

OR012*Investigating interactions between land use and honeybee - microbiota associations***Julia Jones**, Thierry Gosselin, Camilla Ip, William Hughes

There is growing concern about the serious losses of honeybee colonies in many areas due to a multifactorial combination of new and existing threats, principally parasites and disease, pesticide exposure and food availability. Honeybees and other bees host a community of mutualistic and commensal microbes in their guts which play an important role not only in the nutritional biology of a honeybee, but also in its general health, resistance to disease and potentially susceptibility to pesticides or pollutants. While the microbe community appears to be broadly similar across honeybee populations, it is very likely that its precise composition will change depending on pesticide exposure and the particular plant species that a honeybee colony has foraged on, and thus upon land use in the area of the colony. However, the potentially profound impact of land use on honeybee microbiota, and thereby on honeybee health, has not previously been investigated. Here we analyse the variation of the 16S rRNA sequence using Illumina next-generation sequencing technology to characterise the gut microbial community of honeybee foraging in agricultural and suburban habitats in the southern United Kingdom. We compare the communities to determine the impact of land use on the microbiota, and the implications of this for honeybee health.