix, Chapter 14*) supports several conclusions about the evolution of this gene family. *A. mellifera* has lost multiple Gr lineages and failed to expand any of them (45, 46), but gene losses are not restricted to *A. mellifera*, with some occurring in *N. vitripennis* and/or *P. barbatus*. The existence of at least 18 Gr lineages is inferred, with *A. mellifera* having lost function in 10 of them, *P. barbatus* in 4, and *N. vitripennis* in 5. *P. barbatus* has expanded two gene lineages independently of the two expansions seen in *N. vitripennis*. Expansion A is considered to be orthologous to the NvGr48-50 gene lineage and a large set of ≈ 50 highly degraded pseudogenes in *A. mellifera* (represented by AmGrX-Z), and expansion B is somewhat younger. We hypothesize that these are bitter taste receptors that lost function in *A. mellifera* at the time at which they transitioned to nectar feeding, ≈ 100 Mya (47). Bitter taste perception may be essential for *P. barbatus* to avoid unpalatable seeds (e.g., plant secondary compounds).

The Or family also appears to be considerably expanded in *P. barbatus*, with 344 apparently functional genes among a total of 399 genes (the largest total known for any insect) compared with a total of 166 in *A. mellifera* and 225 in *N. vitripennis* (Dataset S2). We counted 365 ± 10 and 345 ± 10 glomeruli in five queens and five workers, respectively (*SI Appendix, Chapter 15*), supporting an $\approx 1:1$ relationship of Or genes to glomeruli resulting from convergence of the axons of all neurons expressing a particular Or on one glomerulus (48, 49). A particularly large expansion of a nine-exon gene subfamily to 169 genes suggests that these genes might comprise the cuticular hydrocarbon receptors (*SI Appendix, Chapter 14*). Cuticular hydrocarbons have gained many novel functions important in the context of social behavior, such as colony recognition and queen signaling (50, 51).

P. barbatus has 72 genes in the cytochrome P450 superfamily, compared with 46 in *A. mellifera* and 92 in *N. vitripennis* (5, 6). P450 subfamilies involved in detoxification of xenobiotics show some expansion, whereas those implicated in pheromone metabolism are enigmatically less expanded (*SI Appendix, Chapter 16*).

Evolutionary Rate and Pseudogene Accumulation. An evolutionary rate analysis based on amino acid substitutions of the three hymenopteran species with a genome sequence, with *D. melanogaster* as an outgroup, showed that a significant part of the *P. barbatus* genome (4,774 orthologous genes conserved over approximately 350 million y) evolves at a similar rate as the *A. mellifera* genome, and the *A. mellifera* and *P. barbatus* genomes show slightly higher substitution rates than the *N. vitripennis* genome (Fig. 3 and *SI Appendix, Chapter 31*). This analysis suggests that the slow evolutionary rate reported for *A. mellifera* may not be associated with sociality, but rather is specific to the Hymenoptera.

A notable feature of *P. barbatus* chemosensory and P450 genes is that the pseudogenes commonly have multiple major mutations suggesting that they are mostly “middle-aged” pseudogenes. Normally a range of pseudogene ages can be inferred in the chemoreceptor gene families from young pseudogenes with

single mutations to gene fragments. We estimated the relative ages of the pseudogenes in Ors, Grs, and cytochrome P450s in *P. barbatus*, *A. mellifera*, and *N. vitripennis* by counting the number of obvious pseudogene-causing (“pseudogenizing”) mutations per gene (stop codons, intron boundary mutations, small frame-shift insertions or deletions, or large insertions or deletions). As shown in Fig. 3, there is a contingent of considerably older pseudogenes in these gene families in *P. barbatus*. The pattern in *P. barbatus* is in contrast to *A. mellifera* and *N. vitripennis*, which have a greater number of young pseudogenes. We hypothesize that the ant lineages that gave rise to *P. barbatus* experienced a major change in chemical ecology ≈ 10 – 30 Mya, possibly as a consequence of the increase in elevation of the Sierras and Andes to their present height (52, 53). These western mountain ranges created rain shadows on their eastern sides and spawned the great American deserts. The North American members of the genus *Pogonomyrmex* underwent a significant radiation adapting to these new habitats (16), so the gene expansions in the chemoreceptors and P450s might be adaptations to novel seeds and plant families and their associated toxic components and chemical signatures. Accumulated pseudogenes may therefore reflect a shift toward a more specialized diet concurrent with the adaptive radiation of *Pogonomyrmex* spp. (54).

Innate Immunity Genes. Social insects live in dense groups with high connectivity, putting them at increased risk for disease outbreaks, but they also have social immunity to minimize the introduction and spread of pathogens (55, 56). Very efficient social defenses (e.g., hygienic behaviors) or novel immune pathways were hypothesized to explain the presence of few (roughly half) innate immunity genes in *A. mellifera* compared with *D. melanogaster* (and more recently in the red flour beetle, *Tribolium castaneum*) (5, 38). However, the more recently sequenced genomes of *N. vitripennis* (6) and *Acyrtosiphon pisum* (pea aphid) (37) also have “depauperate” complements of immune genes relative to flies and beetles, which suggests that the gene complement of flies and beetles might be a derived condition within insects. Indeed, the number of innate immune genes in *P. barbatus* is more similar to the other hymenopterans (*SI Appendix, Chapter 17*). Although all of the major signaling pathways are present in *P. barbatus* (IMD, Toll, Jak/STAT, and JKN), only a few recognition proteins were identified, which suggests either a highly focused immune system or an alternative unknown pathogen recognition system. Interestingly, we found expansions of antimicrobial peptides relative to *A. mellifera*. These expansions may correspond to a transition to living within the soil and an increased exposure to bacterial and fungal pathogens.

Developmental Networks and Polyphenism. The production of alternative phenotypes during development may occur through the regulation of several key nodes in specific networks during development (57–59). In ant colonies, queens and workers fill divergent adaptive roles—dispersal and reproduction vs. colony maintenance—and their functional differences are reflected in differences in morphology, physiology, and behavior, such as in wings and ovaries. *P. barbatus* workers are completely devoid of wings at the adult stage and have ovaries a fraction of the size of the queen’s. In analogy to honey bees (60), we hypothesized that CpG DNA methylation may play a role in the differential regulation of genes in the wing and reproductive development networks of workers and queens. This hypothesis was computationally evaluated by examining the CpG dinucleotide content (39) of wing and reproductive developmental pathway genes relative to the genome (*SI Appendix, Chapter 18*). These developmental networks contain significantly fewer CpGs than random genes, suggesting that they are more methylated than most genes because methylated cytosines are more prone to deamination (6, 39, 61). These results are in contrast to data on *A. mellifera*, where housekeeping

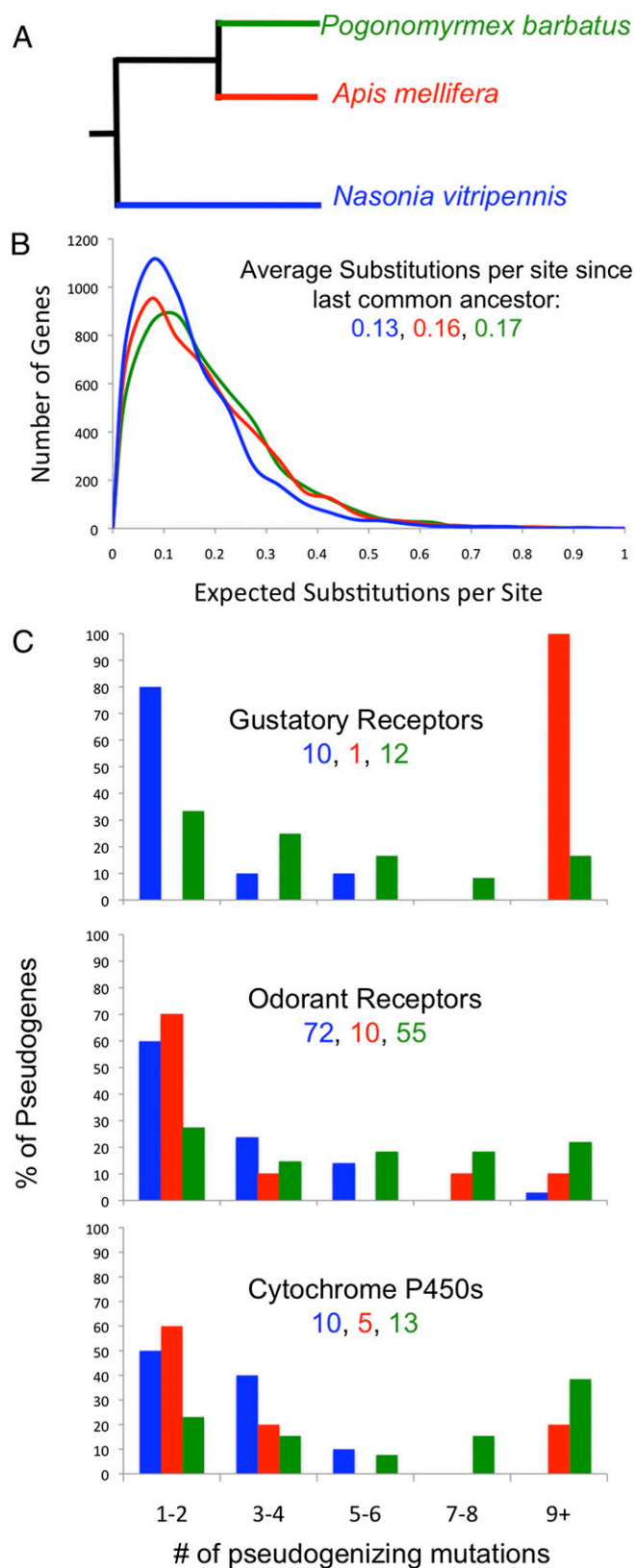


Fig. 3. Evolutionary rate and the accumulation of pseudogene-causing ("pseudogenizing") mutations in three gene families in the ant *P. barbatus* (green), the honey bee *A. mellifera* (red), and the jewel wasp *N. vitripennis* (blue). (A) The relationships among analyzed taxa. (B) A comparison of the evolutionary rates based amino acid substitutions in a set of 4,774 orthologs shared among the three species and *D. melanogaster* (the outgroup). (C) The

genes are the main targets of methylation (39, 61) (which is also in contrast to vertebrates), and suggest a potentially divergent role of methylation in harvester ants compared with honey bees.

Gene Regulation and Reproductive Division of Labor. Various gene families/pathways were specifically targeted for manual annotation because of their known role in queen-worker caste determination (3). These families/pathways included the insulin/TOR-signaling pathway (*SI Appendix, Chapter 19*), yellow/major royal jelly genes (*SI Appendix, Chapter 20*), biogenic amine receptors (*SI Appendix, Chapter 21*), and hexamerin storage proteins (*SI Appendix, Chapter 19*). These candidate caste genes will be targeted for studying gene expression differences between castes using RNAi. The RNAi pathway is intact in *P. barbatus* (*SI Appendix, Chapter 22*), and RNAi has already been successfully implemented in another ant (62).

Similar to the other sequenced hymenopterans, *P. barbatus* has a full methylation toolkit (*SI Appendix, Chapter 24*). All three DNA methyltransferase genes (*Dnmt1–3*) and three methyl-binding proteins (*MBD*) are present in *P. barbatus*, but interestingly there is only a single copy of *Dnmt1* compared with two in *A. mellifera* and three in *N. vitripennis* (6). The loss of multiple copies of maintenance methyltransferase(s) in ants may have implications for the inheritance of epigenetic information.

We analyzed genes within 100 kb of four microsatellite markers diagnostic for the J-lineages (63) with the hypothesis that some genes physically linked to the markers may cause the incompatibility between the lineages that leads to the loss of phenotypic plasticity and genetic caste determination (24) (*SI Appendix, Chapter 19*). One interesting candidate from this analysis, *lozenge* (*lz*), has many described mutants in *D. melanogaster*, including sterility due to a loss of oogenesis and a spermathecum (64–67), two traits characteristic of worker ants.

Materials and Methods

Genome Sequencing and Assembly. The genome and transcriptome of *P. barbatus* were sequenced entirely on the 454 XLR titanium platform at SeqWright. Five runs were dedicated to unpaired shotgun reads on DNA isolated from a single haploid male ant, which generated over 6 million reads averaging 370 bp in length (after trimming). Two runs used 8-kb paired-end libraries based on DNA from four brothers of the previous male ant; this yielded a total of nearly 2.9 million reads, each averaging 262 bp in length (after trimming). The assembly presented in this paper was created by a CABOG 5.3 (68) open source assembler. We substituted the OVL overlap module for the recommended MER overlayer for performance reasons (see CABOG documentation at <http://sourceforge.net/apps/mediawiki/wgs-assembler>).

The transcriptome was sequenced using a single 454 titanium run, which generated 10.4 Mb of sequence across 726,000 reads. The transcriptome was assembled using the Newbler v2.3 assembly software (Roche).

The genome of *P. barbatus* was annotated with the automatic annotation pipeline MAKER (69). The ab initio predictions of MAKER were further refined to produce an official gene set used for computational analyses (*SI Appendix, Chapter 2*). This set (OGS1.1) included all nonredundant ab initio predictions from all gene predictors used by MAKER that were supported by an InterProScan domain (26) and excluded any that were flagged as possible repeat elements. A second official gene set (OGS1.2) was produced to include refined genes on the basis of manual annotation and has been submitted to NCBI. Manual annotations followed a standard methodology described in the

accumulation of pseudogenizing mutations in three ecologically relevant gene families (Gr, Or, and cytochrome P450s). The number of pseudogenes found in each species is below the gene family name in each panel. Only one gene represents the Grs in *A. mellifera*; all other *A. mellifera* Gr pseudogenes had accrued a very high number of mutations and most are fragments. Of those analyzed here, the pseudogenes in *P. barbatus* tend to be much older than those in *A. mellifera* and *N. vitripennis* (ANOVA: $F_{2,156} = 4.7$, $P = 0.01$).

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