Titre Projet. A Methodological platform in environmental genomics for the Spatial Analysis of associations between Genes, Environment and Phenotypes (SAGEP)

Acronyme: SAGEP

Axe ECCOREV 2: vulnérabilités des écosystèmes terrestres et aquatiques: Gestion de la biodiversité: Organisation et évolution de la biodiversité.

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Scientific context

This project is related to the study of the adaptive genetic diversity and how it can change in response to global change ("évolution de la biodiversité"). More specifically, one of the main focus of this project is to investigate species ability to adapt to rapid environmental changes (e.g. climate change). This first requires being able to detect signature of natural selection in heterogeneous of fluctuating environments.

Related open key questions are: whether adaptation occurs through the rapid fixation of new mutations or draws from standing genetic variation? How many genes are involved? What is the impact of gene flow on the evolution of local and temporal adaptation?
All those questions are related to the study of biodiversity organisation ("Organisation de la biodiversité"). We will focus both on terrestrial and marine ecosystems (see below chosen species)

Objectives
Recently, the identification of signatures of natural selection in genomic scans has become an area of intense research, stimulated by the increasing ease with which genetic markers can be discovered and genotyped or sequenced. Loci identified as subject to selection may be functionally important, and hence candidates for involvement in disease (medicine) or other environmental adaptation (agronomy, conservation). However, efficient spatial methods for the detection of loci under selection are lacking. Whereas various cases of molecular adaptation have been described in model species (e.g. Drosophila), such knowledge remains to be developed for non-model organisms. In this project we propose to fill those gaps. The major objectives of the research proposed here are to improve our knowledge of the statistical methods

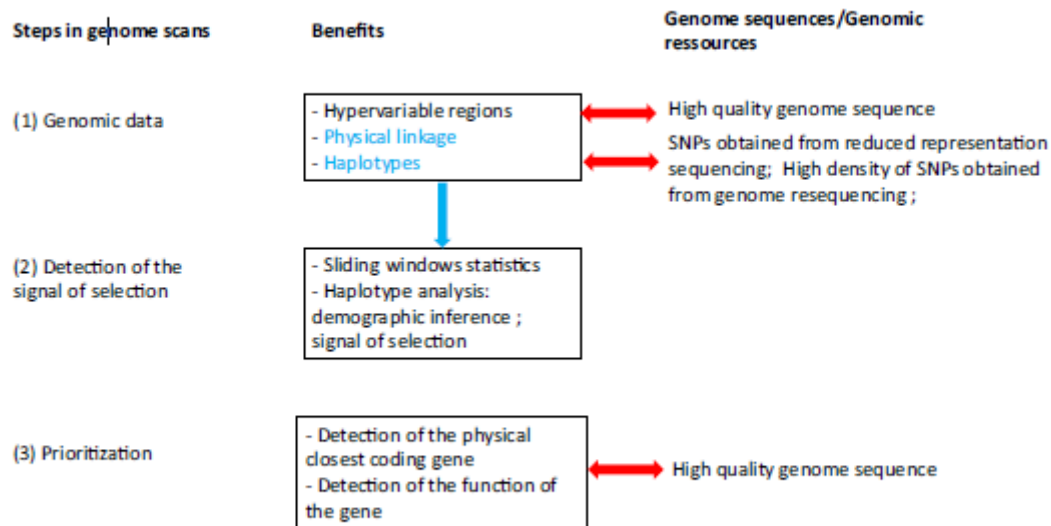for detecting the signal of selection and how non-model species may adapt to environmental changes.

Fig. 1 Schematic representation of the benefits of using additional genomic resources (mainly reference genomes) in the different steps of genome scans.

Publications:

Manel S, Perrier C, Pratlong M, Abi-Rached, L. Paganini, J. Pontarotti, P. Aurelle, D. (2016) Genomic resources and their influence on the detection of the signal of positive selection in genome scans. *Molecular Ecology* **25**, 170-184.

Lien avec d'autres projets

Les échanges au cours de cette réunion sont également en lien et alimentent d'autres projets des membres de ECCOREV (D. Aurelle et P. Pontarroti: étude de l'adaptation chez le corail rouge initiée par un financement ECCOREV et poursuivi dans le cadre de l'ANR ADACNI et de la thèse de Marine Pratlong financée par le labex OT-Med; Alex Baumel et S. Manel, projet ECOSUD). S. Manel et Didier Aurelle prévoient de soumettre un projet à l'ANR (génomique comparative).