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EVOLUTION OF CO-OBLIGATE SYMBIOSES IN APHIDS AND GENOME REDUCTION IN ENDOSYMBIONTS

par

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- Organisms across the tree of life are associated with diverse microbial partners, conferring to the host new adaptive traits that enable it to explore new niches. This is the case for insects and other invertebrates thriving on unbalanced diets, which harbour mutualistic intracellular microorganisms, mostly bacteria, that supply them with the required nutrients. The genomes of these mutualistic organisms tend to evolve to become small and compact, coding mainly for a reduced house-keeping machinery and the genes involved in their symbiotic function.

- Aphids (Hemiptera: Aphididae) typically harbour the obligate endosymbiotic bacterium *Buchnera*, which is required for the supply of essential amino acids and some vitamins. However, several aphids from the Lachninae subfamily have been shown to consistently harbour secondary endosymbionts, mainly *Serratia symbiotica*. These secondary endosymbionts can expand the metabolic capability of the symbiotic consortium and even replace or complement functions formerly performed by the ancient obligate symbiont. Through whole-genome sequencing and fluorescence in situ hybridisation of the endosymbiotic consortia of different aphid species belonging to four out of five Lachninae tribes, we explored the co-obligate status of their harboured *S. symbiotica* strain as well as the cell shape, tissue tropism and identity of the non-*Serratia* secondary endosymbionts. While *S. symbiotica* is the most common and putatively ancient secondary endosymbiont, it has been replaced at least in four ocassions. The genomes of the *Buchnera* endosymbionts revealed that a putatively ancient loss of the genes involved in the synthesis of two essential vitamins could be behind the establishment of secondary obligate endosymbionts within this subfamily.

- Finally, we found that the genomes of *S. symbiotica* strains from different aphids actually represent discrete stages along the genome reduction continuum (from free-living to reduced obligate endosymbiont), and the analyses of these genomes allowed us to dissect the genome reduction process within a single bacterial taxon evolving in a similar biological niche (aphid-*Buchnera*).