HORIZON 2020

The molecular drivers of deep-sea adaptation in brittle stars

Rapports

Informations projet

DEEPADAPT

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Periodic Reporting for period 2 - DEEPADAPT (The molecular drivers of deep-sea adaptation in brittle stars)

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Résumé du contexte et des objectifs généraux du projet

The deep ocean covers about two-thirds of the world's ocean floors; yet, it is one of the least known environments of the planet. Despite its remoteness, the deep ocean provides critical ecosystem services (e.g. carbon sequestration; nutrient regeneration) and a wealth of resources of interest for humans (e.g. anti-cancer molecules; deep-sea fisheries; mining for rare metals). Given its extreme environmental conditions (crushing hydrostatic pressure, freezing temperature, absence of sunlight), life in the deep sea requires several specific adaptations. Surprisingly, little is known about the molecular mechanisms underlying adaptation to such environments. Which and how many genes are involved in adaptation? What is the extent of convergent evolution across distantly related taxa? Answering these questions is important for society because deciphering mechanisms of stress-driven adaptation will provide insights on the resilience of deep marine biodiversity to the ongoing environmental changes.

The objectives of this project are:

i) Decipher the molecular mechanisms of adaptation to the deep sea in brittle stars

ii) Test the extent of convergent evolution among distantly related families.

iii) Generate a reference genome of abyssal brittle stars

I found that molecular functions related to the production of proteins are essential components of deep-sea adaptation.

Furthermore, I uncovered strong levels of convergent evolution, as the same genes and functions were repeatedly targeted by natural selection in species that shared a common ancestor several millions years ago.

I also uncovered that due to the particular life-history traits of deep-sea species (e.g. high longevity), many of them tend to have large genomes essentially composed of repeated regions. I further showed that the evolution of genome size is not an adaptive process in brittle stars.

Finally, I generated a reference genome for the abyssal species Ophiosphalma armigerum, and uncovered cryptic speciation and hybridization in the deep ocean.

These results bring a better understanding of the molecular mechanisms underlying the formation of species in the deep sea, and shed light on the molecular mechanisms allowing life in the deep ocean.

Travail effectué depuis le début du projet jusqu’à la fin de la période considérée dans le rapport et principaux résultats atteints jusqu’à présent

Brittle stars (Ophiuroidea) are a useful group of marine invertebrates to fulfill these objectives, as they are abundant in the deep-sea and they colonized this environment several times independently, thus highlighting their strong adaptive abilities.

I investigated deep-sea adaptation using a comparative genomics approach and state-of-the-art analytic tools in three complementary work packages (WP):

- Work Package 1: The aim of WP1 was to test genomic adaptive evolution in the deep sea among distantly-related families. I examined the molecular evolution of ~400 genes in ~700 brittle stars species. I found that protein biogenesis (including protein folding and translation) is a key metabolic adaptation to deep-sea conditions. The results of this study have been published in the open access journal Genome Biology and Evolution.
- Work Package 2: The aim of WP2 was to uncover the drivers of genome size evolution in the deep ocean. I performed whole genome sequencing of ~80 species representative of all brittle stars and I examined the environmental, biological and genomic factors impacting the evolution of genome size. I found that the specific life-history traits of deep-sea species (i.e. high longevity, low metabolism) lead to generally increased genome sizes for these species. Furthermore, I uncovered that genome size is

mediated by changes in repeat content, especially transposable elements, and not by changes in ploidy or whole-genome duplications. I completed data analyses of this WP, and will submit the corresponding manuscript to the diamond open-access journal 'Peer Community Journal' by the end of April 2022.

- Work Package 3: The aim of WP3 was to examine the genomic architecture of speciation along depth. I used a population genomics approach by generating a reference genome for the deep-sea species Ophiosphalma armigerum. Furthermore, I performed whole genome sequencing of 120 Ophiosphalma individuals from different localities worldwide and depths (~2500m and ~4000m) to uncover the genetic architecture of local adaptation. I uncovered an example of recent cryptic speciation along depth, as morphologically-similar populations from the same locality at different depths were showing convincing signatures of reproductive isolation. Furthermore, I uncovered that closely-related species were showing signatures of hybridization, suggesting that mechanisms of reproductive isolation are postzygotic in these species. There were unforseen delays in this WP, so I am currently running further analyses and I am planning to submit the corresponding manuscript to the open-access journal 'Science Advances' by the end of September 2022.
- DIssemination: To fulfill the dissemination and exploitation objectives of DeepAdapt, i.e. promoting my research and fostering interactions among deep-sea scientists, I took part in the organization of the 16th Deep-Sea Biology Symposium, a hyrbid conference with onsite and online attendance possible. This was not only an excellent opportunity to present my research to the deep-sea community, but also a strategic way to promote myself and develop my scientific network by interacting closely with international deep-sea experts. Given the current generalisation of the hybrid conference format, I led the publication of a manuscript about the challenges and opportunities of hybrid meetings. I am the senior author and sole corresponding author of this paper. This manuscript is under review in the open-access journal 'Frontiers in Marine Sciences', and a preprint is available on the BioRxiv preprint server: https://doi.org/10.1101/2022.03.18.484941

In addition to open-access publications, I shared the results of my research by participating in 7 international conferences, I was invited to speak at 5 seminars, I participated in 5 outreach events and I wrote 3 blogposts for the general public, ensuring that the results of this project are widely disseminated in the scientific community and beyond.

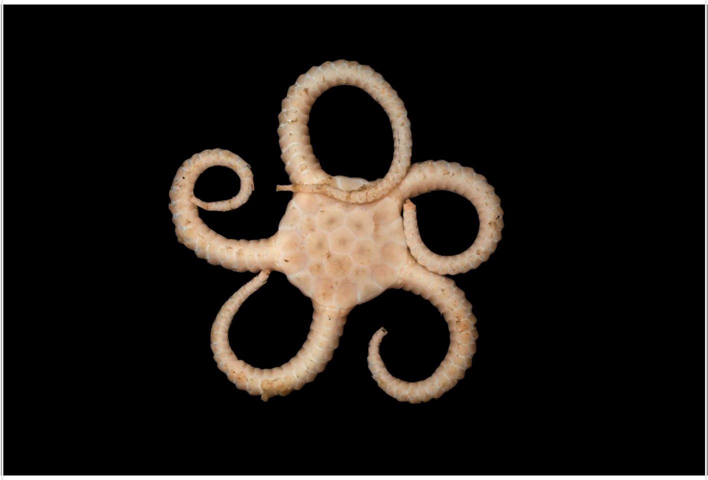
Progrès au-delà de l’état des connaissances et impact potentiel prévu (y compris l’impact socio-économique et les conséquences sociétales plus larges du projet jusqu’à présent)

This project advances the understanding of deep-sea biology beyond the state of the art, because it has generated unprecedented genomic resources for deep-sea animals and brought forward the understanding of how species adapt to this extreme environment.

I showed that natural selection can convergently act on the very same genes and functions, despite millions of years of divergence between different species, highlighting the strong and constant selective pressure deep-sea species experience.

I also uncovered that the evolution of genome size is non-adaptive in deep-sea species, which explains why most of them have very large genomes. Finally, I uncovered examples of recent cryptic speciation and hybridization in the deep ocean, which further the understanding of how species form

in the largest biome of the planet.
I expect these studies to have a strong impact, not only in evolutionary biology, but also for the conservation of deep-sea biodiversity. Indeed, the results provide insights on the resilience of deep marine biodiversity to present and future environmental changes such as climate change.



DEEPADAPT: the abyssal brittle star Amphiophiura bullata

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