LACK OF CONGRUENCE BETWEEN THE PHYLOGENIES OF *ZOOTERMOPSIS* TERMITES AND THEIR MICROBIAL SYMBIONTS: EVIDENCE OF HORIZONTAL TRANSMISSION? S. J. Taerum[1] and G. H. Gile[1], [1]School of Life Science, Arizona State University, staerum@asu.edu

Introduction: Mutualistic microbes have dramatically altered the niche breadth of plants, animals and fungi. This has driven and shaped the evolution of both multicellular hosts and associated microbes in many associations. A common hypothesis in symbiosis theory is that vertically inherited mutualistic microbes should diverge and speciate along with their hosts, resulting in the hosts and microbes having congruent phylogenies [1]. However, incongruencies are frequently observed because of horizontal transmission of microbes between related species. More knowledge on the interplay between vertical and horizontal transmission is required for a better understanding of host-microbe coevolution.

Lower termites are an ideal group of organisms for the study of host-microbe symbiosis and coevolution. These insects primarily feed on wood which contains recalcitrant materials such as cellulose. Lower termites depend in part on protists in the groups Parabasalia (i.e., “parabasalids”) and Oxymonadida (“oxymonads”) to digest the cellulose [2]. These symbionts inhabit the hind guts of their temite hosts, and are both obligate and vertically transmitted. Cocladogenesis between termites and their mutualist protists has been demonstrated within termite families [e.g., 3]. However, coevolutionary patterns have never been closely examined within a termite genus. Here, we tested for evidence of host-microbe coevolution between termites in the genus *Zootermopsis* and their protist symbionts.

The genus *Zootermopsis* contains four taxa (three species, one of which has been divided into two subspecies), all of which occur only in western North America: *Zootermopsis nevadensis nevadensis Zootermopsis nevadensis nuttingi*, *Zootermopsis angusticollis*, and *Zootermopsis laticeps* [4]. The ranges of *Z. nevadensis nuttingi* and *Z. angusticollis* overlap almost entirely, running along the west coast of North America from the Pacific Northwest down to southern California. Most of the range of *Z. nevadensis nevadensis* is east of the Sierra Nevada, although the range slighty overlaps with those of *Z. nevadensis nuttingi* and *Z. nevadensis nevadensis* in northern and southern California. Finally, the range of *Z. laticeps* is from central Arizona to western Texas.

Until the present study, only the protist community of *Z. angusticollis* was closely examined [5]. In that study, the authors identified seven parabasalid species: *Trichomitopsis minor*, *Trichomitopsis parvus*, *Trichomitopsis termopsidis*, Trichonympha *campanula*, *Trichonympha collaris*, *Trichonympha postcylindrica*, and *Trichonympha sphaerica*. We assessed the gut protist communities of the other three *Zootermopsis* taxa and compared with that of *Z. angusticollis*.

We collected the four *Zootermopsis* taxa, and isolated individual parabasalid cells from the termite guts. We then used a combination of Sanger sequencing and morphological assessments to identify the protist species. In addition, we conducted amplicon sequencing of the whole termite guts using Illumina high-throughput sequencing.

Based on sequence data, the gut protist communities of *Z. nevadensis nuttingi* and *Z. nevadensis nevadensis* appeared to be identical to that of *Z. angusticollis*. *Zootermopsis laticeps* contained three species (one of *Trichomitopsis* and two of *Trichonympha*) that have not yet been described.

The similarities in protist communities between *Z. angusticollis*, *Z. nevadensis nevadensis*, and *Z. nevadensis nuttingi* suggest that horizontal symbiont transmission may occur between these species, possibly facilitated by overlapping ranges as well as hybridization between the species and subspecies. The different community in *Z. laticeps* may be due to geographical isolation from the other *Zootermopsis* species, as well as differences in habitat conditions. Further research is required to better understand the evolutionary history of the termite genus and its associated microbes.

References: [1] Bright M. and Bulgheresi S. (2010) *Nat. Rev. Microbiol., 8,* 218–230. [2] Inoue T. et al. (2000) *Termites: Evolution, Sociality, Symbioses, Ecology,* 275-288. [3] Noda S. et al. (2007) *Mol. Ecol., 16,* 1257–1266. [4] Thorne B. L. et al. (1993) *Ann. Entomol. Soc. Amer. 86,* 532-544. [5] Tai V. et al. (2013) *Plos One 8*, e58727.