

OR009*Preservation and degradation in stored pollen of honeybees***Kirk Anderson**, Vanessa Corby-Harris

The honeybee colony is a complex homeostatic unit, filled with nutritionally rich resources and a broad spectrum of microbial microenvironments. Increasing evidence points to a core gut microbiota, but the structure and function of microbial communities throughout the hive and food stores are relatively unknown. Pollen stored in wax cells, or 'beebread', is a critical aspect of colony health, supplying the bulk of proteins, vitamins and lipids for colony growth. Because beebread is warm, moist, and sugar rich, it provides a suitable niche for potentially pathogenic or spoilage microorganisms. To explore the structure and function of beebread, we used 454 amplicon sequencing of 16S rDNA to reveal beebread bacterial communities from two neighboring colonies sampled at six equally spaced time points over the course of a year. Community signatures were indicative of preservation and degradation, the former defined as an abundance of lactic and acetic acid bacteria, the later characterized as a complex nitrogen processing community. Consistently found in all beebread samples were facultative anaerobes typically abundant in nitrogen rich environments. These included many different bacteria capable of digesting complex plant polymers providing access to the pollen protoplasm. In these beebread samples, the release of nitrogen rich cell contents of pollen is evidenced by the strong presence of a comprehensive nitrogen processing bacterial community. During pollen degradation, carbon slowly made available from cellulose and other complex plant polymers would provide sustained fuel for nitrogen processing and these metabolic systems may be mutually reinforcing.