Gut bacteria community

- key components in the ecological and evolutionary success of animals
- can benefit host by helping to
  - digest food
  - detoxify harmful molecules
  - protect against pathogens and parasites
  - modulate development and immunity
- only beginning to understand many of the causes and consequences of changes in the gut bacterial community

Gut bacteria community

- *Nasonia* wasps – beneficial gut bacteria instrumental in the speciation process (Brucker et al. 2013)

- Bumblebees - specific microbiota protects against the widespread natural parasite *Crithidia bombi* (Koch and Schmid-Hempel 2011)

- Termites – reduced gut microbial diversity in reproductives causes reduced colony growth and colony fitness (Rosengaus et al. 2011)

Honey bees

- Ecologically and economically important pollinator
- Experiencing declines in some areas
  e.g. In Britain managed colony numbers have declined by approximately 75% in the past 100 years (Carreck 2008)
- Interest in the role of microbes in the health of honey bees and other pollinators is increasing, recent studies have highlighted the possible roles of pathogens for pollinator declines
- Microbiota / bacteria can be vertically transmitted from mother to offspring, and can also be acquired environmentally

Honey bee bacterial communities

- Do honey bees exposed to different landscape types harbour different bacterial communities?
- What role do these bacterial communities play in pollinator health and biology?
- We need
  - Real landscape diversity
  - Characterised bacterial communities

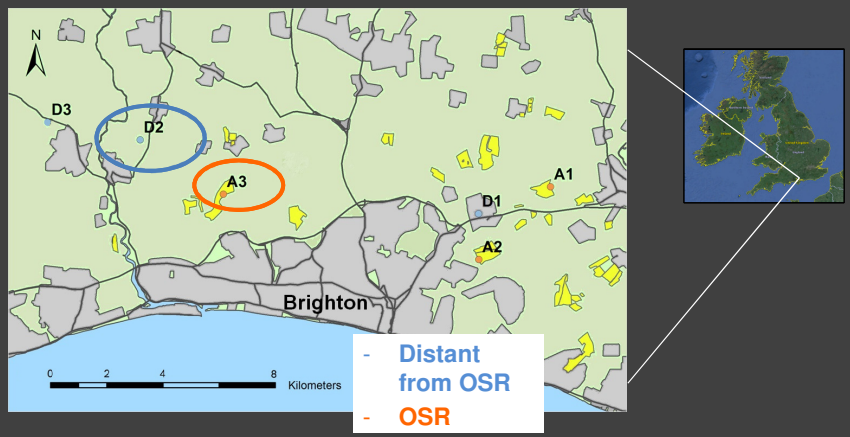
Diversity in the British landscape

- Large diversity of land use in Britain – many crops farmed, many urban areas, and also national parks
- Neonicotinoids are now the most widely used insecticides in the world – routinely used to dress seeds of oilseed rape, sunflower and maize




Diversity in the British landscape

Diversity in the British landscape



Bacterial community amplicon sequencing

- sampled forager honey bee workers
- amplicon sequencing - V4 region 16S rRNA gene (Illumina MiSeq)
- identified thousands of bacterial reads
- bioinformatics pipeline and comparative analyses

Bacterial community amplicon sequencing

Illumina sequencing of community amplicons

- useful to reduce genome complexity
- characterise bacteria symbionts present
- reliable representation of bacteria present in the entire community

barcoded samples sequenced with Illumina MiSeq

- generate sequencing library of a specific orthologous region

efficient and cost effective

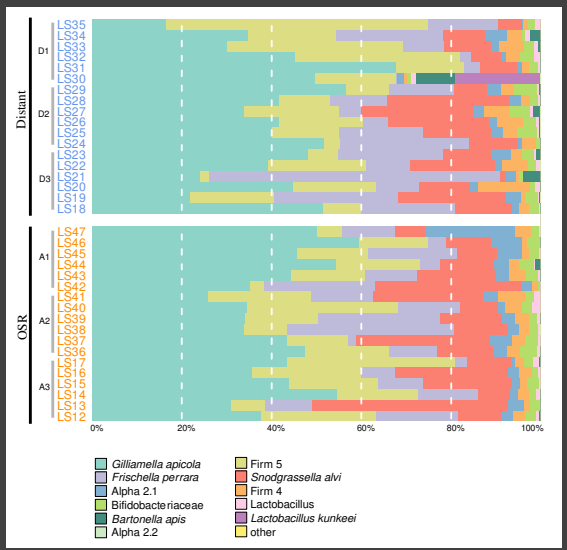
- e.g. can sequence 35 samples from different landscapes in 1 Illumina MiSeq run,
- 1 Illumina MiSeq (10 million filtered reads)
- identify 26 thousand unique reads

(Caporaso et al. 2012)

Honey bee gut bacteria and landscape

- high resolution identification of bacterial communities
- verify core bacterial community
- honey bees exposed to different landscape types show significant differences in their gut microbial communities
  (PERMANOVA p<0.001)

Which bacteria are different?



- key honey bee gut bacteria found to be different
- lower abundance of *Bartonella apis* (dominant member of the gut community) of honey bee workers foraging on OSR
- higher abundance of Alpha 2.1 (Acetobacteraceae, Class Alphaproteobacteria) in bees on OSR
- higher abundance of Alpha 2.2 in bees on agricultural regions distant to OSR
- small differences in other bacteria also common in hive material

Jones et al. 2017

What do the differences mean?

- key honey bee gut bacteria found to be different in bees exposed to different landscapes
- What does this mean?
  - gene functional category found to be enriched in honey bee gut bacteria is carbohydrate metabolism and transport
  - carbohydrate related function enriched across all bacterial taxa – proteins that show homology to drug resistant efflux pumps
  - potentially selected upon when bees are exposed to different environments e.g. forage, pesticides
  - *B. apis* has recently been shown to encode genes which may be involved in the degradation of secondary plant metabolites

Engel et al. 2012, Segers et al. 2017

Honey bee gut bacteria, local environment and behaviour

Honey bee gut bacteria and behaviour

Do bees performing different behaviours have different bacterial associations?

Why is this interesting

Bacterial associations

- Invertebrates and vertebrates host diverse microbial gut communities
- Effects are wide ranging, and many we are only beginning to understand

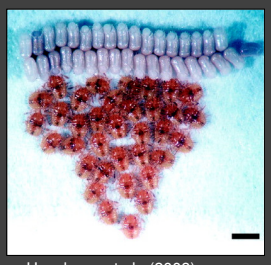
Bacterial associations

- a low oral dose of a bacterium produces anxiety-like behaviour in mice via the gut – brain pathway
- probiotic bacteria influence emotional behaviour in mice
- changes in the diet of rodents, which considerably alter the composition of the microbiome, have also been shown to improve memory and learning
- in wild red squirrels with elevated stress levels, there is a concomitant reduction in the diversity of the oral microbial community

Bacterial associations

- bacteria in the locust gut produce a key component of the pheromone derived from their faecal pellets that promotes aggregation behaviour in locusts

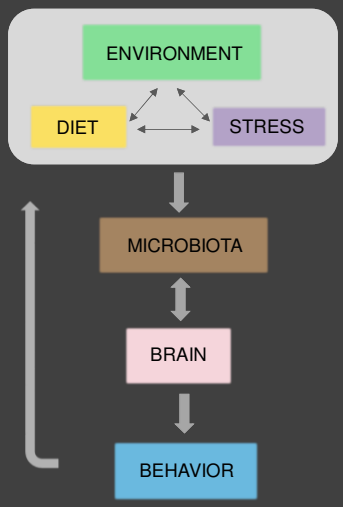
- experimental depletion of a key gut symbiont of stinkbug nymphs results in the occurrence of wandering nymphs, whereas nymphs infected with sufficient amounts of the symbiont rest



Hosokawa et al. (2008)

Bacterial associations

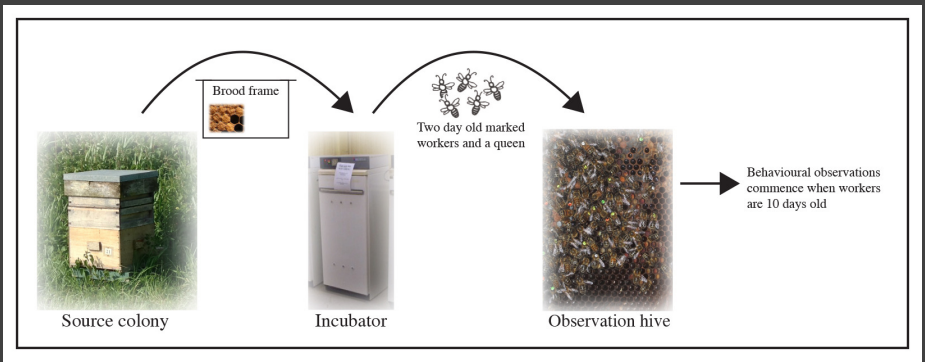
- Invertebrates and vertebrates host microbial gut communities with diverse roles
- Causes and consequences are wide ranging, and many we are only beginning to understand



Honey bee gut bacteria, local environment and behaviour

- Honey bees give us the possibility to examine associations between bacteria and behaviour in one of the most behaviourally diverse creatures!

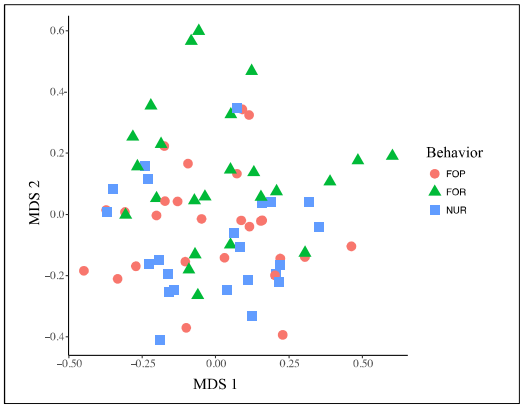
Honey bee gut bacteria, local environment and behaviour



Jones et al. 2018

Honey bee gut bacteria and behaviour

- Global difference in bees performing different behaviours (PERMANOVA $p<0.05$)
- Foraging workers harbour different relative abundances of some bacteria to workers performing in nests tasks of nursing and food processing

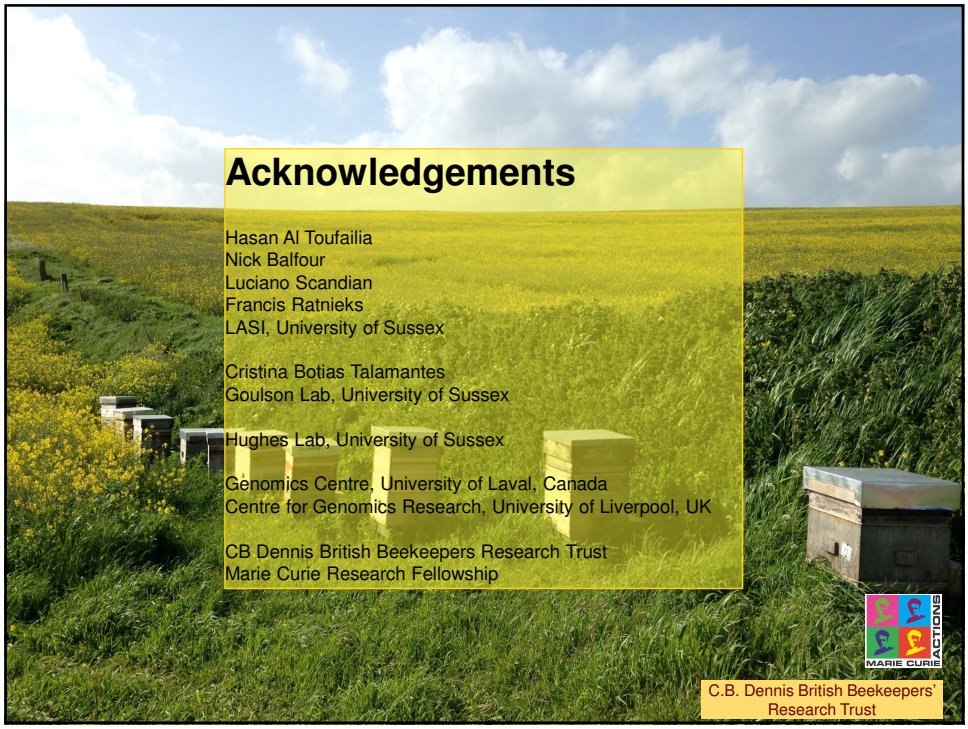


Summary

- high resolution characterisation of honey bee bacterial communities
- evidence that bees exposed to different land use types harbour different bacterial communities
- evidence that bees performing different behaviours and therefore exposed to different local environments have different bacterial associations

Future directions

- framework for investigating bacterial community differences and implications for pollinators world-wide
- functional analyses of differentially represented bacteria



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