

OR208*The gut microbiota of termites: evolutionary origin and functional adaptations***Andreas Brune**

Termites degrade lignocellulose with the help of their intestinal gut microbiota. The general role of the microbial symbionts in the digestive process is slowly emerging, but the specific functions of individual populations and their evolutionary origin are still in the dark. Characterization of the hindgut community in a wide range of termite and cockroach species by pyrosequencing of bacterial 16S rRNA genes revealed strong differences among the major host groups, with dramatic changes in the relative abundance of particular bacterial taxa. When mapped onto the host tree, these changes coincided with major events in termite evolution. The acquisition of cellulolytic protists, which are abundantly present in all evolutionary lower termites, gave rise to large populations of bacterial symbionts that specifically colonize the flagellates. These flagellate symbionts were recruited among the gut bacteria and apparently serve to complement deficits in the nitrogen metabolism of their flagellate hosts. When the flagellates were lost in higher termites (family Termitidae), the availability of wood particles for bacterial colonization opened up new niches for fiber-digesting populations that had until then prevailed only in low numbers. Many of the bacterial lineages characteristic of the termite gut microbiota are present also in many cockroaches. While some members of this core microbiota seem to represent diet-specific lineages that have been independently acquired from the environment (host selection), others probably became associated with an ancestral cockroach already in the early Cretaceous (cospeciation).