



15th International Auchenorrhyncha Congress and 10th International Workshop on Leafhoppers and Planthoppers of Economic Importance

Bacterial and fungal associates of Delphacidae (Fulgoroidea: Delphacidae): using next generation amplicon sequencing to find evidence of symbiont turnover and replacement in an economically important insect lineage

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The Delphacidae are the most speciose planthopper family with over 2100 described species (Bourgoin 2014), and are significant pests of the world's most important food commodities, including rice, wheat, barley, maize, and sugarcane (Wilson & O'Brien 1987). Based on early light microscopy studies (Müller 1940) and more recent studies using DNA sequence data (Urban & Cryan 2012), these insects also harbor multiple co-evolved obligate microbial endosymbionts, many of which remain uncharacterized. Recently, full genome sequencing of the rice pest *Nilaparvata lugens* and its associated symbionts (Xue *et al.* 2014) has revealed the presence of a fungal symbiont, and the absence of the bacterial endosymbiont, *Sulcia meulleri*. *Sulcia* is hypothesized to be the primary endosymbiont of Auchenorrhyncha, as it has been detected in Fulgoroidea, Membracoidea, Cercopoidea, and Cicadoidea, and has been shown to provide nutrients essential to the host insects' survival (Moran *et al.* 2005; McCutcheon & Moran 2010). These recent findings are consistent with the hypotheses of Müller (1962) who proposed that delphacids have experienced turn-over and replacement of symbionts across their evolutionary history. To date, DNA sequence based evidence of delphacid symbionts has only been generated for several species, primarily crop pests that are placed among the Delphacini, the most recently diversifying delphacid lineage (Urban *et al.* 2010). As such, it is unclear what symbionts were ancestrally present in Delphacidae, what the succession of symbionts may have been, and in what lineages symbiont replacement and turn-over may have occurred. Using next-generation DNA amplicon sequencing, as well as Sanger sequencing, the bacterial and fungal associates of delphacids were surveyed and characterized for taxa sampled from across the phylogeny of this family, as well as taxa sampled from Cixiidae. Interpreting microbial associations in the context of the delphacid phylogeny of Urban *et al.* (2010) reveals evidence of a complex multi-symbiont system, with endosymbiont turnover potentially occurring early in the evolution of this insect family. Understanding of this dynamic symbiotic system provides unusual insights into symbioses, in general, and may also provide vital insights for the effective management of insects that pose significant threats to world food production.

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