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Metabolomic insight in species sensitivity differences within periphytic communities

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Context & objectives

- Periphyton, as an assemblage of various taxa (microalgae, diatoms, bacteria, fungi), is a relevant model to evaluate the impairment of ecosystem functions in aquatic systems facing global change. [1,2]
- There is a paucity knowledge about the differences in species sensitivity to chemical stress within these communities, which is critical to their structure and functioning [3,4].
- Untargeted metabolomics is a relevant approach to assess the whole molecular phenotype of organisms and their consortium facing environmental stress, especially the chemical stress [5, 6]

Aims :

- (1) To highlight common vs distinct metabolome response between periphytic species facing chemical stress
- (2) Explore and compare the chemical landscape of various periphytic species

Experimental & Analytical workflow

Biological models (3 periphytic species and their co-culture)

- ✓ **Cyanobacteria**
Phormidium sp. (PMC847)
- ✓ **Green algae**
Scenedesmus costatus (TCC744)
- ✓ **Diatom**
Gomphonema parvulum (TCC612)
- ✓ **Co-culture**

Chemicals (2 model herbicides and their mixture)

- ✓ **Atrazine**
 - *Surface water conc.*: 0.1-10 µg/L
 - *Ecotoxicity*:
Algae growth 96h (NOEC) : 100 µg/L
Algae growth 72h (EC50) : 69 µg/L
- ✓ **S-metolachlor**
 - *Surface water conc.*: 0.1-10 µg/L
 - *Ecotoxicity*:
Algae growth 96h (NOEC) : 12 µg/L
Algae growth 72h (EC50) : 17 µg/L

Exposure experiment

- T0** (n=6)
- Control
- T7** (n=4 for each condition)
- Control
 - Atrazine (10, 100, 1000 µg/L)
 - S-Metolachlor (10,100, 1000 µg/L)
 - Mixture (10x10, 100x100, 1000x1000)

Metabolomic Workflow

Quenching (N₂) + Storage (-80°C)

Freeze-Drying

Biphasic extraction

- Lipophile Phase (MTBE)
- Hydrophile Phase (MeOH/H₂O)

Data acquisition

UPLC-XevoG2-S ToF (Waters®)
ESI+/-, MSe:
(1) Full HRMS 50-1500 m/z
(2) Coll 6V vs 10-40V

✓ All T0 and T7 conditions

UPLC-Qexactive+ (ThermoScientific®)
ESI+/-, DDA-top5
100-1500 m/z
MS1- Réso 120000
MS2- Réso 35 000

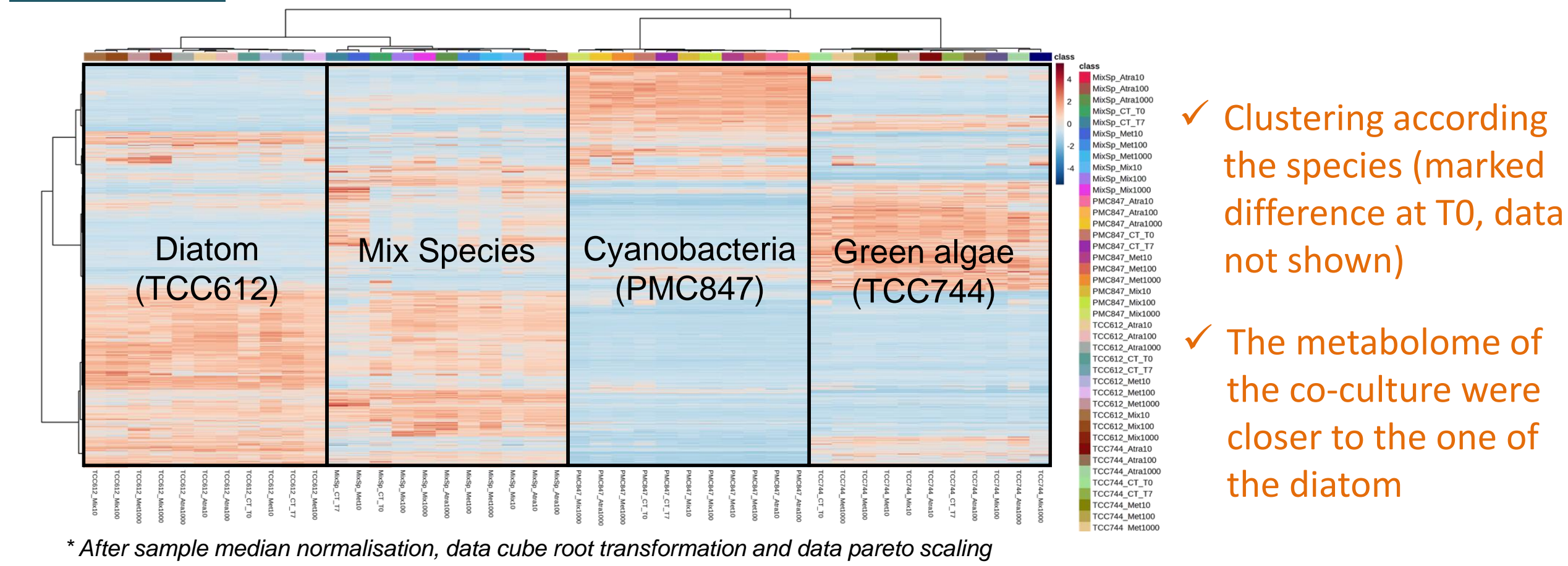
✓ Only T0 condition (i.e. Chemical landscape)

Data processing and chemometrics

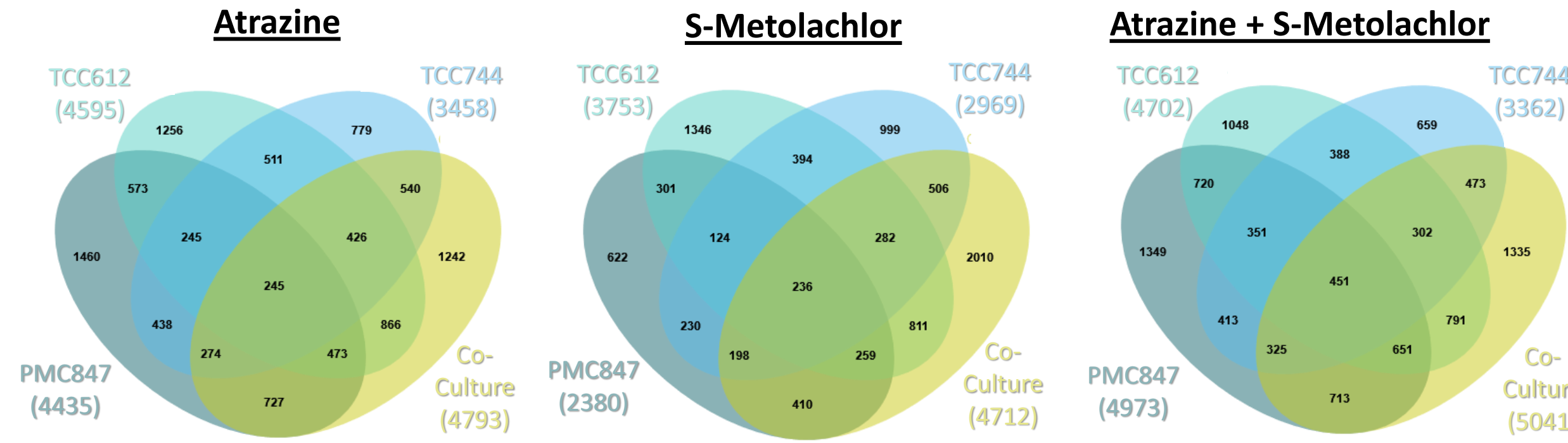


Results

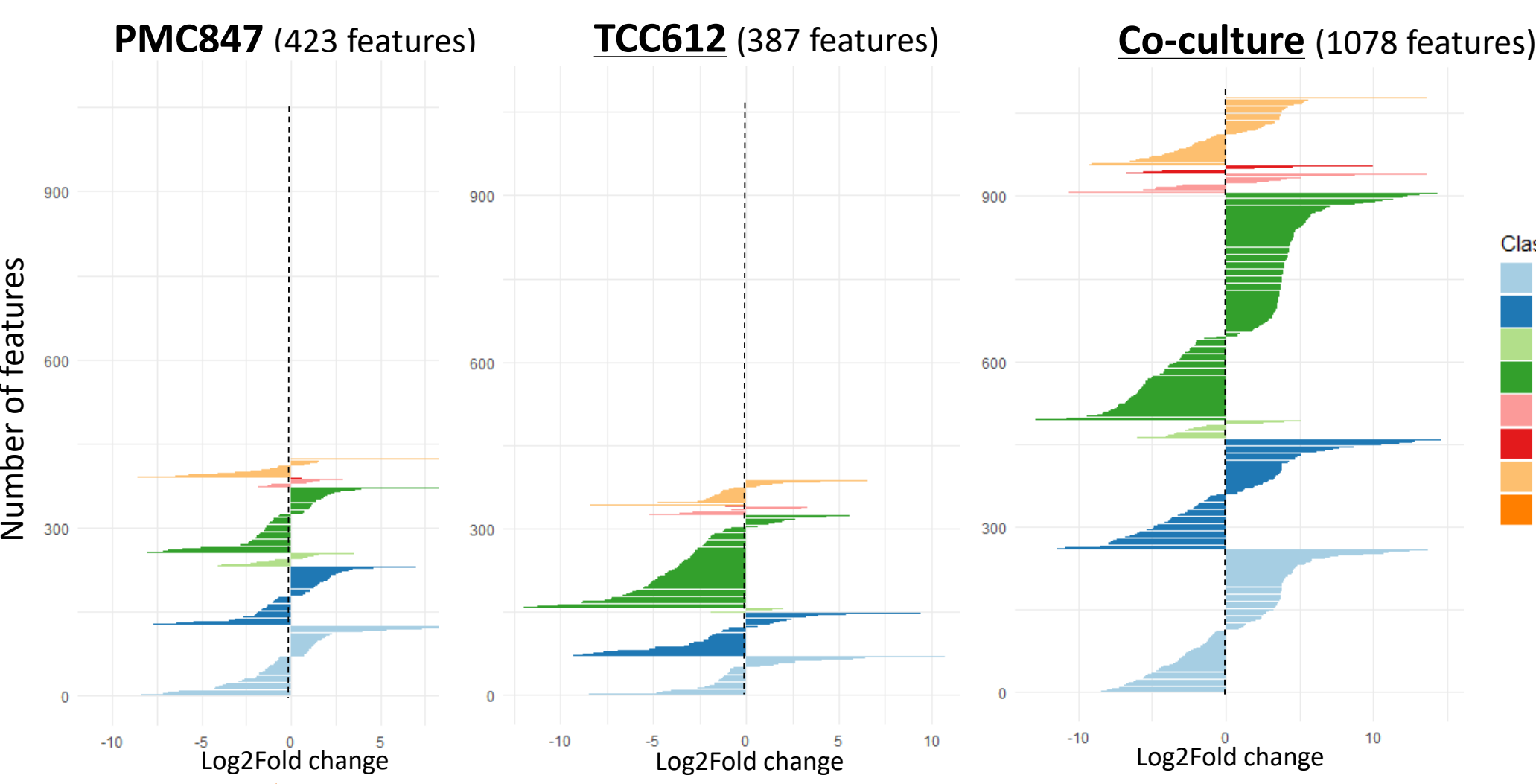
1. Hierarchical clustering* of all the metabolome fingerprints



2. Interspecies differences in the signals significantly** modulated

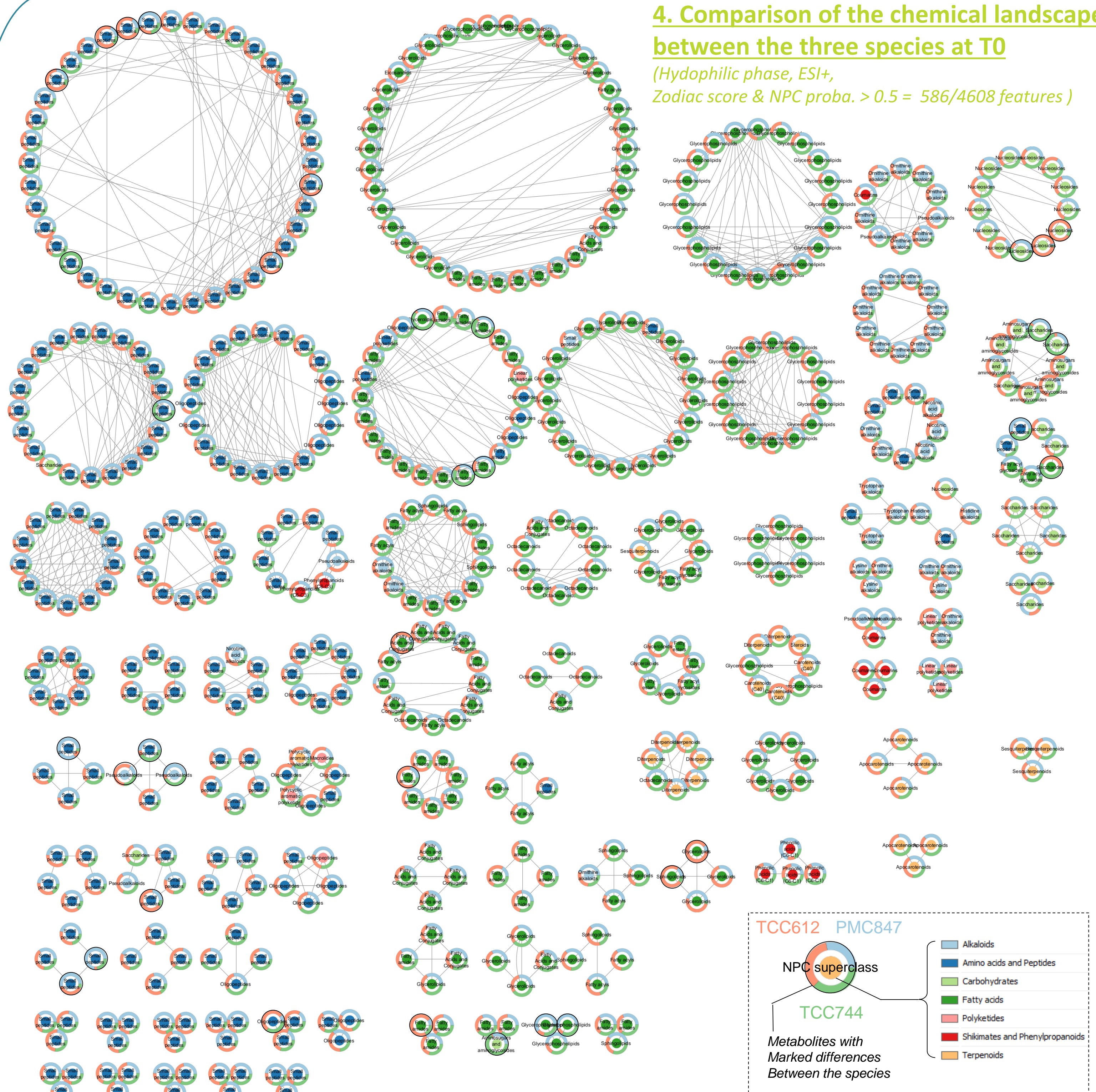


3. Interspecies differences in the responsive putative metabolites classes (Atrazine)



4. Comparison of the chemical landscapes between the three species at T0

(Hydrophilic phase, ESI+, Zodiac score & NPC proba. > 0.5 = 586/4608 features)



Major outcomes & Perspectives

- The clustering according the species highlighted marked differences in the metabolome of the species, even at T0 (data not shown)
- Overall, marked species differences in the response to the herbicides in terms of identity, number and fold change (down- vs up-regulation) of features or annotated metabolites (NPC_pathway)
- In accordance with species difference in the metabolome fingerprints at T0 (data not shown), the chemical landscape revealed abundance discrepancies between the three species, with some metabolites only present in two or even one species.

➢ Next steps :

- (1) To enlarge the chemical landscapes by integrating hydrophilic ESI- and lipophilic ESI+/- datasets
- (2) To compare the response of each species to the different herbicides to highlight potential specific toxicity pathways

References :

- [1] Leenhardt et al. (2022). Summary of the collective scientific expertise. INRAE; IFREMER. doi.org/10.17180/d7a0-f411
- [2] Morin S, Artigas J. Environ Toxicol Chem. 2023 Sep;42(9):1867-1888. doi: 10.1002/etc.5708
- [3] Chaumot, A., Garric, J., & Morin, S. (2010). Sciences Eaux & Territoires, (1), 26–29. https://doi.org/10.14758/SET-REVUE.2010.1.06
- [4] Sabater, S. (2017). Microbial Ecotoxicology. Springer, doi.org/10.1007/978-3-319-61795-4_14
- [5] Bedia et al. (2018) Environmental Research in Comprehensive Analytical Chemistry Volume 82, 2018, https://doi.org/10.1016/bs.coac.2018.07.006
- [6] Creusot N, Chaumet B, Eon M, Mazzella N, Moreira A, Morin S. Environ Sci Pollut Res Int. 2022 Apr;29(20):29332-29347. doi: 10.1007/s11356-021-17072-7.