



L'Animation Scientifique



> JEUDI 18 NOVEMBRE 2021, 13h45 \ 14h30

Giant genomes uncover ecological speciation in the deep ocean

The deep ocean is the largest biome on Earth and yet it is among the least studied environments of our planet. Hence, the genomic mechanisms underlying the formation of species in the deep sea remain virtually unknown. Here we present the assembly of one of the largest sequenced invertebrate genomes. We used 10x chromium linked-reads, ONT long reads and transcriptomic reads to generate a draft genome assembly. The abyssal brittle star *Ophiosphalma armigerum* (Echinodermata: Ophiuroidea) genome is 8 Gb large and contains about 52% repeats. We further sequenced 123 *O. armigerum* individuals spanning the whole species geographic (from the North Atlantic Ocean to South Australia) and bathymetric range (from 2200 m to 4800 m depth). We found significant bathymetric structuring among bathyal (~2500 m) and abyssal (~4000 m) populations, suggesting ecological speciation along a depth gradient in *O. armigerum*. We then describe genomic islands of speciation and candidate genes for deep-sea adaptation. When focusing on the individuals from abyssal depths, we uncovered high levels of gene flow among localities around Australia. Remarkably, trans-oceanic connectivity was detected as individuals from the North Atlantic Ocean and individuals from South Australia were connected by significant levels of gene flow at abyssal depths. This study provides unprecedented marine invertebrate genomic resources and sheds light on speciation and connectivity mechanisms in the largest biome of the planet.

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Séminaire accessible sur ZOOM :

<https://umontpellier-fr.zoom.us/j/94437658185>
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