XVII INTERNATIONAL SYMPOSIUM ON
SCHISTOSOMIASIS
PERSPECTIVES ON SCHISTOSOMIASIS ELIMINATION
NOVEMBER 10-13TH 2024 | SALVADOR - BAHIA

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TITLE

BIOMPHALARIA GLABRATA, A NEW MODEL TO INVESTIGATE THE EVOLUTION OF MEIOTIC RECOMBINATION

AUTHORS

Rudler, A.[1]; Murphy, L.[1]; Allienne, J.F.[1]; Rognon, A.[1]; Dellong, A.[1]; Grunau, C.[1]; Cosseau, C.[1]; Clement, J.A.J.*[1]

AFFILIATIONS

[1] IHPE, Univ Montpellier, CNRS, IFREMER, Univ Perpignan Via Domitia, Perpignan, France

ABSTRACT

Meiotic recombination is a conserved mechanism that plays an important role in genetic diversity and genome evolution. By shuffling parental alleles to produce novel haplotype, recombination increases the efficiency of selection at linked loci and thus facilitates population adaptation. During meiosis, DNA double-strand breaks initiates homologous recombination at specific loci called hotspots. In many mammals, their localization corresponds to specific DNA sequences bound by the zinc finger (ZnF) array of PRDM9. These hotspots are also marked with specific epigenetic modifications (H3K4me3 and H3K36me3) that are catalyzed by PRDM9 itself. A remarkable property of PRDM9 is the high diversity and fast evolution of its ZnF domain. The consequence is the fast evolution of recombination map for species having a PRDM9 for hotspot localisation and thus a potentially higher evolvability.
PRDM9 appears in the last common ancestor of metazoans but its partial or complete loss have been surprisingly reported in many taxa. Species lacking a full-length PRDM9 have evolutionary stable hotspots that are located near promoter-like regions, that are evicted by PRDM9. The involvement of PRDM9 in meiotic recombination has not been yet explored outside vertebrate species, one reason being that invertebrate model species (drosophila, nematode) have no PRDM9. Here, we propose to fill these gaps by investigating PRDM9 function in meiotic recombination in closely-related species of freshwater snails, including Biomphalaria glabrata and Biomphalaria pfeifferi and Bulinus truncatus, for which we recently identified full-length PRDM9 conservation by exploring their recently published genome assemblies.
This project will address the following questions: Where are meiotic hotspots located along the genome of freshwater snails? Is PRDM9 essential for meiotic progress and fertility? Can we find evidence of PRDM9 function in the localisation of hotspots?
We will use complementary approaches such as population genomics, genotyping of PRDM9 zinc finger array, molecular mapping of histone modifications and DNA breaks in snail gonads (ChIPseq approaches), histology and genetic manipulation of snail.
Preliminary results about PRDM9 ZnF diversity showed hypervariable amino-acid at positions contacting DNA and diversity in number and order of ZnF between individuals and populations. This indicates a probable involvement of PRDM9 in specifying recombination hotspot. The epigenetic profiling is currently being optimized and will be applied to our snails lines already selected for different Prdm9 alleles.
This project should help to identify the molecular bases behind the adaptation of freshwater snails to their biotic and abiotic environments.

KEYWORDS

Meiosis, Freshwater Snail, Recombination, Epigenetic Profile, Gonads

FINANCIAL SUPPORT

ANR