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Title: "Functions of chromatin in transcription, stress response and meiotic recombination in *Arabidopsis thaliana*"

Abstract

Chromatin composition and accessibility affects multiple biological processes on cellular scale, such as initiation of gene transcription or meiotic recombination. In turn, those molecular changes, affect genetic diversity and stress-response on the populational and organismal levels.

In the first part of the thesis, I have investigated functions of chromatin modifications on expression of stress-response genes in model plant species *Arabidopsis thaliana*. We thoroughly characterized, histone variant H2A.Z acetyltransferase NuA4 that is necessary for expression of genes related to growth and development. On the other hand, NuA4 stimulates deposition of H2A.Z into gene-bodies of stress-responsive genes, which ultimately leads to their silencing in non-inductive conditions. Later, I investigated roles of histone deacetylase enzyme HDA19, that can specifically remove acetyl groups from H2A.Z and H3 at responsive genes. Interplay between histone acetylation and deacetylation forms equilibrium preventing spurious expression of stress genes.

In the later section I explored possible roles of chromatin modifications with dCas9-based tools. I provided a set of evidence that local recruitment of expression inducer peptide VP64, leads not only to increased transcription of the targeted gene but also to rearrangements in chromatin which can affect meiotic crossover formation in the targeted locus.

In the second part of the thesis, I developed bioinformatic pipelines used in NGS data analysis with emphasis on crossover detection in *Arabidopsis*. First, I designed web-based tool that allows easy browsing of genotyping-by-sequencing datasets coming from different mutant backgrounds. Additionally, I developed a code that provides a simple and effective way to determine crossover site in NGS data generated via seed-

Z komentarzem [PZ1]: Może żeby to przejście od regulacji transkrypcji do rekombinacji było bardziej płynne mógłbyś napisać, że ten "local recruitment" prowadzi nie tylko do zwiększenia transkrypcji genu, ale także wpływa na meiotic crossover formation

Z komentarzem [PZ2]: Nie wiem czy "demonstrated" pasuje w tym kontekście, ja bym raczej napisał że "I developed bioinformatics tools (albo softwares) for NGS data analysis..."

Z komentarzem [PZ3]: Fast comparison of what?

typing. Seed-typing is a method for investigating meiotic recombination at the hotspot scale.

To sum up, I demonstrated various aspects of my PhD research activities, ranging from studies on chromatin roles in the regulation of gene expression and meiotic recombination to development of computational approaches in biological data analysis.