

Figure 1: Phylogenetic composition of the natural bacterial communities from Lake Zurich after 120 hours of exposure to predation by a protistan predator. Community A represents the natural community, while community B was exposed at time 0 to an invasion by a grazing-resistant strain. The presence of the invader seems to promote the development of a different community, with a significant increment of all the main groups and a consistent reduction of the betas. Observing this group more in detail it is possible to notice that the competition with the grazing-resistant strain is highly affecting the Chromatiales group, reducing in abundance by ten times, while the Aeromonadales seems to keep their dominance independently by the presence of the invader, as much as the Burkholderiales.

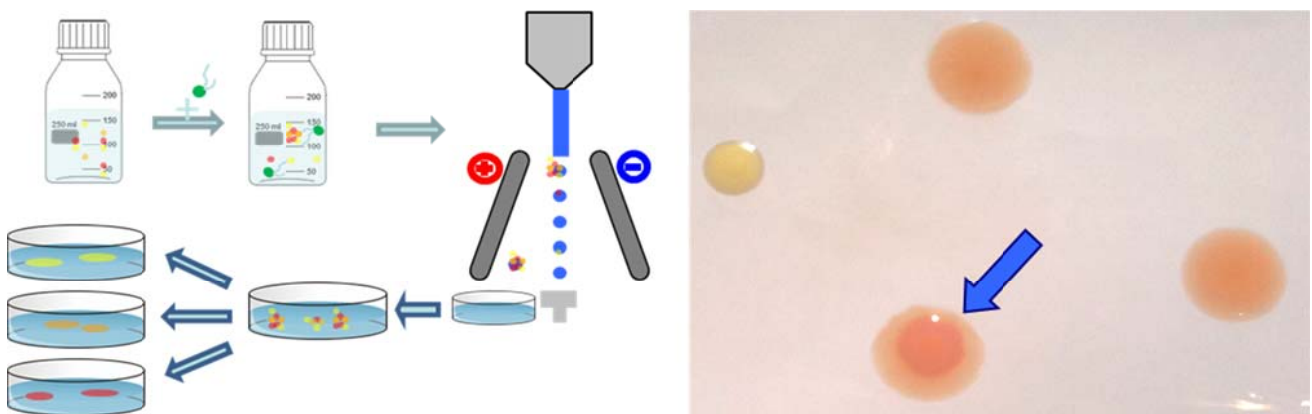
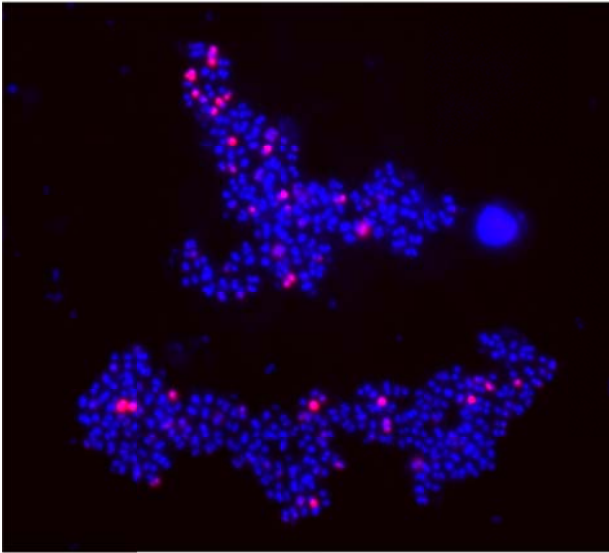


Figure 2: Identification, sorting and isolation of co-aggregating bacterial strains: water samples from the experimental treatments exposed to high grazing pressure were collected and, without other manipulations loaded in the flow cytometer. From the cytometric signature of the largest aggregates single events (aggregates) were collected and sorted to agar plates. The blue arrow in the photo indicates a co-aggregate where the two participating strains were able to grow also on solid substrate.



**Large aggregates ( diameter > 10  $\mu\text{m}$  ), under predation**

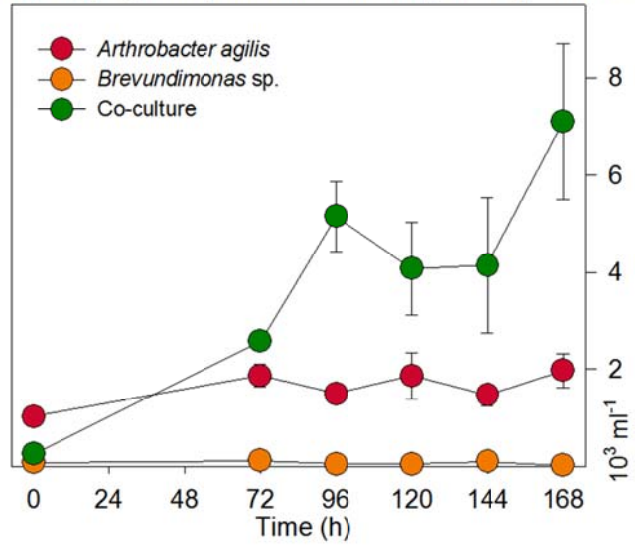


Figure 3: Co-aggregates composed of *Brevundimonas* (in violet) and *Arthrobacter* (in pink, epifluorescence microscopy). The number of large aggregates (essentially co-aggregates) in the co-culture is 4 times higher than in the pure culture of *Arthrobacter*, while *Brevundimonas* in pure cultures is not able to prevent predation by aggregation at all.