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SÉMINAIRE

Targeted RAD sequencing across the genomes of insect populations and broods

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The reduction of DNA sequencing costs over recent years has enabled whole genome sequencing to become relatively affordable for most organisms. However, sequencing many individuals, from multiple populations can still be financially limiting and require extensive computational power. Since its development in 2008, restriction-site associated DNA (RAD) sequencing has offered an effective method for sampling non-random, interspersed sequences across a genome. In brief, the approach involves digesting genomic DNA with a restriction enzyme, ligating adapters to these sites and sequencing the fragments with illumina technology. Publications based on the RAD method have addressed many biological questions ranging from population genetics to linkage mapping and phylogeography, using 10's or 100's of individuals from broods or wild collections. Here I will provide an overview of the RAD method, and highlight various approaches to analyze RAD datasets. Data generated by myself and colleagues, from tropical butterflies, pest moths and polymorphic ladybirds, will be presented to demonstrate our approach for assembling genetic linkage maps (with and without a reference genome), bulked segregant analysis, genome wide phylogenies and comparative genomics. Although there are both benefits and drawbacks to RAD sequencing, it is a universal genetic approach that could be considered for many organisms.