Revealing the microbiota of the subterranean aphid *Anoecia corni* through metagenomic sequencing

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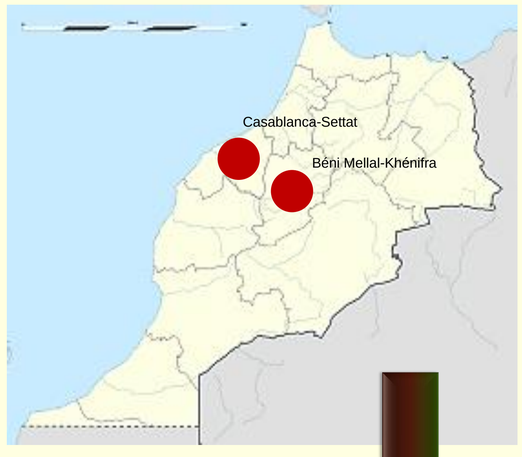
Biological Context

Many insect species harbor bacterial partners that can significantly influence their evolutionary ecology[1,2]. As compared to other insect groups, aphids harbor a bacterial microbiota that has a reputation for being poorly diversified, only restricted to the presence of the obligate nutritional symbiont *Buchnera* and some facultative symbionts[3,4]. However, studies that have addressed the microbial diversity in aphids remain based on a very limited number of species.

The dogwood-grass aphids (*Anoecia corni*) aphid species spends much of its life cycle in a subterranean environment and is in close contact with the vast microbial flora of the rhizosphere[5]. One hypothesis is that the lifestyle of this aphid species may promote the acquisition of a richer bacterial diversity compared to aphid species whose life is restricted to the aerial parts of the host plant. In this exploratory study, we used 16S rRNA amplicon Illumina sequencing approach to evaluate the bacterial diversity associated with specimens collected in the “Moroccan granary”.

Sample collection



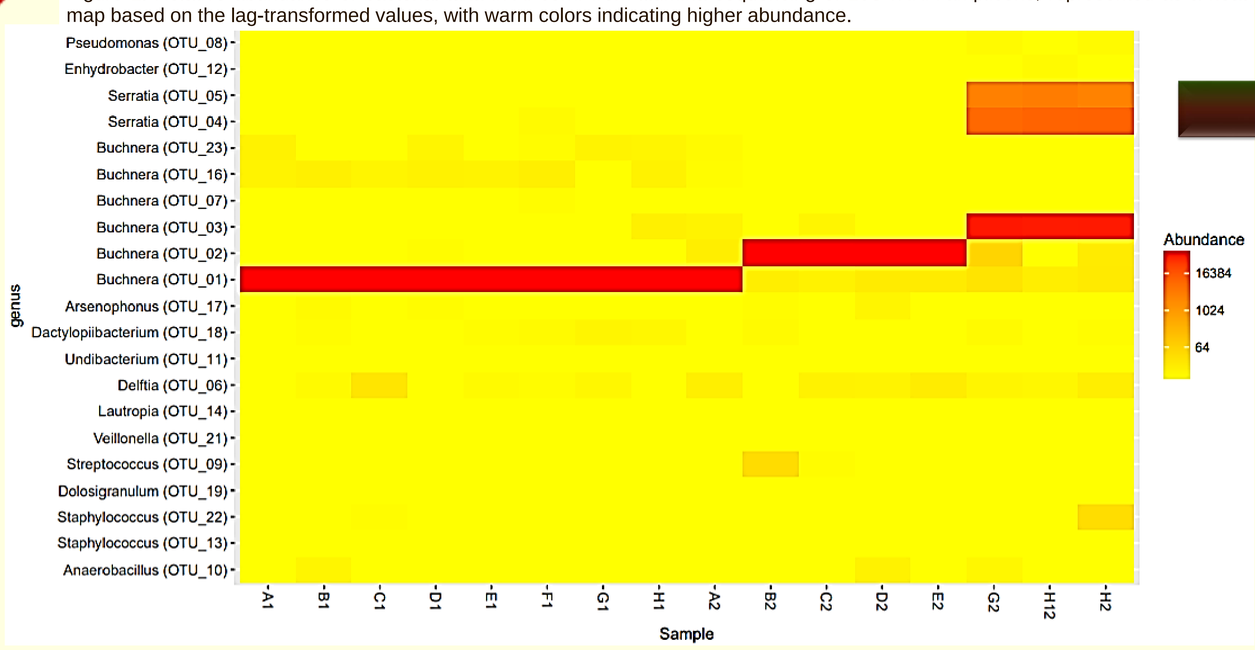
Anoecia corni specimens were collected in Morocco (regions of Béni Mellal-Khénifra and Casablanca-Settat).

DNA extraction & PCR

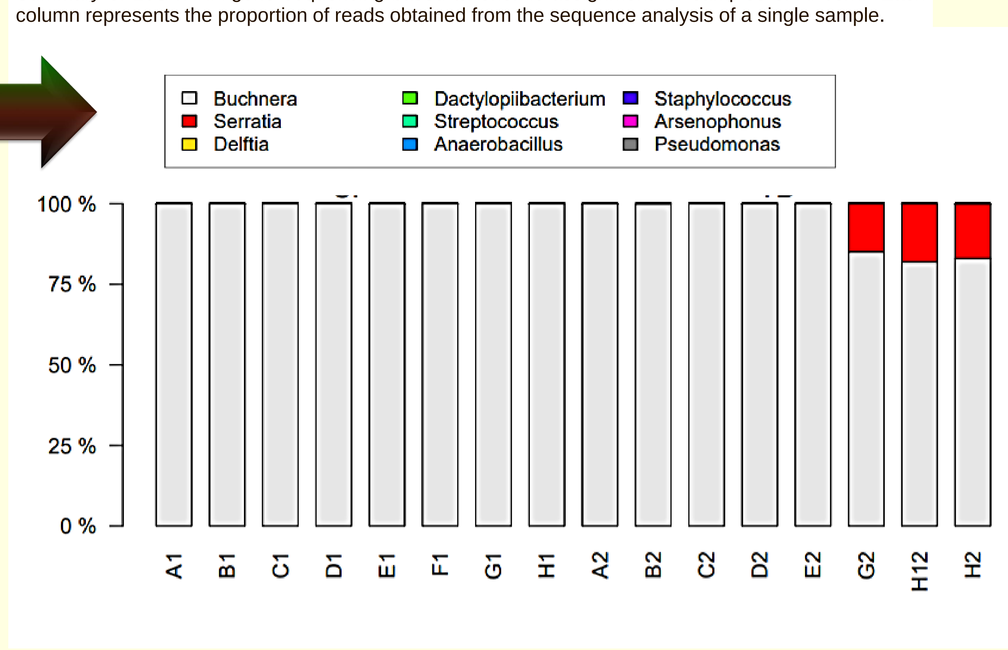
DNA extraction & sequencing librairies preparation according to the Illumina MiSeq system instructions 16S workflow. V3-V4 variable region of the 16S bacterial rRNA gene was amplified using universal primers. Data analyses were carried oud as described in Fakhour et al. 2018[6].

Results & discussion

Figure 1. Relative abundance of bacterial taxa in *A. corni* from Illumina sequencing of 16S rRNA amplicons, represented as a heat map based on the lag-transformed values, with warm colors indicating higher abundance.



Summary of 16S rRNA gene sequencing-based taxonomic assignment for samples of *A. corni*. Each column represents the proportion of reads obtained from the sequence analysis of a single sample.



- Quite high α-diversity compared to other aphid species: 22 OTUs corresponding to 14 bacterial genera. But : low abundance (Figures 1 & 2). Most of the identified genera have already been detected in other insect groups and correspond to bacteria perceived as gut bacteria, plant associates, plant pathogens or environmental bacteria (e.g. *Delftia* spp., *Dactylopiibacterium* spp., and *Anaerobacillus* spp.).
- *Arsenophonus* and *Serratia symbiotica* are the only facultative symbionts identified in *A corni*.
- Besides the obligate symbiont *Buchnera*, *S. symbiotica* is the most abundant bacterium detected in infected aphids (the largest proportion of reads) (Figure 2).

Conclusions & Perspectives

- α-diversity of bacterial communies found *A. corni* is quite rich (→ not limited to the presence of endosymbiotic bacteria).
- Origin & functional significance of this diversity? Environmental contaminations, commensals, mutualistic or parasitic partners?
- Biological significance of the presence of *S. symbiotica*? (→ future: molecular typing approaches – e.g. MLST).
- The microbial flora of the rhizosphere = potential reservoir for the emergence of new symbiotic associations in insects.

References: 1. Gil, R. & Latorre, A. Life 9, 21 (2019); 2. Engel, P. & Moran, N. A. FEMS Microbiol. Rev. 37, 699–735 (2013); 3. Oliver, K. M., Degnan, P. H., Burke, G. R. & Moran, N. A. Annu. Rev. Entomol. 55, 247–266 (2010); 4. Jing, X. et al. Mol. Ecol. 23, 1433–1444 (2014); 5. Ivens, A. B. F., Kronauer, D. J. C. & Boomsma, J. J. Conserv. Genet. Resour. 3, 73–77 (2011); 6. Fakhour, S. et al. FEMS Microbiol. Ecol. 94, (2018).