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Unravelling the genetic mechanisms of extreme heterochiasmy: Sexual dimorphism in frog meiosis

OUR LAB

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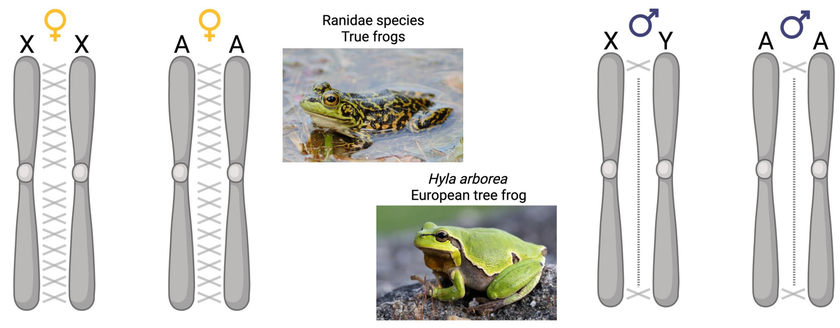
Scientific Background

Many frogs have extreme heterochiasmy and homomorphic sex chromosomes.

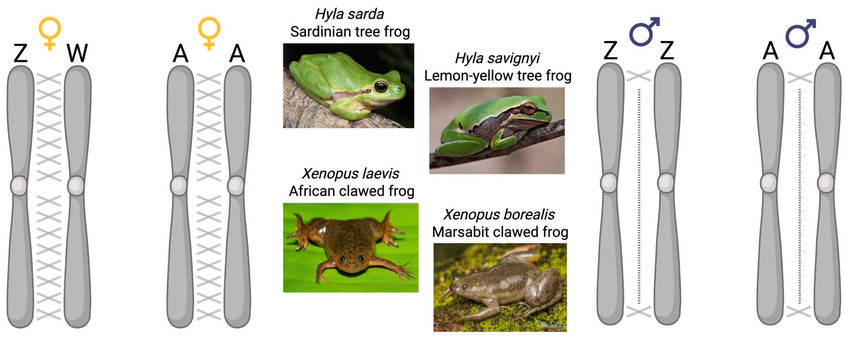
Extreme heterochiasmy refers to drastic sex-specific differences in meiotic recombination rate and distribution.

Homomorphic sex chromosomes exhibit few differences in size and gene content, making them cytologically indistinguishable.

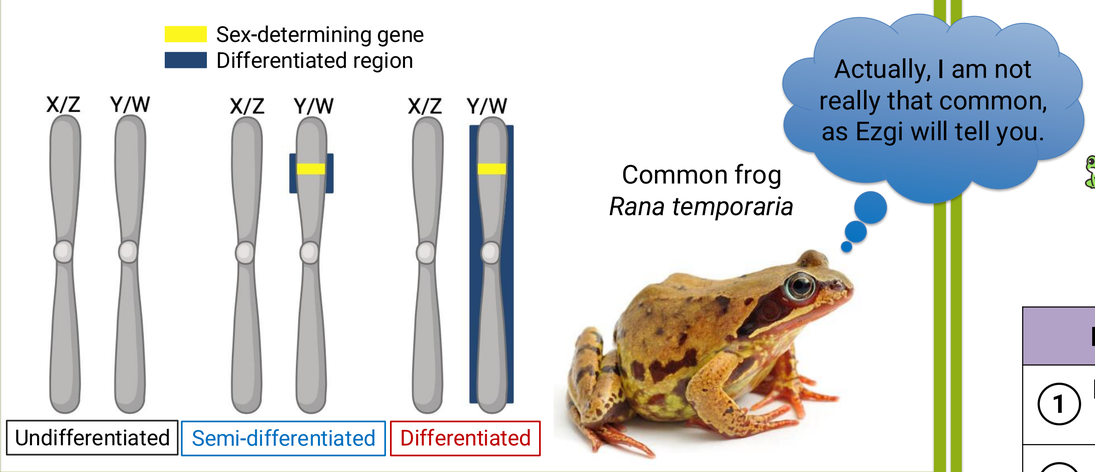
Male-specific telomere-restricted recombination in **male heterogametic** species



Male-specific telomere-restricted recombination in **female heterogametic** species

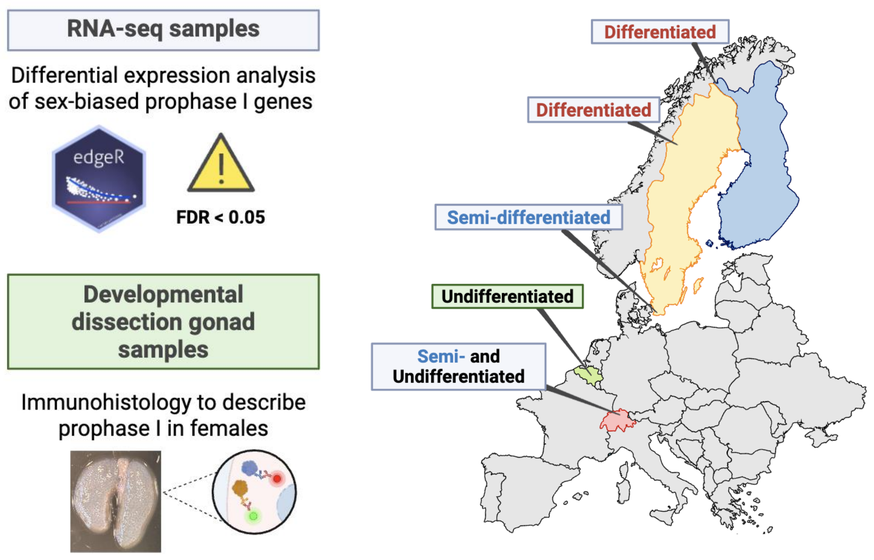


In true frogs, homomorphic sex chromosomes harbor **Y-specific haplotypes** of variable length induced by extreme heterochiasmy, rather than sexually antagonistic selection, therefore challenging the canonical model of sex chromosome evolution.

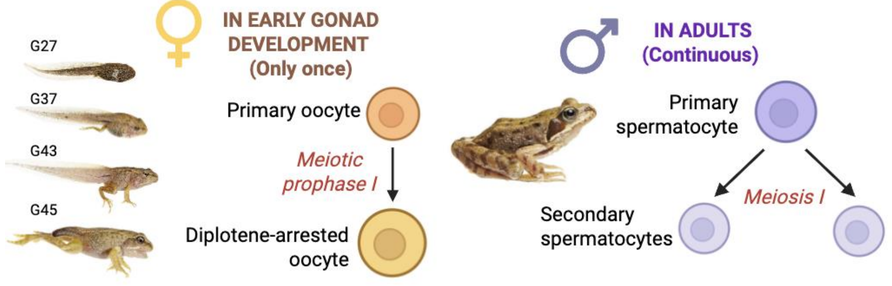


Methodology and Sample Design

Studied *Rana temporaria* populations: analytical workflow, geographic distribution, and sex chromosome differentiation

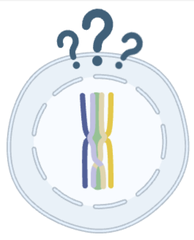


Meiosis I initiates at different developmental stages in females and males



Figures were created with BioRender.com

Research Questions

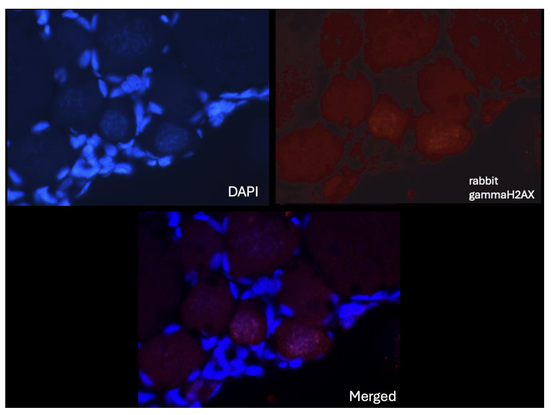


What molecular mechanisms govern extreme heterochiasmy during frog meiosis?

Which sex-specific genes are involved in prophase I and recombination regulation, and how might their expression contribute to extreme heterochiasmy?

Results

Prophase I successfully staged in *Rana temporaria* females



Progression of prophase I in female froglets

Transcriptionally active diplotene-arrested oocytes

Sex-biased meiotic prophase I gene expression revealed by RNA-seq differential expression analysis

Expectations

Meiosis I occurs at different life stages in females and males; therefore, **meiosis I-related genes** are expected to be **female-biased in froglets** and **male-biased in adults**.

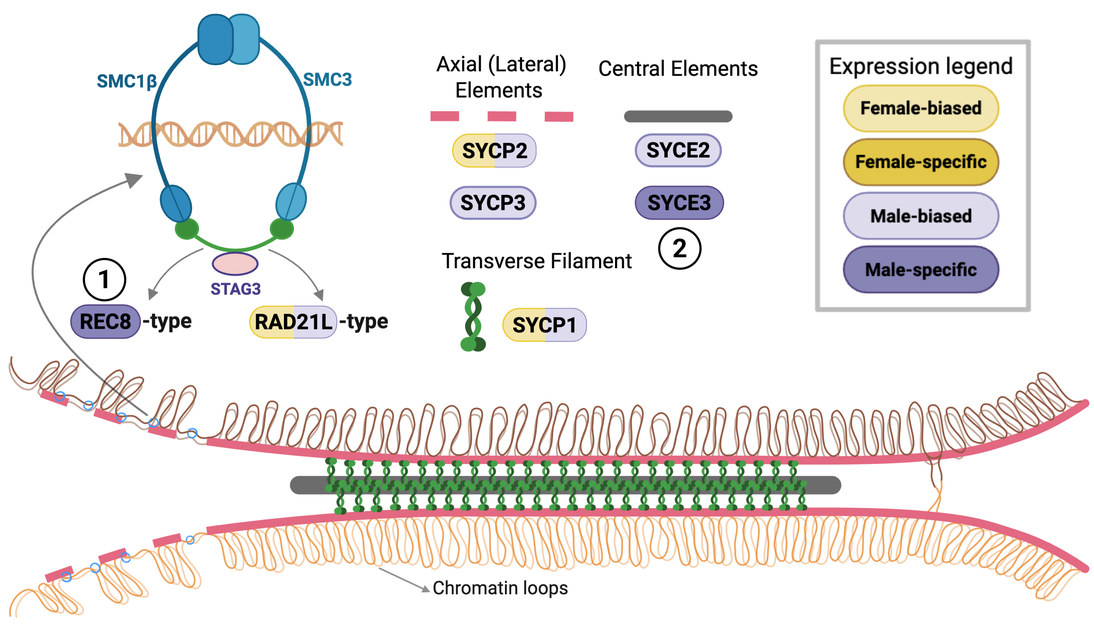
Due to **genome-wide telomere-restricted recombination in males**, genes employed in
- crossover resolution
- meiotic cohesion and synaptonemal complexes (in case of recombination suppression via epigenetic restriction of homolog pairing)
are expected to show **reduced or unbiased expression** in adult testes.

Sex-biased expression of **double strand break (DSB) machinery** is expected in both sexes, given its critical role in unsynapsed region stability and silencing.

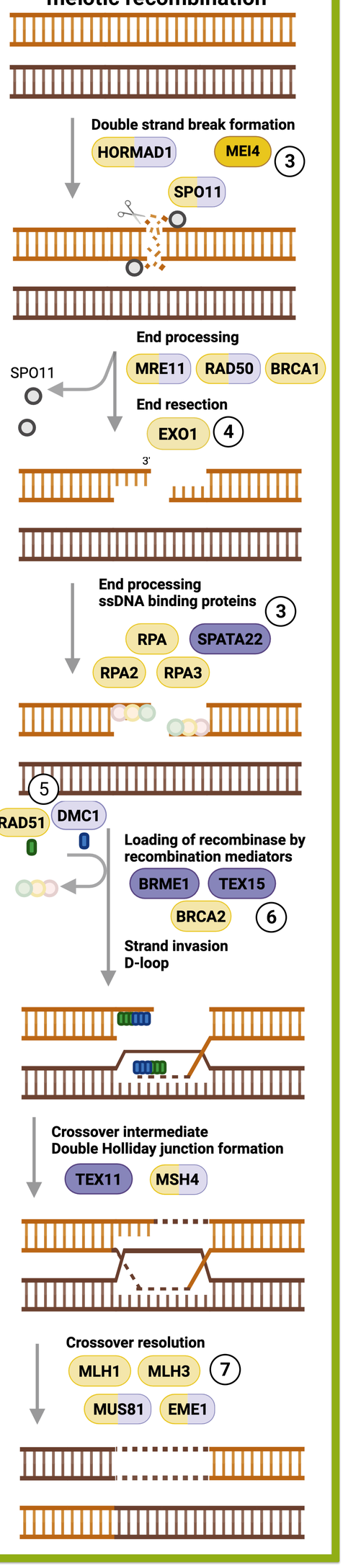
Results

Male-specific	Sex-specific	Female-bias
(1) Meiotic cohesin complex	(3) DSB machinery proteins	(4) End resection and processing
(2) Central element in synaptonemal complex	(5) (6) Preference on recombinases and their recruitment mechanisms	(7) Crossover resolution

Gene expression in chromosome axis assembly

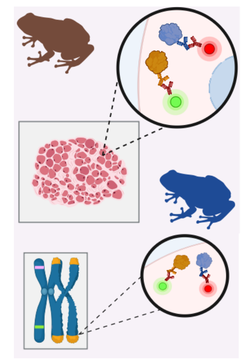


Gene expression in meiotic recombination



Conclusions

- Synaptonemal complex and DSB formation related genes are abundantly expressed in adult testis.
- Sex-specific end resection and processing likely to be employed due to extreme heterochiasmy.
- **Crossover-specific resolution marked by MLH1-MLH3 showed a consistent female-bias across all stages, as expected under extreme heterochiasmy.**
- Sex-specific transcript variants of MUS81 control unbiased resolution.

What is next?

Cytogenetic analysis of gonads from *Rana temporaria* (XX/XY) and *Bufo bufo* (ZW/ZZ) to investigate sex-specific:
1. Axis-loop structure
2. Recombination suppression mechanisms via epigenetic modifications
3. DSB and crossover dynamics
4. Roles of differentially expressed genes.