

# PhD position on patterns and determinants of phylogenetic and functional diversity of skin microbiome in freshwater fish.

## **Keywords:**

Microbial communities, microbiota, high-throughput sequencing, skin, Teleostei, *Silurus glanis*, biological invasions

## **Host lab:**

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## **Funding:**

The selected student will apply to the doctoral school (SDU2E) competition to obtain the doctoral contract. See <https://www.adum.fr/as/ed/page.pl?site=sdu2e&page=candidater>

Beginning of the thesis: October 2019

## **Project description:**

### **Context**

Every plants and animals establish interactions with microorganisms that could be accidental or obligatory, temporary or persistent, and imply more or less strong molecular or cellular responses ranging from beneficial through neutral to detrimental (pathogenic). These host-microorganisms interactions are well studied in Humans, especially since the Human Microbiome Project was launched in 2007 (Turnbaugh et al. 2007) and the high-throughput sequencing methods have been democratized. Knowledge about bacterial community in microbiomes remains limited to gut microbiomes and to a restricted number of host Vertebrate models such as Human and mouse. Studies focusing on teleosts are scarce whereas they are a good model to study host-microorganisms interactions (Lescak & Milligan-Myhre 2017), with a high number of fish species existing worldwide that belong to very contrasting phylogenetic lineages.

Skin is a complex and dynamic ecosystem, colonized by many microorganisms (bacteria, archaea, virus, fungi, macroparasites) that represent a defence barrier against pathogens (Ángeles Esteban 2012). Bacterial communities are able to react quickly to local selective pressures, thanks to their high plasticity (low generation time, high mutational rate, high phenotypic plasticity, gene flow). Both influenced by environment and host (health, mobility, immunity) characteristics, skin microbiome is relevant to study mechanisms of bacterial community assembly and identify the genetic and environmental factors that control bacterial density, composition and diversity. In teleost, skin and the associated-mucus it constantly secretes shelter a microbiota that exerts essential functions for development and homeostasis of host immunity and recycling and elimination of catabolism products (Lowrey et al. 2015, Kelly & Salinas 2017).

Knowledge relative on teleost skin microbiota are still scarce, and mostly concern marine fish species. In freshwater ecosystems, fish skin microbiome has been poorly characterized (less than ten species mostly of economical interest and/or harvested such as carp species and salmonids. First investigations suggested that skin microbiota composition is host-specific in several marine fish species (Larsen et al. 2013, Chiarello et al. 2015). Chiarello et al. (2018) show skin microbiomes in 44 coral reef species are particularly correlated to host phylogeny and ecological traits, revealing a phyllosymbiosis pattern. At the intraspecific scale, gut health in Yellowtail kingfish (Legrand et al 2017) and genetic differentiation between Atlantic salmon populations (Webster et al. 2018) or Brook charr (Boutin et al. 2014) are likely to influence skin microbiome structure. Other factors like pH (Sylvain et al. 2016), salinity (Schmidt et al. 2015, Lokesh & Kiron 2016), captivity conditions (Tarnecki et al. 2016), seasonality (Larsen et al. 2015) may also induce intraspecific variability in fish skin microbiome. Beside deterministic factors, several work point out the contribution of unselective neutral processes in gut microbiome structuring (Jeraldo et al. 2012, Burns et al. 2016, Sieber et al. 2018). Ecological and evolutive forces that structure skin fish microbiome remain unclear. The description of skin microbiome

of phylogenetically and functionally contrasting fish species in natural communities appears necessary for drawing general patterns of skin microbiome variability among freshwater fishes.

Skin microbiota is generally more diversified than surrounding bacterioplankton, suggesting better resources and physical habitat on fish surface than in water column. The occurrence of strictly anaerobic bacterial phylotypes in skin mucus of whiting proves that mucus layer contains anaerobic niches (Smith et al. 2007). Ammonia-oxidizing bacteria were identified in gill mucus of the common carp and the zebra fish (Kessel et al. 2016). Studies on human microbiome demonstrate that metabolic pathways can be between individuals and body zones despite large differences in microbiome compositions (Turnbaugh et al. 2007, Lozupone et al. 2012). Similar observations were made on microbial communities associated to the algae *Ulva australis* (Burke et al. 2011). These first elements underline the interest to identify functional roles of microorganisms while functional diversity is largely neglected in researches on microbiome (Colston & Jackson 2016, Tropini et al. 2017).

### **Objectives and methods**

The objective is to describe and understand how bacterial communities are structuring on freshwater wild fish skin surface. We will answer to the following questions:

- (1) Which bacterial taxa and which functional genes compose skin microbiome?
- (2) Is the association between microorganisms and fish host-specific?
- (3) What do determine phylogenetic and functional variability of skin microbiome?

The PhD student will determine the roles of host (species, trophic behaviour, ontogeny, genotype) and environment (geographic place, bacterioplankton composition, biotic interactions, chemical environment) in explaining and assess host-associated microbial communities from sampling in situ and experiments in laboratory.

Bacterial diversity will be analysed using high-throughput sequencing (Illumina MiSeq) at several scales: fish community, population and individual. Several sampling campaigns are planned:

- First, mucus sampling will be performed on individuals from several fish species in different communities to estimate the contribution of the interspecific variability of host on microbiome structure. We hypothesize that microbiome density, composition and diversity significantly differ between host species and that microbiome composition similarity is correlated with phylogenetic and/or trophic position proximity.
- Second, mucus will be sampled on European catfish individuals in six populations from three French watersheds during three seasons (April-May, July-August, October-November) to identify how does microbiome phylogenetic and functional diversity change in time and space. We will hypothesize that changes in environmental conditions and biogeographic origin of hosts can modulate phylogenetic and functional structure of microbiomes. Functional structure of bacterial communities will be analysed from GeoChip microarray (Zhou et al. 2015). The last generation of GeoChip contains more than 167,000 distinct probes, covering near 400,000 coding sequences from around 1500 functional gene families involved in microbial carbon, nitrogen, sulphur, and phosphorus cycling, energy metabolism, metal homeostasis, or stress tolerance.
- Third, mucus will be sampled on European catfish individuals to understand the role of host intraspecific variability on microbiome. We will hypothesize that host life history traits, like trophic behaviour, activity, sex, ontogeny, health status) influence microbiome structure.

Bacterioplankton composition will be systematically analysed.

Finally, complementary experiments in microcosms will be performed to identify mechanisms of bacterial acquisition by manipulating water quality, temperature and presence of other fish individuals and/or species (horizontal transmission).

### **Profile and skills required:**

Strong knowledge in community ecology and functional ecology, skills in formulating hypotheses, abstraction ability. Advanced skills in molecular biology. Good level in multivariate statistics, skill in the R programming. Good level in English reading and writing.

### **Candidate selection:**

Candidates should send the following material by e-mail to frederic.santoul@univ-tlse3.fr and stephanie.bouletreau@univ-tlse3.fr :

- cover letter explaining your motivation
- CV

- results and ranking in Master degree
- contact information of two reference persons

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