



## GENOME WATCH

# Buzz off, that's my bee!

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This month's Genome Watch explores the interactions of bee bacterial symbionts with each other and with their apian hosts.

Metagenomics of the human gut microbiota is a well-established field, and it is now apparent that this microbial community comprises hundreds of species, which are involved in many complex interactions. By contrast, the microbiota of the bee gut is simpler, with 95% of gut bacteria in adult worker honey bees represented by only eight phylotypes<sup>1</sup>. The commercial and environmental importance of bees is well-reported, but their value as a model for host–microbiota interactions is only now being realized using whole-genome sequencing.

The genome sequences of gut symbionts from various bee species were recently published<sup>2–4</sup>. Using the Illumina HiSeq2000 and PacBio RS, Kwong *et al.* sequenced three isolates of *Gilliamella apicola* and of *Snodgrassella alvi* to a depth of >500x coverage<sup>2</sup>. One type strain from each species was sequenced to completion and circularized, and the other four strains were sequenced to draft status. Both species are dominant members of the gut microbiota of honey bees and bumble bees, and annotation of the type strains provided evidence that each occupies a different, but complementary, metabolic niche. *G. apicola* is heavily dependent on carbohydrate metabolism, whereas *S. alvi* has lost this ability, and the metabolic networks of each species suggest that they might provide each other with nutrients.

Intriguingly, this study also provided the first experimental evidence that *S. alvi* strains are only able to colonize bees from their native host genus and can out-compete non-native

species even when they are initially at a tenfold numerical disadvantage. Comparative genomic analysis also revealed that little or no horizontal gene transfer (HGT) occurs between *S. alvi* and *G. apicola* strains from two different bee species, which is indicative of specific, long-term host–microbiota associations. However, HGT seems to occur between isolates that reside in the same host, which highlights the importance of interactions between gut symbionts.

Bees are social insects, and the transmission of symbionts between individuals that live in close proximity probably helps to maintain a similar microbiota. McFrederick *et al.* focused on the less well-studied halictid bee species *Megalopta centralis* and *Megalopta genalis* to determine whether social structure has a role in shaping their bacterial communities<sup>3</sup>. Both species are found in solitary and social nests, which enabled the role of social structure to be distinguished from that of host species. Using 454 pyrosequencing, a total of 12 nests of *M. genalis* (four social nests and eight solitary nests) and six nests of *M. centralis* (three social nests and three solitary nests) were sampled, and the results were collated with publicly available data. Data analysis showed no evidence of bacterial community clustering by social structure, although clustering by host species was strong, which is consistent with the findings of Kwong *et al.*<sup>2</sup>.

In large-scale sequencing projects, there is a high risk of capturing contaminating sequences from unintended sources. While sequencing the bumble bee *Bombus impatiens*, Martinson *et al.* also sequenced a novel gammaproteobacterial member of the *B. impatiens* gut microbiota<sup>4</sup>. At just less than 2 Mb, the genome is at least 500 kb smaller than that of the *G. apicola* and *S. alvi* type strains, which is consistent with a highly restricted host range, owing to specific

long-term co-evolution with its host. Indeed, the authors found that this new species, which is known as '*Candidatus Schmidhempelia bombi*' and is a close relative of *G. apicola*, has not been found in any other insect so far.

These newly sequenced bee gut symbionts have revealed multiple genes that are candidates for determining host specificity. These include genes that mediate interactions with the host epithelium, such as those that encode type IVa pili in *G. apicola* and *S. alvi*, as well as type VI secretion system (T6SS) proteins in *G. apicola* and T1SS proteins in *S. alvi*. Proteins from T1SSs, T5SSs and T6SSs were also found in '*Ca. Schmidhempelia bombi*'. Fli pili systems, which are involved in adhesion to the gut wall and biofilm formation, were also identified in some strains.

Given the simplicity of the bee gut microbiota and the widespread availability of affordable genome sequencing methods, it seems to be only a matter of time before we have a more comprehensive understanding of the function and community structure of the microbiota that is associated with these invertebrates. This should benefit many disciplines, from host–bacteria co-evolution and bacterial symbiosis to bee conservation.

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1. Moran, N. A. *et al.* Distinctive gut microbiota of honey bees assessed using deep sampling from individual worker bees. *PLoS One* **7**, e36393 (2012).
2. Kwong, W. K. *et al.* Genomics and host specialization of honey bee and bumble bee gut symbionts. *Proc. Natl Acad. Sci. USA* **111**, 11509–11514 (2014).
3. McFrederick, O. S. *et al.* Host species and developmental stage, but not host social structure, affects bacterial community structure in socially polymorphic bees. *FEMS Microbiol. Ecol.*, **88**, 398–406 (2014).
4. Martinson, V. G. *et al.* Genomic features of a bumble bee symbiont reflect its host environment. *Appl. Environ. Microbiol.* **80**, 3795–3803 (2014).

### Competing interests statement

The author declares no competing interests.

