



TITLE: Pangenome Evolution in the Marine Bacterium *Alteromonas*

NAME: Mario López-Pérez

E-mail: mario.lopezp@umh.es

Affiliation: Universidad Miguel Hernández (Spain)

We have examined a collection of the free-living marine bacterium *Alteromonas* genomes with cores diverging in average nucleotide identities ranging from 99.98% to 73.35%, i.e., from microbes that can be considered members of a natural clone (like in a clinical epidemiological outbreak) to borderline genus level. The genomes were largely syntenic allowing a precise delimitation of the core and flexible regions in each. The core was 1.4 Mb (ca. 30% of the typical strain genome size). Recombination rates along the core were high among strains belonging to the same species (37.7–83.7% of all nucleotide polymorphisms) but they decreased sharply between species (18.9–5.1%). Regarding the flexible genome, its main expansion occurred within the boundaries of the species, i.e., strains of the same species already have a large and diverse flexible genome. Flexible regions occupy mostly fixed genomic locations. Four large genomic islands are involved in the synthesis of strain-specific glycosidic receptors that we have called glycotypes. These genomic regions are exchanged by homologous recombination within and between species and there is evidence for their import from distant taxonomic units (other genera within the family). In addition, several hotspots for integration of gene cassettes by illegitimate recombination are distributed throughout the genome. They code for features that give each clone specific properties to interact with their ecological niche and must flow fast throughout the whole genus as they are found, with nearly identical sequences, in different species. Models for the generation of this genomic diversity involving phage predation are discussed.