



Contribution ID : 30

Type : **Oral**

New microbial players in oxygen-minimum-zone biogeochemistry

Tuesday, 4 September 2018 10:45 (35)

Key microbial players from oxygen minimum zones (OMZs) have been identified, but the majority remains unrecognized or uncharacterized. The application of single-cell genomics -in combination with microbial-community gene content, transcription, and process rate measurements- offers the possibility to gain some insight into the distribution, metabolic potential, and activity of previously uncharacterized bacterial and archaeal groups. Such approach is revealing new potentially important players for OMZ biogeochemistry, as well as the presence of some apparently overlooked pathways. Quantifying the importance of such microbial processes at the local and global scale and putting them into a general ecological framework remain a challenge.

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Session Classification : 04 Microbial Communities and their Impact on Biogeochemical Cycles in Oxygen Minimum Zones