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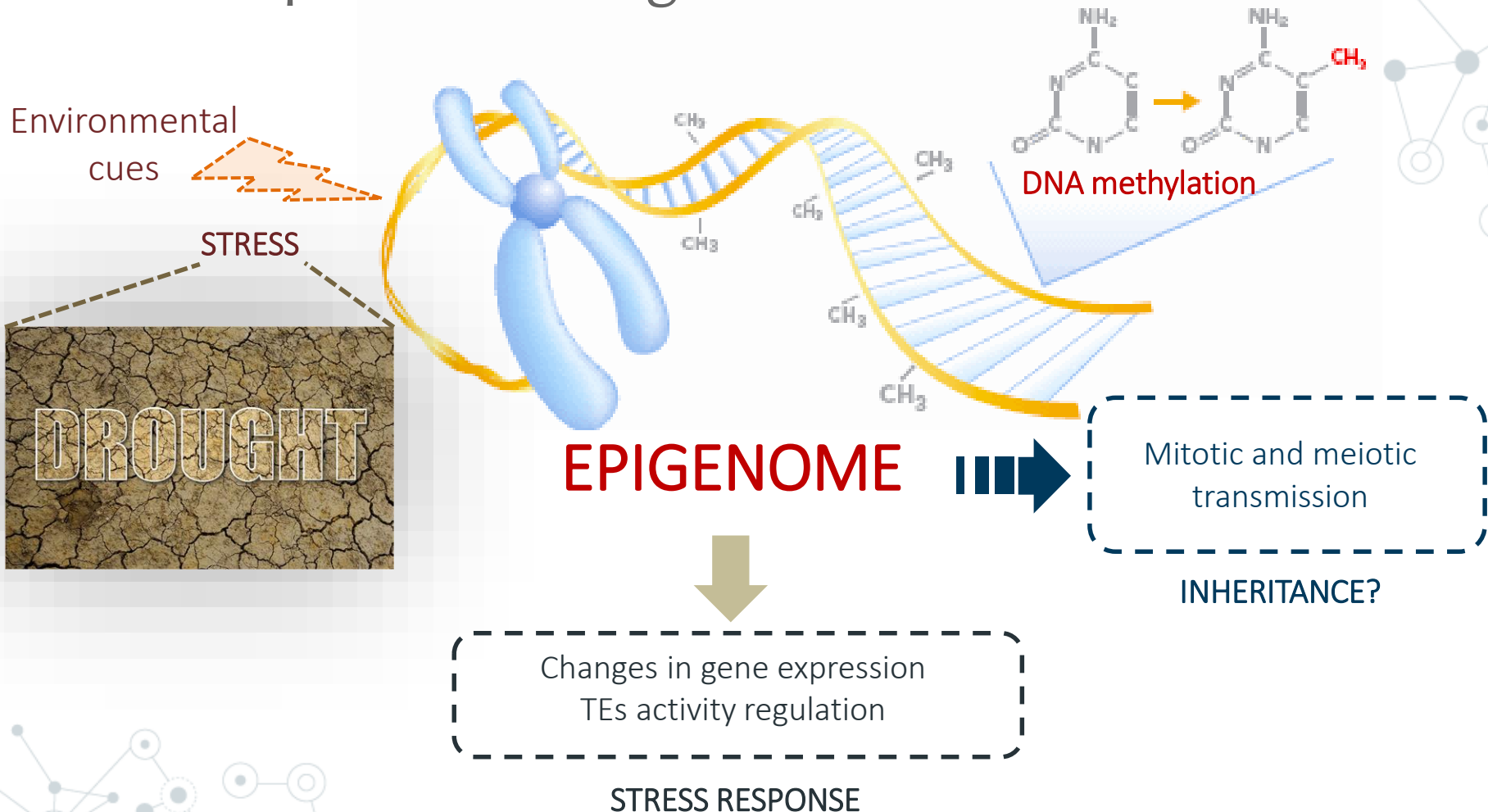
PhD thesis

Focused on the plant epigenomics
and transcriptomics in the context
of abiotic stress responses

Supervisors: prof. dr hab. Iwona Szarejko
dr Mirosław Kwaśniewski

Epigenetic changes

AIM: Analysis and characterization of barley methylome and its response to drought stress conditions



My genetic model

Barley (*Hordeum vulgare* L.)

Barley is a **good** study object:



One of the most important cereals



Can be a model to other monocot crops



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Key ingredient in beer and whisky production



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Barley is actually a **bad** study object for genomics:



Genome 50x (!) bigger than of model plant *Arabidopsis thaliana* (5.3 Gbp)



Its genome consists mainly of repetitive sequences - as much as 84% (genes only 3%)



The genome is still shattered in thousands of contigs - no consensus physical map



Barley as a plant → DNA methylation studies are more complex

- Extremely high level of DNA methylation
- Every sequence context can be methylated (CG, CHG, CHH – H: C, A or T)
- CHG and CHH only partially methylated

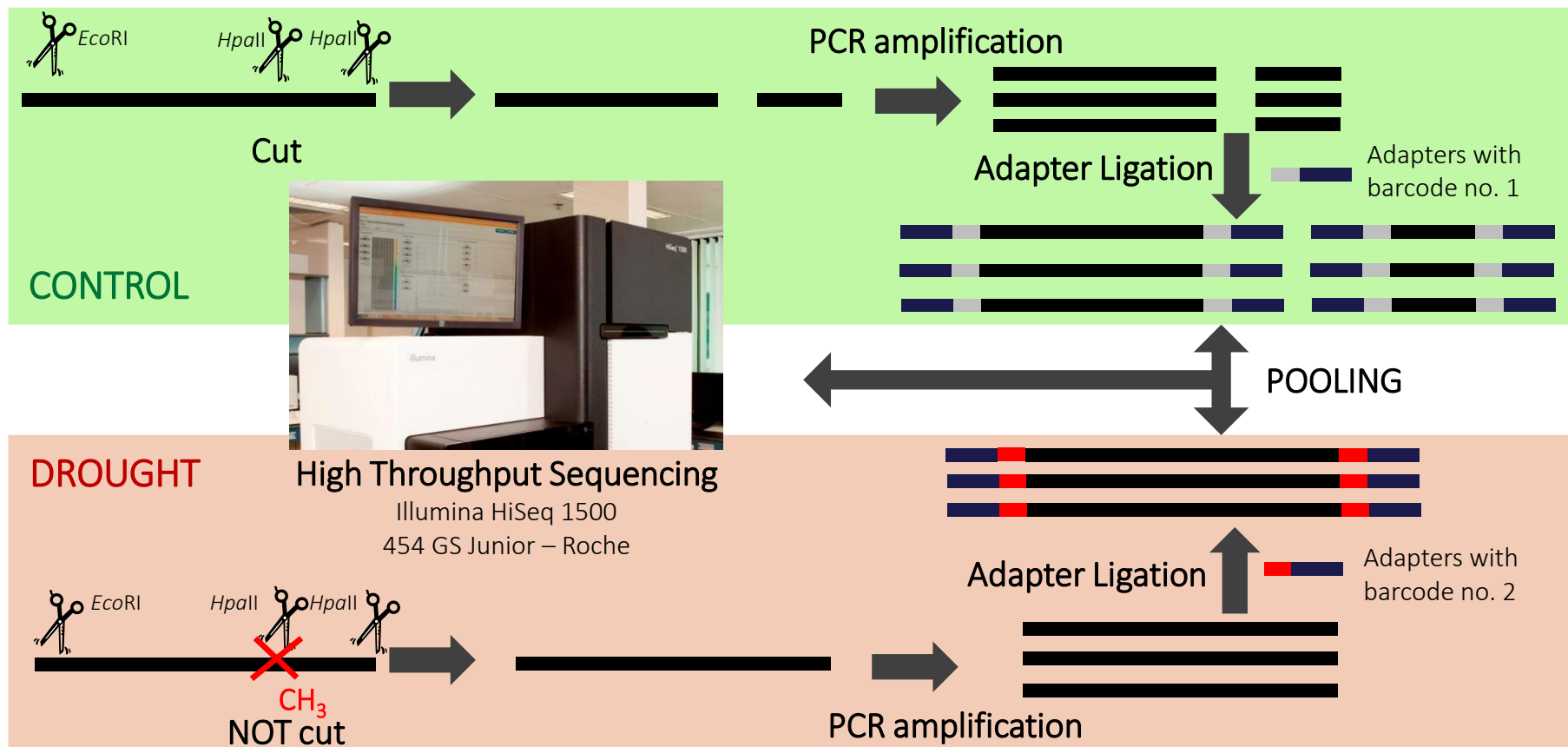


New NGS approach to study DNA methylation

DNA methylation study: **MSAP-Seq** (Methylation Sensitive Amplification Polymorphism Seq)

Gene expression: **RNA-Seq**

MSAP-Seq allows for an identification of specific sites undergoing DNA methylation changes in organisms with large and complex genomes

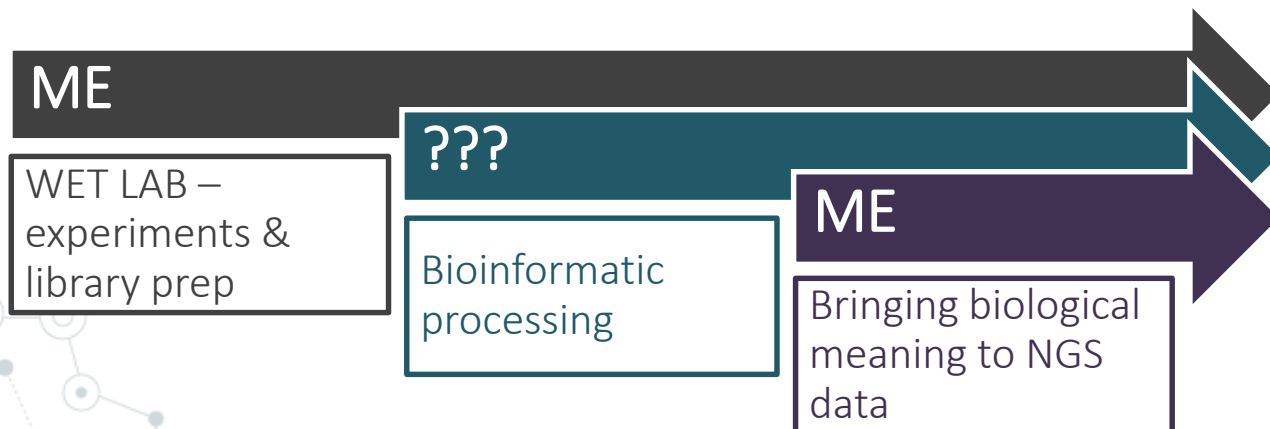


My NGS experience

Setting up experiments and preparing libraries for:

- ✓ Methyl-Seq
- ✓ RRBS (Reduced Representation Bisulfite Sequencing)
- ✓ RNA-Seq
- ✓ SmallRNA-Seq
- ✓ Shotgun sequencing
- ✓ Targeted amplicon sequencing
- ✓ Metagenomics based on 16S-rDNA tags

Previously 454 – now Illumina HiSeq



Thank You!

