## Horizontal gene transfer from diverse bacteria to an insect genome enables a tripartite nested mealybug symbiosis

The smallest reported bacterial genome belongs to *Tremblaya princeps*, a symbiont of *Planococcus citri* mealybugs (PCIT). *Tremblaya* PCIT not only has a 139 kb genome, but possesses its own bacterial endosymbiont, *Moranella endobia*. Genome and transcriptome sequencing, including genome sequencing from *Tremblaya* symbiont of *Phenacoccus avenae* (PAVE), which lacks intracellular bacteria, reveals that the extreme genomic degeneracy of *Tremblaya* PCIT likely resulted from acquiring *Moranella* as an endosymbiont. In addition, at least 22 expressed horizontally transferred genes from multiple diverse bacteria to the mealybug genome likely complement missing symbiont genes. However, none of these horizontally transferred genes are from *Tremblaya*, showing that genome reduction in this symbiont has not been enabled by gene transfer to the host nucleus.

Acquisition of Moranella symbiont may trigger extreme genome degeneracy in Tremblaya PCIT. 10 Genome reduction in Tremblaya PAVE occurs to a degree consistent with other previously reported 11 tiny symbiont genomes, and Tremblaya PCIT gene set is an almost perfect subset of Tremblaya PAVE. 12 These results suggest that much of the reductive genome evolution observed in Tremblaya (down to 13 approximately 170 kb) occurred before the acquisition of Moranella in the common ancestor of Planococcus 14 citri and Phenacoccus avenae and that the extreme genomic degeneracy observed in Tremblaya PCIT 15 (from 170 kb to 140 kb) was likely due to the acquisition of Moranella by Tremblaya at some point in the 16 lineage leading to *Planococcus citri*. This scenario is consistent with studies showing that massive and 17 rapid gene loss can occur in bacteria that transition to a symbiotic lifestyle (Mira et al., 2001; Moran Mira, 18 2001; Nilsson et al., 2005), after which gene loss slows, and gross genomic changes become infrequent, 19 even over hundreds of millions of years (McCutcheon and Moran, 2010; Tamas et al., 2002; van Ham et al., 2003). 21

Pathways for translation, synthesis of essential amino acids, vitamins and peptidoglycan in *Tremblaya* PCIT are complemented by *Moranella*, mealybug genes originated from bacteria-to-mealybug horizontal gene transfers (HGTs) and mealybug genes of eukaryotic origin. In PCIT, ten HTGs group closely with other alphaproteobacterial sequences in phylogenetic trees, and nine HTGs from Gammaproteobacteria,

22

two from Bacteroidetes, and one that is phylogenetically unresolved. The majority of these HGTs are not present in *Tremblaya* and *Moranella* genomes.

The presence of a large number of HTGs involved in peptidoglycan production and recycling is consis-28 tent with the hypothesis that cell lysis is the mechanism used to share gene products between Moranella 29 and Tremblaya PCIT (Koga et al., 2013; McCutcheon and von Dohlen, 2011). This idea was initially sug-30 gested based on a lack of transporters encoded on the Moranella genome combined with the large number 31 of gene products or metabolites involved in essential amino acid biosynthesis and translation that would 32 need to pass between Moranella and Tremblaya PCIT for the symbiosis to function (McCutcheon and 33 von Dohlen, 2011). Subsequent electron microscopy on mealybugs closely related to PCIT showed that 34 although most gammaproteobacterial cells infecting the Tremblaya cytoplasm were rod shaped, some were 35 amorphous blobs seemingly in a state of degeneration (Koga et al., 2013). The results suggest a plausible mechanism for how the insect host controls this process: by differentially controlling the expression of 37 the horizontally transferred genes, the host could regulate the cell wall stability of Moranella. Increasing 38 the expression of murABCDE genes would increase the integrity of Moranellas cell wall, and increasing the expression of mltD/amiD would tend to decrease Moranellas cell wall strength. As Tremblaya PCIT 40 encodes no cell-envelope-related genes and likely uses host-derived membranes to define its cytoplasm, it 41 would be unaffected by changes in gene expression related to peptidoglycan biosynthesis. This hypothesis 42 is testable, because the levels of Tremblaya and Moranella are uncoupled in mealybugs closely related to PCIT; in males in particular, Moranella levels drop to undetectable levels while Tremblaya persists (Kono et al., 2008). In situations where Moranella is reduced with respect to Tremblaya, low expression of murABCDEF and increased expression of mltD/amiD would be expected.