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**Ecogenomics of Microbes**

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**TITLE: Evolution of vibrios in natural environment: lessons from a metagenomic study of skin mucus of the eel (*Anguilla anguilla*)**

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**Brief biography.** Miguel Carda is Doctor in Biotechnology by the University of Valencia (Spain) (2017) and, currently, post-doctoral researcher at the University of Valencia (Spain). His research has been focused on metagenomic, genomic and molecular biology. He has been formed at the laboratories of F. Rodríguez Valera (Alicante), C. Amaro (Valencia) and M. Waldor Harvard (USA). Carmen Amaro is Full Professor of Microbiology at the University of Valencia (Spain). She is the leader of a research group devoted to the study of aquatic pathogens and its impact on Aquaculture. She has mainly focused her research on *Vibrio vulnificus*, a zoonotic pathogen, able to cause death by sepsis in humans and different species of aquatic animals. She has directed more than 20 research projects, has published more than 100 international papers on this matter, all of them in journals of Q1, and has a global H index of 32. Her research received a national award from the Spanish Ministry of Agriculture and Fisheries in 2001.

The hypothesis underlying this work was that the fish's skin-mucosal-surface (SMS) could be an adequate niche for the emergence of accidental human pathogens that cause intestinal diseases. In order to test this, we compared the SMS-microbiome of eels (*Anguilla anguilla*) to that of the surrounding water (W-microbiome). The eel was selected because it is euryhaline, lacks macroscopic scales and is covered by a dense layer of mucus. We also compared SMS-microbiome from eels sampled in different ecosystems, four natural water-bodies (salinity from less than 0.1 to 1 %) and one artificial (an intensive eel farm that uses water of



0.3% salinity). In parallel, we isolated selected bacterial species and compared their genomes with those in databases.

*Gammaproteobacteria* were the most abundant in SMS-microbiome regardless of eel origin (wild or farm), although the composition in genera and species was variable. Remarkably, potentially pathogenic *Vibrio* monopolized wild-eel's SMS-microbiome from natural ecosystems, *V. anguillarum*/*V. vulnificus* and *V. cholerae*/*V. metoecus* being the most abundant ones in SMS from estuary and lake, respectively. Functionalities of the SMS-microbiome differed significantly from those of W-microbiome and allowed us to predict that successful colonizers contain specific genes for i) attachment (mainly by forming biofilms), ii) bacterial competence and communication, and iii) resistance to mucosal innate immunity, predators (amoeba) and heavy metals/drugs. In addition, we found several mobile genetic elements (mainly Integrative Conjugative Elements) as well as a series of evidences suggesting that bacteria exchange DNA in SMS. Finally, the genome of a *V. metoecus* strain isolated from SMS was compared with all published genomes of the same species. The SMS isolate presented characteristics intermediate between *V. metoecus* from water/extra-intestinal infections and *V. cholerae* O1 from cholera patients suggesting that HGT events between close *Vibrio* species could take place in this mucosal environment.

**In conclusion**, we have obtained metagenomic and genomic evidence in favor of the hypothesis on the role of fish mucosal surfaces acting as driving forces for selecting the best adapted bacteria to colonize and persist in mucosal surfaces e.g. the human intestine.