

Eukaryotic communities characterized using airborne DNA from poultry buildings: first insights towards pest control improvement in layer henhouses

Adrien Taudière (adrien.taudiere@zaclys.net), Tony Dejean, Geoffrey Chiron, Marine El Adouzi, Olivier Bonato, and Lise Roy

Dermanyssus gallinae

wikipedia

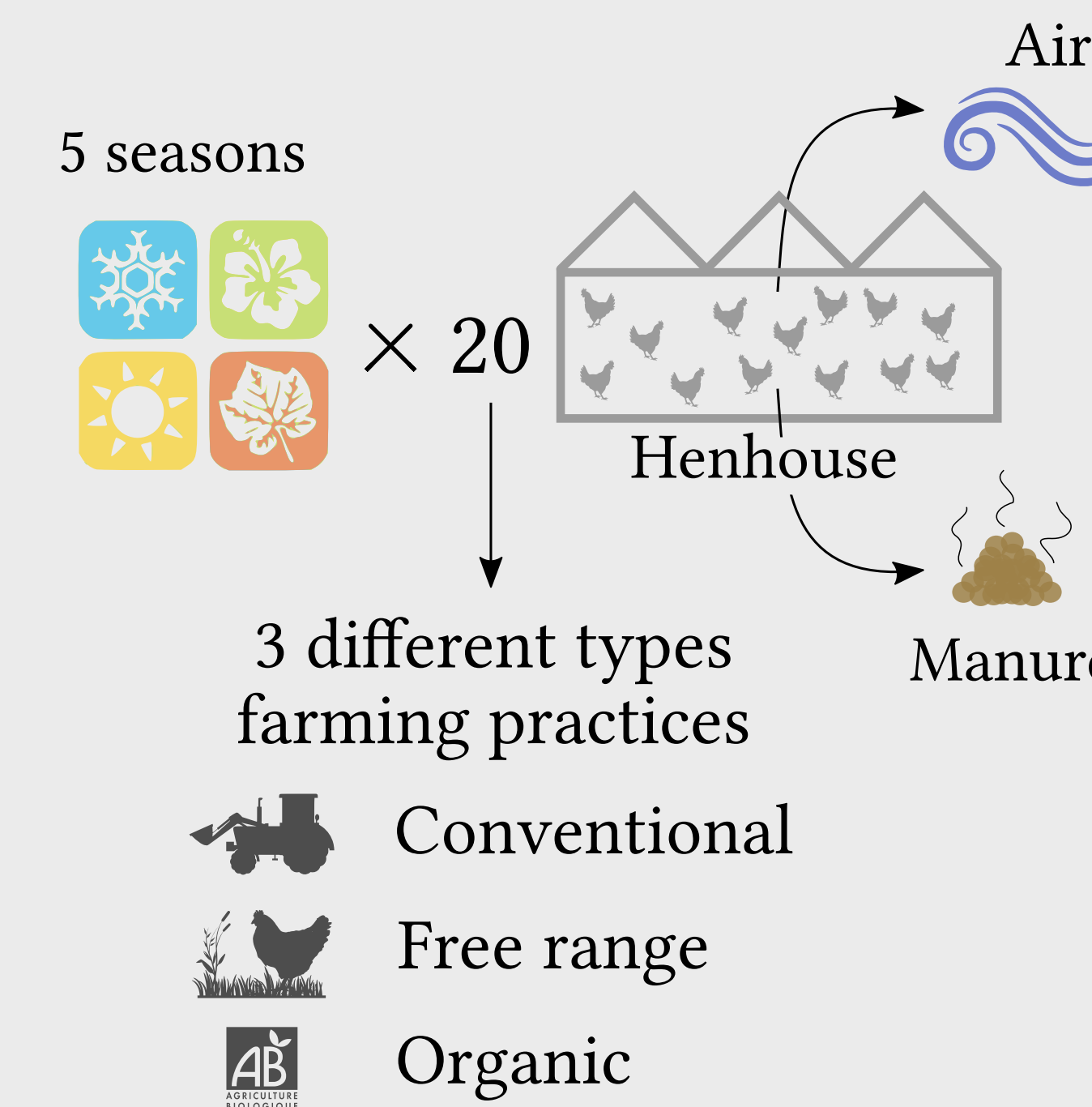


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Context & objectives

- Improving environmentally friendly strategies for **controlling pests** is crucial in modern agriculture and requires a better knowledge of the **ecological networks** involving pest species. The poultry red mite (*Dermanyssus gallinae*) is a haematophagous pest of economic importance in poultry farms. The ecology of *D. gallinae* is poorly known in particular concerning its predators and pathogens.
- Using **airborne DNA metabarcoding** coupled with visual counting of acari morphospecies, we propose a first insight into Eukaryotic communities in the environment of henhouse under different types of farm managements.
- The overall objectives of this study were to (i) characterize the **Eukaryotic communities** in henhouses under different farming practices and their relation with *D. gallinae* abundance and (ii) disentangle interactions within the predatory mite guild (which potentially encompasses predators of *D. gallinae*).

Materials & Methods



Environnemental **metabarcoding** (Illumina) of Eukaryotic communities

204 samples



Visual counting (681 899 individuals) of arthropod morphospecies



Abbreviation for morphospecies:

- ME1: multi-species (incl. *Cornodendrolaeps presepeum*)
- ME2: two cryptic species (incl. *Androlaelaps casalis*)
- ME4: *Proctolaelaps* near *parascolyti*
- ME7: multi-species (incl. *Macrocheles muscaedomesticae*)
- UR1: *Uroobovella fimicola*
- UR2: multi-species (*Uropodina*)

(i) All Eukaryota analysis

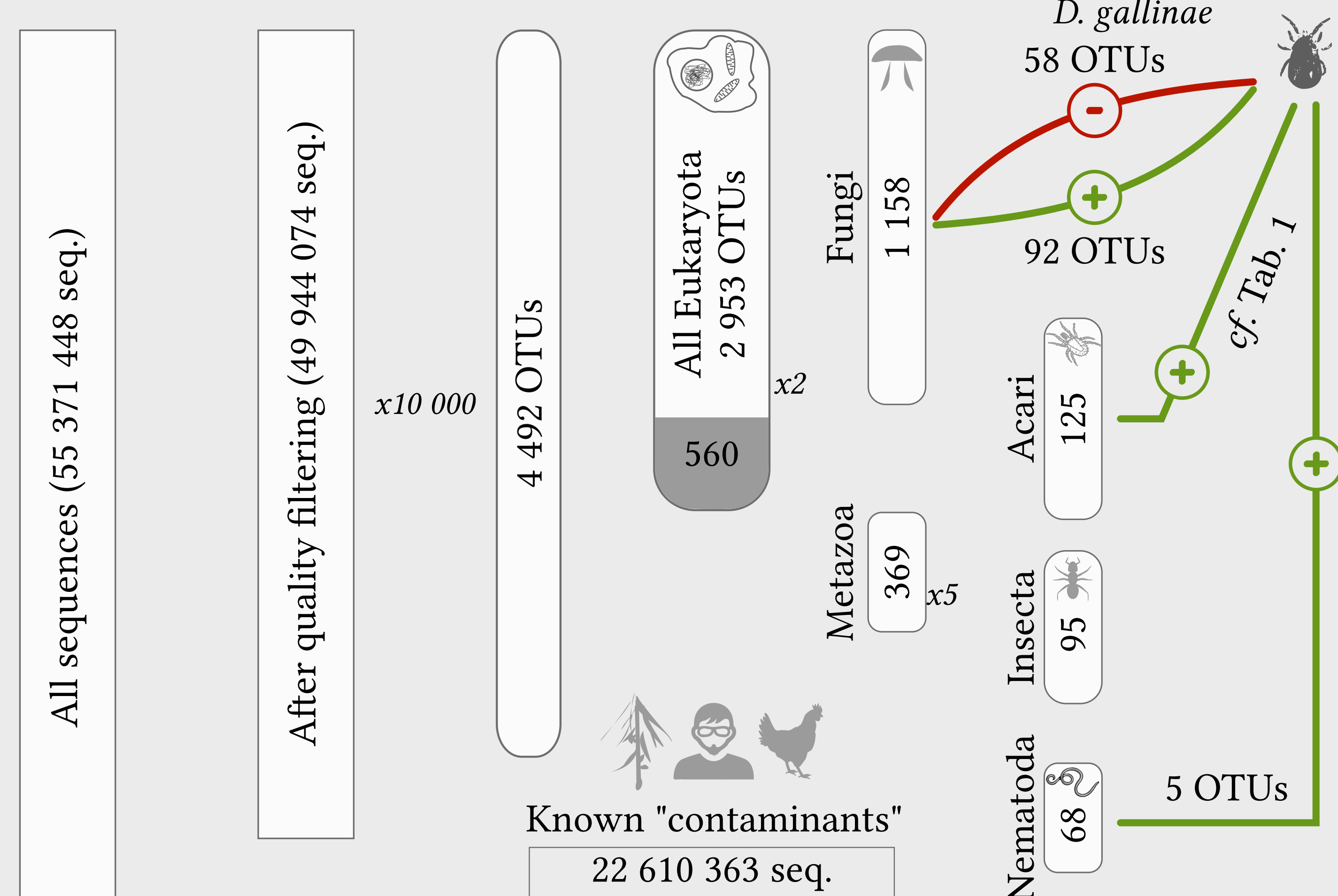


Fig. 1: Number of sequences and operational taxonomic units (OTUs) in the main taxa. The significance of the correlation between the abundance of *D. gallinae* and other OTUs was computed on relative abundance using Spearman rank test and corrected p-values for multi-testing.

- Excluding Cordata and Plants (Fig. 1), *D. gallinae* was the second most abundant OTU (1.2M seq.) after a fungal OTU belonging to the Sordariomycetes family (9.7M seq.).
- Alpha-diversity of Eukaryota and Acari were not affected by **farming practices** (Wilcoxon test: p-values > 0.05; Fig. 2).
- Farming practices explained significantly (Permanova: p=0.001) though very weakly the **variation in Eukaryota communities** (Fig. 3). Moreover, Acari communities vary far less across seasons than communities of other Eukaryota.
- Very few taxa displayed a **significant negative correlation** with the abundance of *D. gallinae*, and all these taxa belong to fungal Kingdom (Fig. 1).

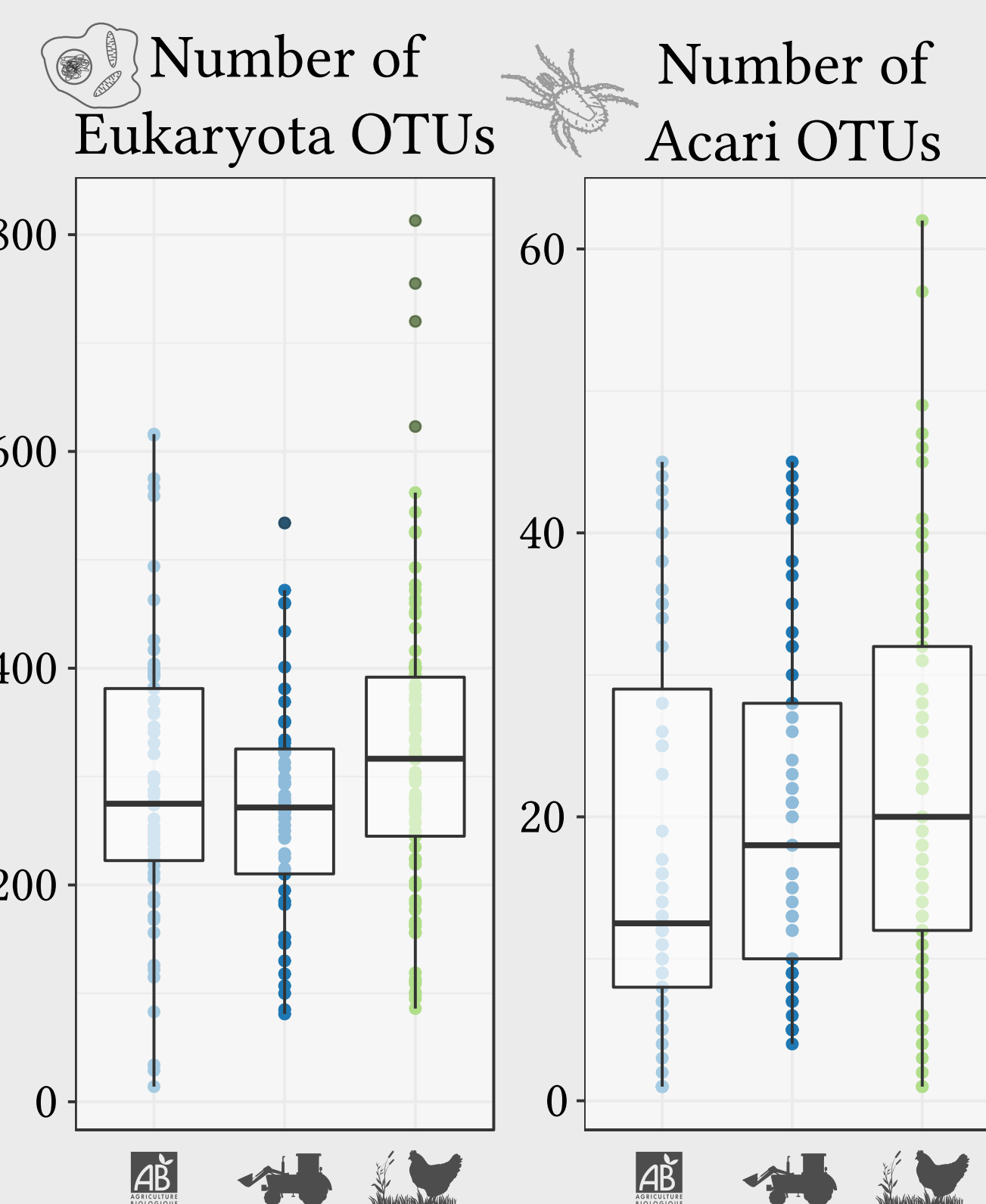


Fig. 2: Number of OTUs according to farm managements



Fig. 3: Variance decomposition of B-diversity (Permanova)

(ii) Focus on Acari

Tab. 1: Correlation between molecular and visual abundance of Acari (*Spearman test*)

	Rho	P-value
Astigmata	0.62	0.0001
Cheyletoidea	0.29	0.0162
ME1	0.28	0.0186
ME2	0.39	0.0009
ME5	0.12	0.3243
ME7	0.27	0.0252
Oribatida	0.21	0.0875
UR1	0.15	0.2162
UR2	0.06	0.6043

Tab. 2: Correlation between the abundance of *D. gallinae* and other Acari (*Spearman test*)

	Rho	P-value	Rho	P-value
Astigmata	0.28	0.0230	0.61	0.0001
Cheyletoidea	-0.11	0.3508	0.31	0.0102
ME1	-0.01	0.9150	0.19	0.1225
ME2	0.47	0.0001	0.41	0.0006
ME5	0.20	0.0977	0.09	0.4435
ME7	0.07	0.5890	0.31	0.0100
Oribatida	0.28	0.0230	0.17	0.1575
UR1	0.10	0.4021	0.22	0.0775
UR2	0.21	0.0814	0.00	0.9781

- Molecular (air) and visual count (morphospecies) measured **consistent abundances** (Tab. 1) but **inconsistent community compositions** (Mantel test on Bray distance among samples: p=0.08).
- None of the acari morphospecies was negatively correlated** with *D. gallinae* for either molecular or visual data (Tab. 2). However, farming practices may blur the overall signal.

Conclusion

- Farming practices is negligible in structuring Eukaryota communities identifiable via DNA in air.
- We identified some species of fungi that may have a negative impact on *D. gallinae*. Moreover, some Acari morphospecies, positively correlated with *D. gallinae*, could be good candidate for biological control by favoring their possible predation on the pest mite.
- We pave the way for further investigations of Eukaryote trophic networks involving the pest mite *D. gallinae* and thus help progress biocontrol in henhouses thanks to DNA metabarcoding.