Population epigenetics

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Résumé

It is becoming increasingly evident that epigenetic processes influence phenotype and interact with genetic variation. Indeed, laboratory studies on plants and animals have shed light on some of the general features of epigenetics, with important evolutionary implications. However, studies aiming to determine the relative contributions of genetic and epigenetic variation to phenotypic variation in natural populations can provide important information relative to this debate, particularly if performed in wild populations encountering naturally different levels of environmental complexity, with different genetic structures and dynamics, and natural ecological processes. Here, we will share our study on population epigenetics in natural population of forest trees in relation to their local adaptation. First, we will present a strategy for population epigenomics. WGBS quantifies genome-wide DNA methylation but has several inconveniences rendering it less suitable for population-scale epigenetic studies. The high cost of deep sequencing and the large amounts of data generated prompted us to seek an alternative approach. Restricting studies to parts of the genome would be a satisfactory alternative had there not been a major limitation: the need to select upstream targets corresponding to differentially methylated regions (DMRs) as targets. Given the need to study large numbers of samples, we propose a strategy for investigating DNA methylation variation in natural populations, considering the structural complexity of the genomes with their size and their content in unique as coding regions versus repeated regions as transposable elements. Second, we will present the epigenetic variability of natural tree populations in comparison to their genetic variability. Finally, our last objective is to improve the accuracy of prediction models of complex traits by integrating epigenetic data layers into existing models, and to test new statistical prediction models combining multiple layers.

Mots-Clés: DNA methylation, epigenetics, tree, adaptation

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