Training proposal

NAME: BAPTESTE

FIRSTNAME : ERIC

ADRESS : Equipe AIRE, Sorbonne Université, 7, Quai Saint Bernard, UMR ISYEB, Bat A pièce 427, 75005 Paris

HDR : Yes

DOCTORAL SCHOOL AFFILIATION: CDV

DEPARTMENT: UMR7205 Institut de Systématique, Évolution, Biodiversité (ISYEB)

Tel: 01 44 27 21 64 Fax: NA Courriel:eric.bapteste@mnhn.fr

Quick summary of the team studies:

AIRE team seeks to generalize evolutionary explanations beyond their traditional approaches and objects of studies. More precisely, we try to expand the evolutionary theories i) by expanding its scope to additional units of selection and new, still unrecognized taxonomic lineages and ii) by expanding their modelling towards more general models, able to account for chimerism and interactions between biological entities, from molecules to ecosystems. Our work is largely interdisciplinary, at the interface of evolutionary biology, microbiology, network sciences, bioinformatics, ecology and philosophy of biology. The research project below concerns one of the topics investigated in the lab: the evolution of ageing across the web of life, to understand when, how and why organisms, their cells and when relevant their tissues age by developing original generic comparative approaches applied to longitudinal series of gene co-expression networks and by generalizing the explanatory scope of the disposable soma theory from animals towards the entire microbial world (prokaryotes and protists).

TEAM MEMBERS, EXPERT IN BIOINFORMATICS:

Philippe LOPEZ, Systems Biology Prof, co-PI of the AIRE team

Eduardo COREL, Assistant Prof in bioinformatics

Jérôme TEULIERE, postdoctoral fellow, developping methods for network comparison

Duncan SUSSFELD, PhD in bioinformatics

KEYWORDS :

Transcriptomics, Bioinformatics, Ageing, Evolutionary Biology

TITLE OF THE PROJECT: **Introducing the first evidence ever of cellular ageing in archaea by transcriptomic analyses**

Brief description:

INTRODUCTION:

Ageing in bacteria and in protists, which were long considered as non-senescent, is very poorly known. Even worse, this phenomenon has never been observed in Archaea. In collaboration with M. Krupovic (Institut Pasteur), we synchronized the development of archaeal cells and performed transcriptomics on samples from different stages of their cellular cycle. These original data will allow, through bioinformatic analyses mastered by our lab to test whether transcription and gene co-expression of these clones gets increasingly dysregulated with time, unveiling a form of ageing in Archaea for the first time.

GOALS:

Between two cell divisions, archaeal clones, cultured in the same lab conditions, with synchronized cell cycles that would not age should follow highly similar genetic programs and express the same genes at the same stages of their cell cycle. Consequently, sub-populations of non-senescent archaea sampled at the same time, should present a constant variability in their gene expression and co-expression. By contrast, if an increasing proportion of random damages with time would affect archaeal cells, the variability in their gene expression and co-expression should increase with time, demonstrating a form of increased dysregulation with time, hence of ageing. Our goal is to test this.

DATA DESCRIPTION:

We will use transcriptomes from cells and population of synchronized archaeal clones.

METHODS:

The M2 trainee will work as a bio-informatician to achieve the above-mentioned analyses, under the co-supervision of Bapteste and Lopez. She or he will gain expertise in comparative transcriptomics and in gene co-expression network analyses. Moreover, she or he will also work as a researcher in evolutionary microbiology when interpreting the results of her/his analyses.

In more details, the M2 trainee will clean transcriptomic data with dedicated tools, using multivariate statistics, and then group these higher quality transcriptomes by chronological age-class, i.e. based on the sampling of these data at precise stages of the cell cycle. The M2 trainee will analyse the differential gene expression of clones as a function of their chronological age using DeSEq2, and the differential gene co-expression between clones from different age classes using gene co-expression networks methods mastered in the Bapteste/Lopez lab. She or he will quantify the variability in i) gene expression and ii) gene co-expression between archaeal clones as a function their chronological age, testing the null hypothesis of an absence of increase in variability with time.

Thus, she or he will enhance her/his expertise in: transcriptomic analyses, multivariate analyses, differential gene expression analyses, co-expression network analyses, evolution of ageing, microbial evolution and scientific writing.

REFERENCES

Bernard G, Teulière J, Lopez P, Corel E, Lapointe FJ, Bapteste E. Aging at Evolutionary Crossroads: Longitudinal Gene Co-expression Network Analyses of Proximal and Ultimate Causes of Aging in Bats. Mol Biol Evol. 2022 Jan 7;39(1):msab302. doi: 10.1093/molbev/msab302. PMID: 34662394

Teulière J, Bhattacharya D, Bapteste E. Ancestral germen/soma distinction in microbes: Expanding the disposable soma theory of aging to all unicellular lineages. Ageing Res Rev. 2020 Jul;60:101064. doi: 10.1016/j.arr.2020.101064. Epub 2020 Apr 5. PMID: 32268207

Liu J, Cvirkaite-Krupovic V, Baquero DP, Yang Y, Zhang Q, Shen Y, Krupovic M. Virus-induced cell gigantism and asymmetric cell division in archaea. Proc Natl Acad Sci U S A. 2021 Apr 13;118(15):e2022578118. doi: 10.1073/pnas.2022578118. PMID: 33782110

Lindner AB, Madden R, Demarez A, Stewart EJ, Taddei F. Asymmetric segregation of protein aggregates is associated with cellular aging and rejuvenation. Proc Natl Acad Sci U S A. 2008 Feb 26;105(8):3076-81. doi: 10.1073/pnas.0708931105. Epub 2008 Feb 19. PMID: 18287048

RELATED PUBLICATIONS FROM THE TEAM:

Watson AK, Lopez P, Bapteste E. Hundreds of Out-of-Frame Remodeled Gene Families in the Escherichia coli Pangenome. Mol Biol Evol. 2022 Jan 7;39(1):msab329. doi: 10.1093/molbev/msab329. PMID: 34792602

Bernard G, Teulière J, Lopez P, Corel E, Lapointe FJ, Bapteste E. Aging at Evolutionary Crossroads: Longitudinal Gene Co-expression Network Analyses of Proximal and Ultimate Causes of Aging in Bats. Mol Biol Evol. 2022 Jan 7;39(1):msab302. doi: 10.1093/molbev/msab302. PMID: 34662394

Teulière J, Bernard C, Bapteste E. Interspecific interactions that affect ageing: Age-distorters manipulate host ageing to their own evolutionary benefits. Ageing Res Rev. 2021 Sep;70:101375. doi: 10.1016/j.arr.2021.101375. Epub 2021 May 31. PMID: 34082078

Teulière J, Bhattacharya D, Bapteste E. Ancestral germen/soma distinction in microbes: Expanding the disposable soma theory of aging to all unicellular lineages. Ageing Res Rev. 2020 Jul;60:101064. doi: 10.1016/j.arr.2020.101064. Epub 2020 Apr 5. PMID: 32268207

Watson AK, Lannes R, Pathmanathan JS, Méheust R, Karkar S, Colson P, Corel E, Lopez P, Bapteste E. The Methodology Behind Network Thinking: Graphs to Analyze Microbial Complexity and Evolution. Methods Mol Biol. 2019;1910:271-308. doi: 10.1007/978-1-4939-9074-0_9. PMID: 31278668