# The meiotic transcriptome of *Zea mays*

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## Summary

In plants, there are currently only <100 genes with known functions in meiotic processes. To find new meiotic genes, we elucidated the meiocyte transcriptome from the *Zea mays* inbred line B73 using a combination of two techniques (Fig. 1):

• **Capillary Collection of Meiocytes (CCM)** is a method for isolating pure meiocytes.

• **mRNA Sequencing (mRNAseq)** is an efficient deep-sequencing approach to detect tissue-specific differential gene expression.

The B73 meiotic transcriptome includes highly expressed, meiocyte-specific genes that have not been characterized before. Examining gene ontology (GO) profiles and known meiotic genes also shows how valuable this dataset is.

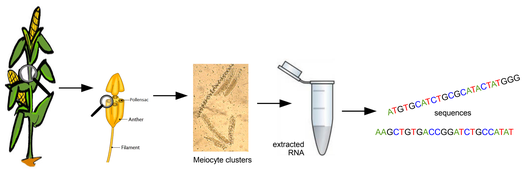



**Figure 1. Overview of the experimental setup**
Maize plants that harbor appropriate male meiosis stages are selected using acetocarmine staining, anthers are dissected and squashed, followed by CCM, RNA extraction, library preparation and sequencing.

## Introduction

So far, most studies on meiotic gene expression in plants used whole anthers. Thus, in these studies the meiocyte transcriptome was contaminated by transcripts from somatic cells. Others studies compared transcriptomes from mutant anthers with wild-type ones. Only recently did studies on *Arabidopsis* use pure meiocytes, which is here done for the first time in a major crop plant.

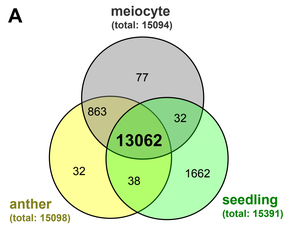
### What is the purpose?

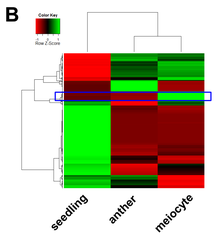
• With meiocyte transcriptome profiling, we aim to increase our **understanding of meiosis**. We can reveal novel meiotic candidate genes and get an overview over which biological processes are present, or which ones are more important. Thus, the data provide us with an optimal starting point for further detailed characterizations.

• The recombination process during meiosis leads to genetic diversity which in turn is the **basis of plant breeding**. Much is not understood or possible yet but might be resolved with increased knowledge. This is especially important considering future challenges such as **a growing population and possible climate changes.**

## Results

**Figure 2. Venn diagram and heat map of expressed genes**
**A:** Genes with at least 5 reads per million. The total number of genes found in pure meiocytes, whole anthers, and 2-week-old seedlings do not differ much. Most genes are shared by all samples, only few genes are unique to single samples or shared by two.
**B:** Genes grouped by their differential expression pattern (read count high = green, low = red, average = black). The blue box contains highly expressed, meiocyte-specific genes.



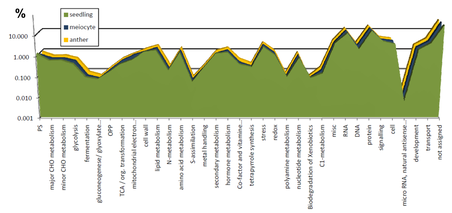




**Figure 3. Comparison of GO distribution**
Gene Ontology (GO) analysis of genes depicted in Fig 2A. The distribution of GO terms is very similar in all samples, with only slight but notable differences: RNA-related genes are significantly enriched in anthers and meiocytes compared with seedling. In contrast, known photosynthetic genes show higher expression levels in seedlings.

**Figure 4. Novel candidate genes in meiotic processes**
A small number of genes show a meiocyte-specific expression pattern (blue box in Fig. 1B). Their GO distribution is shown below, with many unassigned genes and a significantly enriched portion of genes related to RNA and to mitochondrial electron transport/ ATP synthesis. Of all these candidate genes, only few (~5%) have been examined yet.

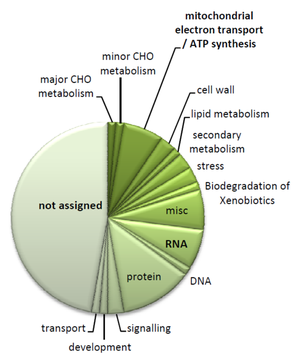
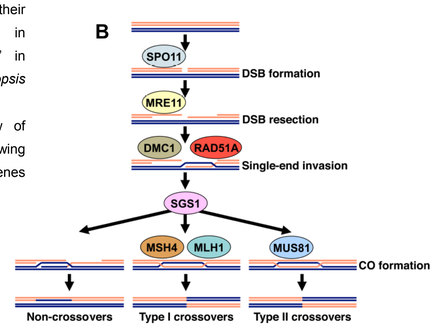



**Figure 5. Homologs of known genes involved in meiotic recombination**
Comparison with the dicot model plant *Arabidopsis thaliana* reveals homologs of genes with reported meiotic functions. Only few of the maize homologs have been characterized yet.
**A:** List of genes involved in meiotic recombination and their expression level ratios in "meiocytes vs. seedlings" in *Zea mays* and *Arabidopsis thaliana*.
**B:** A schematic overview of meiotic recombination showing proteins encoded by genes listed in Fig. 5A.

**A**

| Gene name | Maize M/S | Arabidopsis M/S | further characterized in maize |
|---|---|---|---|
| *DMC1* | 563.7 | 6.0 | |
| *MLH1* | 7.6 | 2.3 | |
| *MRE11A* | 2.9 | 1.4 | Waterworth et al. (2007) |
| *MRE11B* | 2.3 | | |
| *MSH4* | 4.2 | 36.5 | |
| *MUS81-1* | 0.8 | 4.0 | |
| *RAD51A1* | 1.8 | 1.6 | Franklin et al. (1999) |
| *RAD51A2* | 1.3 | | Li et al. (2007) |
| *SGS1* | 0.7 | 0.5 | |
| *SPO11-1* | 4.9 | 2.9 | |
| *SPO11-2* | 11.2 | 2.0 | |

**B**




## Conclusion

• Differential expression suggests candidates for **novel meiotic genes** (Fig. 2 A+B, Fig. 4).

• ~15000 genes are expressed in meiocytes, their amount and GO distribution very similar to somatic tissue (Fig. 2+3). But do all those genes have a function in meiosis?

• **RNA-related genes** are significantly enriched in meiocytes – what is their task?

• Homologs of known **recombination genes** are expressed in *Zea mays* meiocytes; some are even more predominant compared with seedlings than in the model plant *Arabidopsis* (Fig. 5).

## Literature

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*(mRNAseq Arabidopsis meiocytes)*

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*(microarray Arabidopsis meiocytes)*

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*(RAD51, maize)*

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*(MRE11, maize)*

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*(RAD51, maize)*

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