

European Plant Embryogenesis Consortium (EURO-PEC)

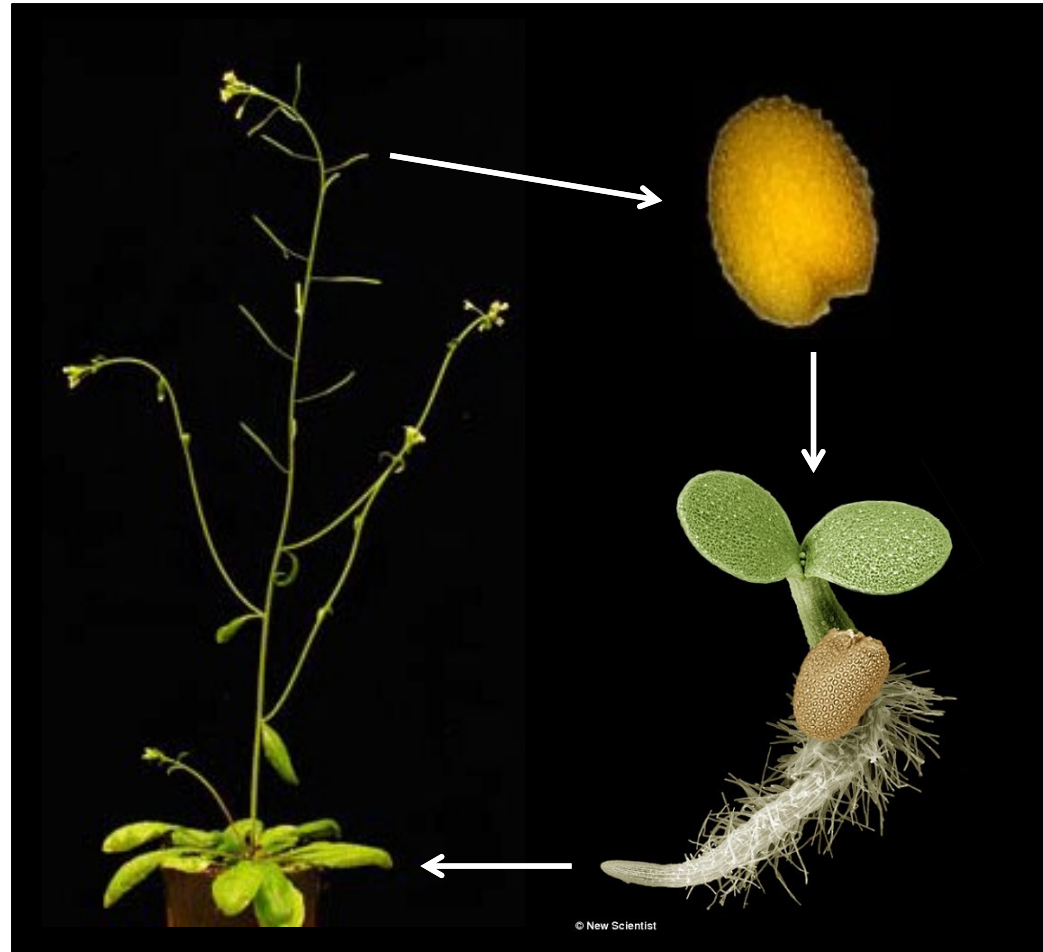
Dolf Weijers
Wageningen University
The Netherlands

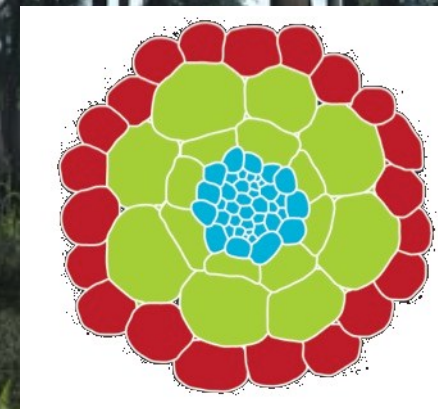
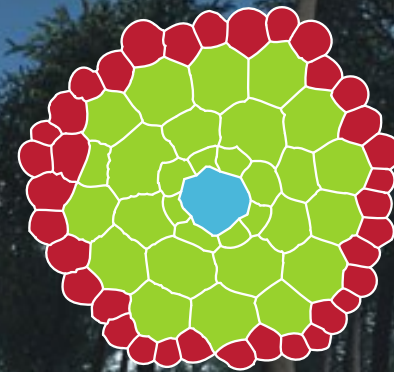
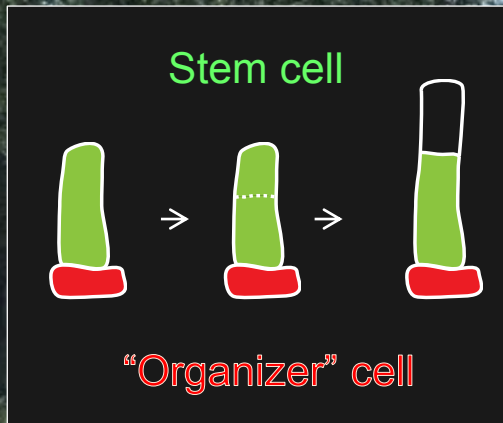
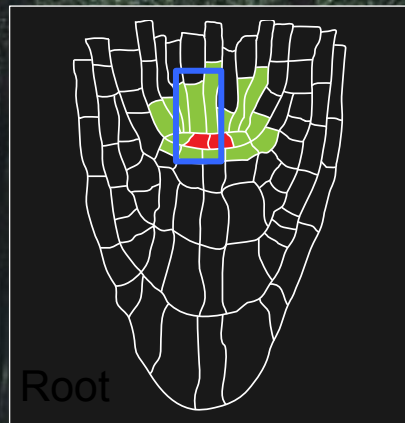
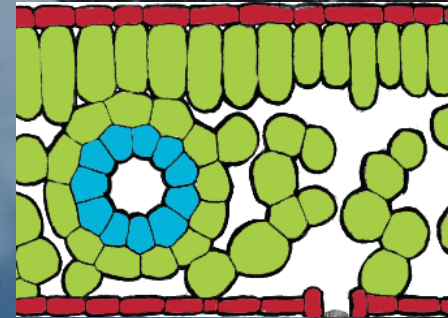
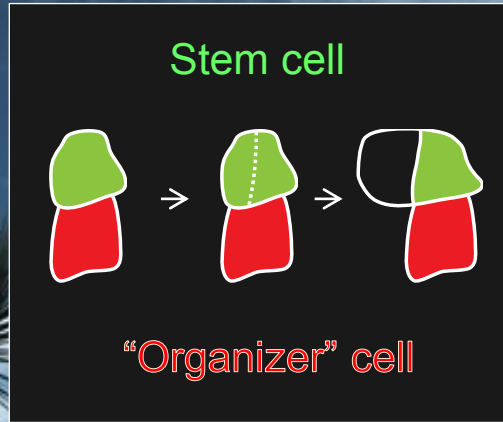
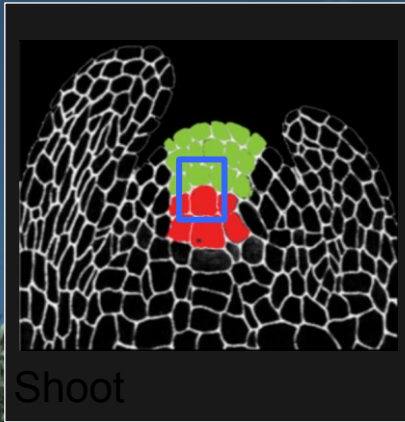


ERA-NET for Coordinating
Action in Plant Sciences



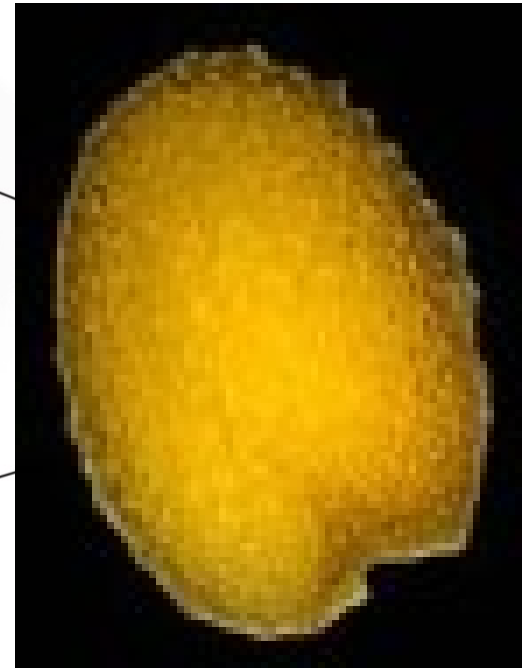
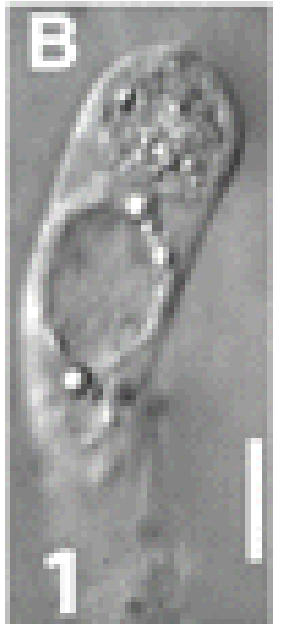
Plant life is cyclical



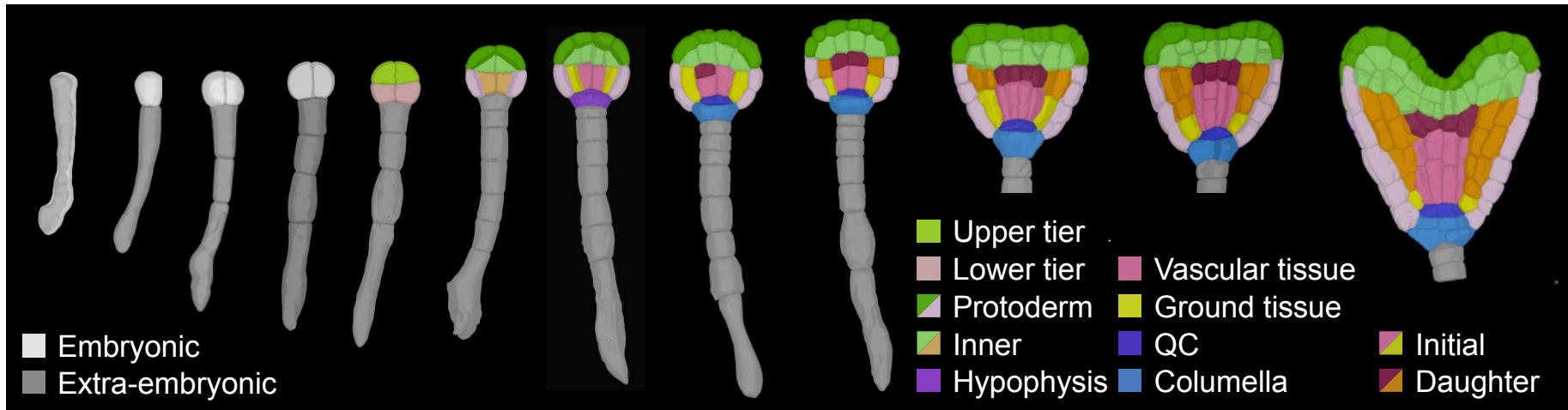


Epidermis
Ground tissue
Vascular tissue

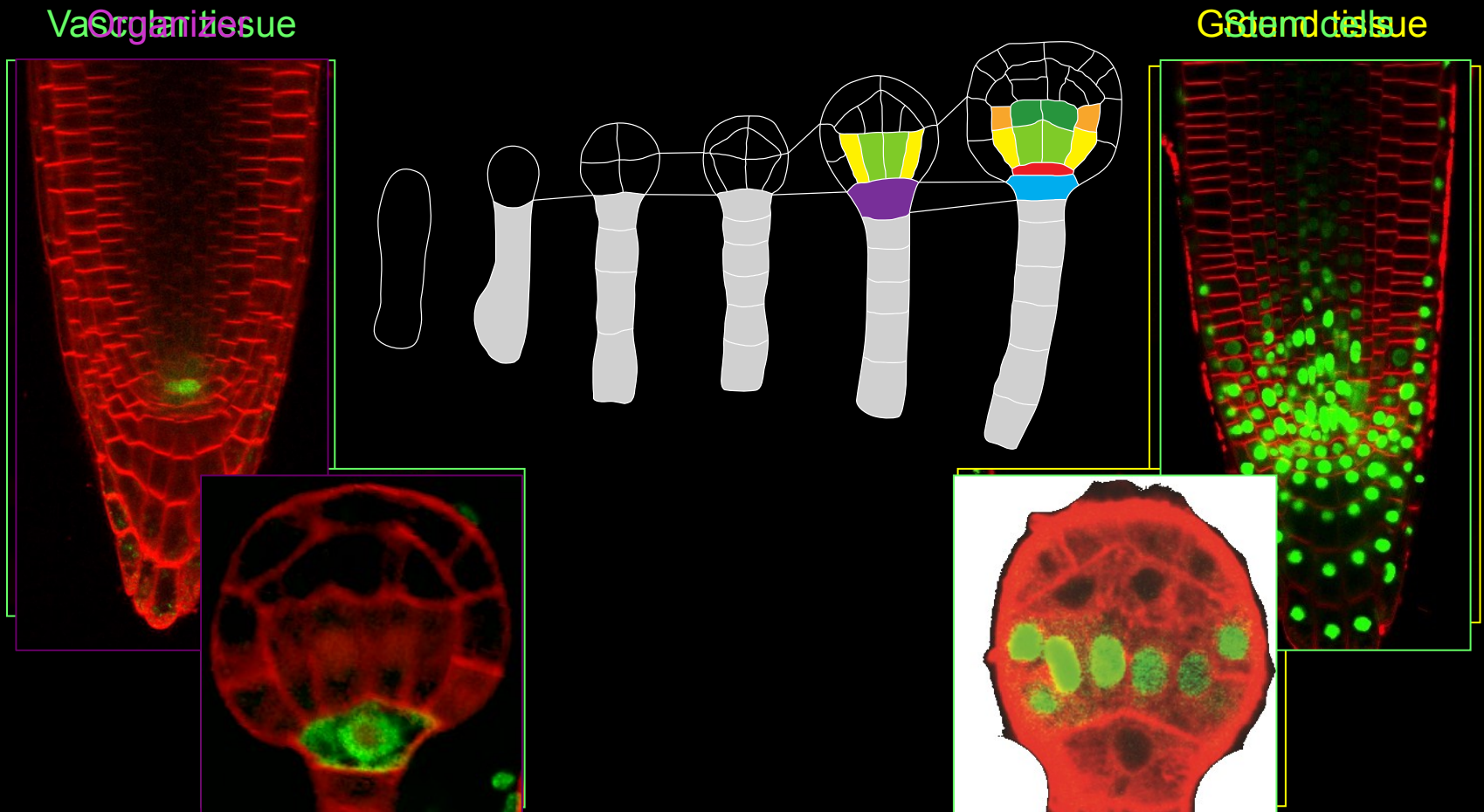
Embryogenesis, a new start



Stepwise increase in complexity



The nexus of development





EURO-PEC partners



Dolf Weijers
Wageningen, NL
(coordinator)



Ben Scheres
Wageningen, NL



Gerd Jürgens
Tübingen, DE



Thomas Laux
Freiburg, DE



Michael Nodine
Vienna, A

**Vascular/ground
tissue**
(*MONOPTEROS*)

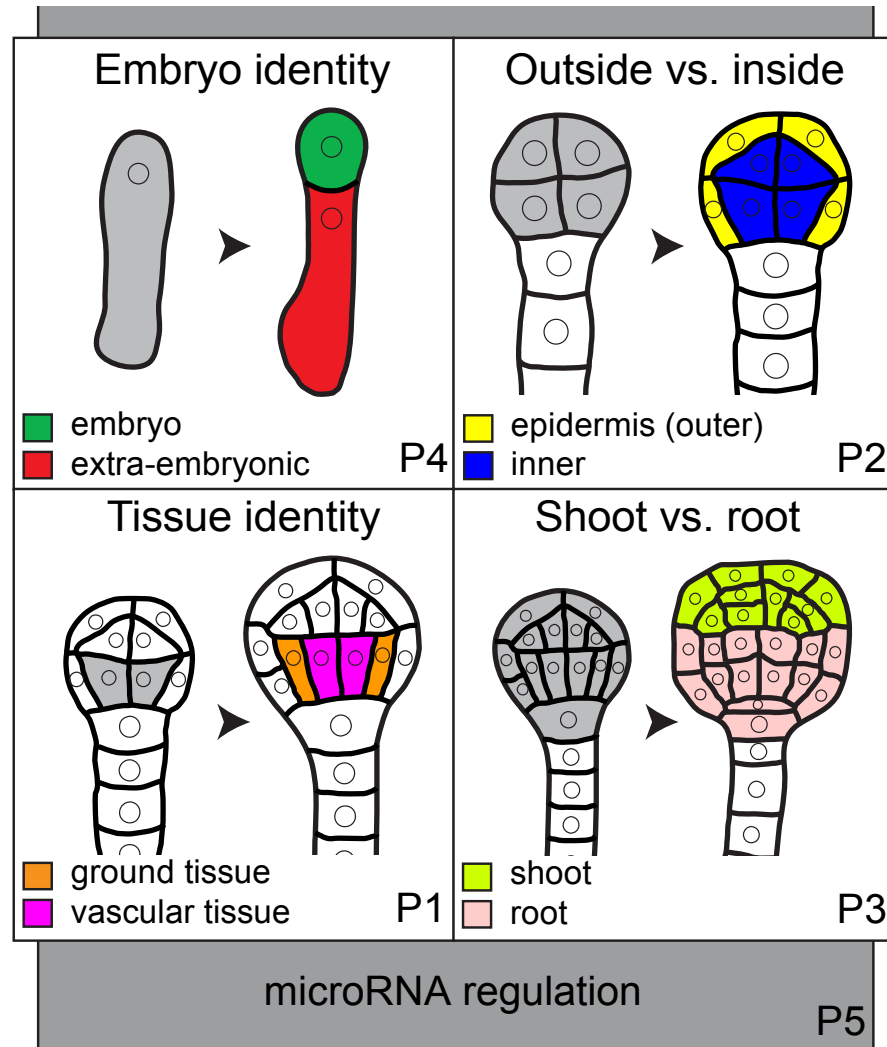
Root identity
(*PLETHORA*)

Epidermis
(*AtML1*)

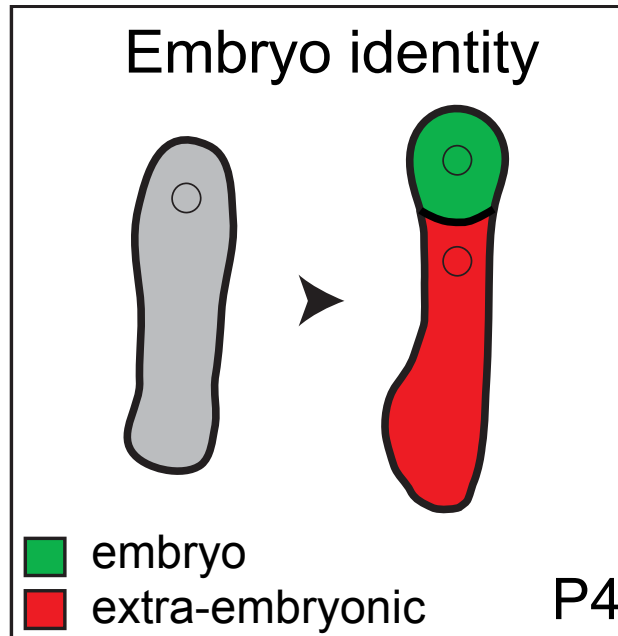
**Early axis
formation**
(*WOX*)

microRNAs

EURO-PEC strategy



Early axis formation



WOX2
expression



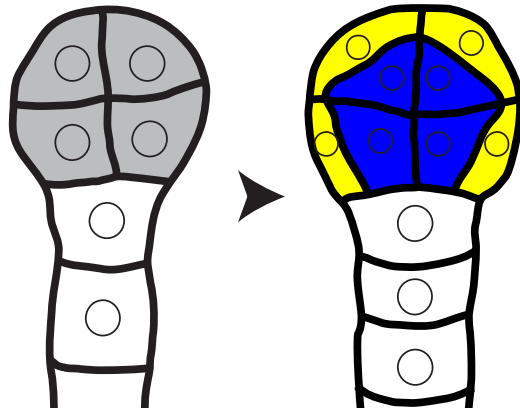
wox2(+)
mutant

- WOX2 transcriptional targets (RNAseq in mutant embryos, ChIP-seq)
- Validation of expression patterns
- Mutant phenotypes

Outside/inside specification



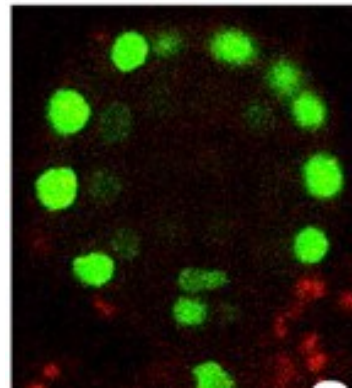
Outside vs. inside



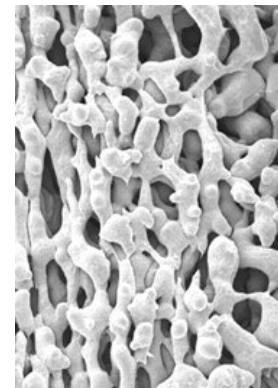
epidermis (outer)

inner

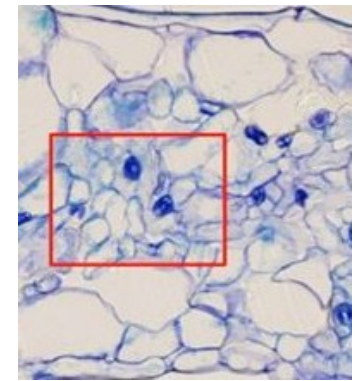
P2



AtML1-GFP



atml1 pdf
mutant



ATML1
misexpression

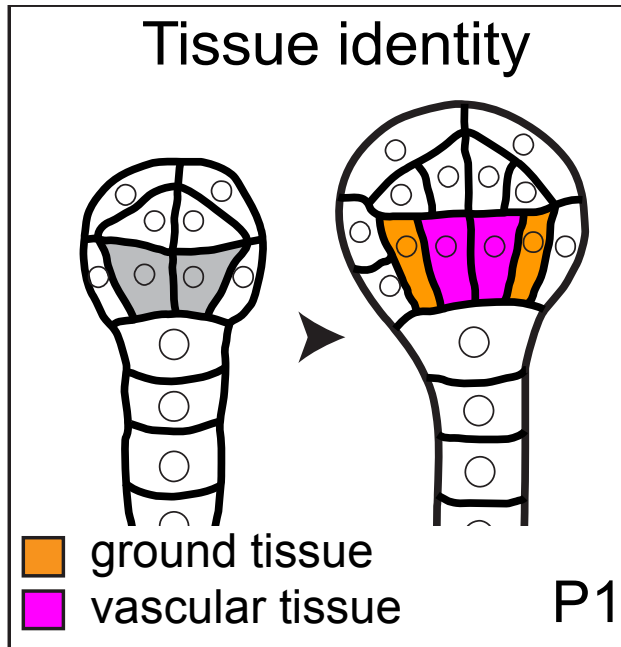
- Identify “outside” and “inside” transcriptomes (FACS, RNAseq)
- RNAseq in *atml1 pdf1* mutant and *ATML1* misexpression embryos
- Validation of expression patterns

Takada and Jürgens., *Development* (2007)

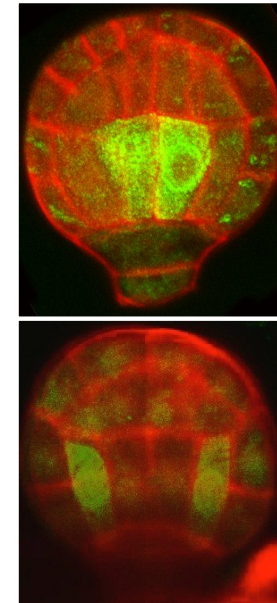
Abe et al., *Development* (2003)

Takada et al., *Development* (2013)

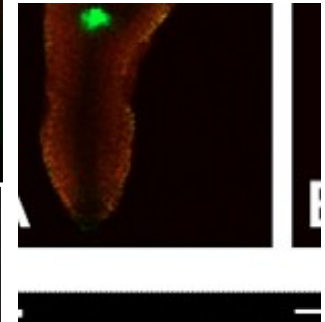
Vascular/Ground tissue specification



mp mutant



INTACT
lines



MP-GFP

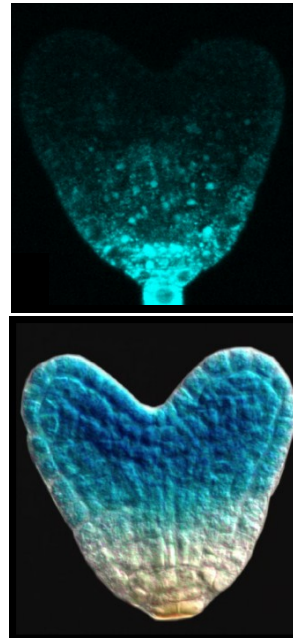
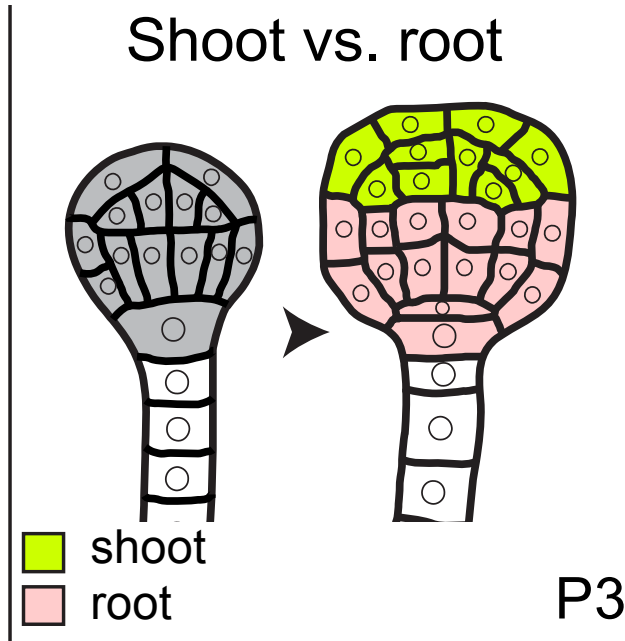
- RNAseq in *mp* mutant vascular and ground tissue (INTACT)
- ChIP-seq on MP in vascular and ground tissue (INTACT)
- Validation of expression patterns

Berleth and Jürgens, *Development* (1993)

Schlereth et al., *Nature* (2010)

Palovaara et al., *TIPS* (2013)

Shoot/Root specification



PLT1

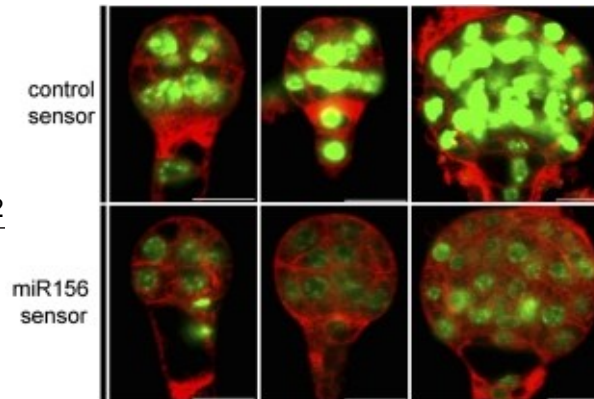
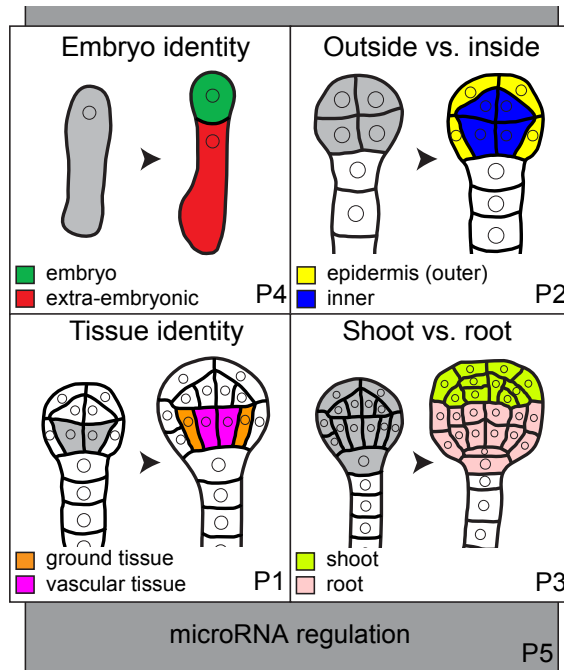
PLT5



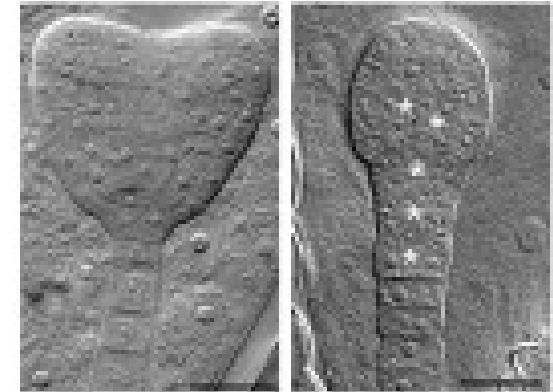
PLT1 misexpression

- Upstream regulation of root vs shoot PLT (yeast 1-hybrid)
- Transcriptional targets of root vs shoot PLT (RNAseq on mutant; ChIP-seq on PLT-GFP)
- Validation of expression patterns and phenotypes

MicroRNA function



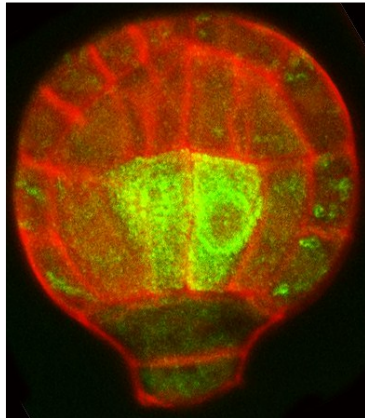
MicroRNA sensor



MicroRNA biogenesis mutant

- Identification of novel miRNA-controlled factors (genetic screen)
- Identification of interactions with known regulators

Unified/standardized methodology



Whole-embryo
RNAseq

P5

Cell specific
transcript profiling

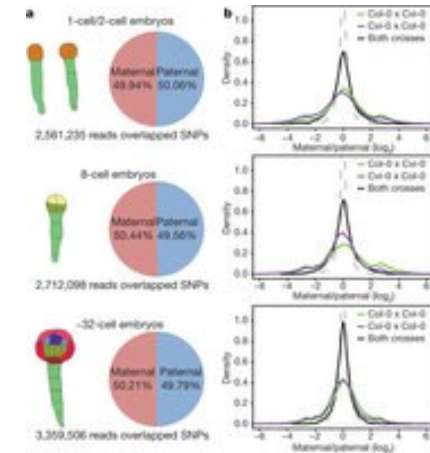
P1,2

Chromatin Immunoprecipitation
(TF ChIP-seq) P1,3,4,5

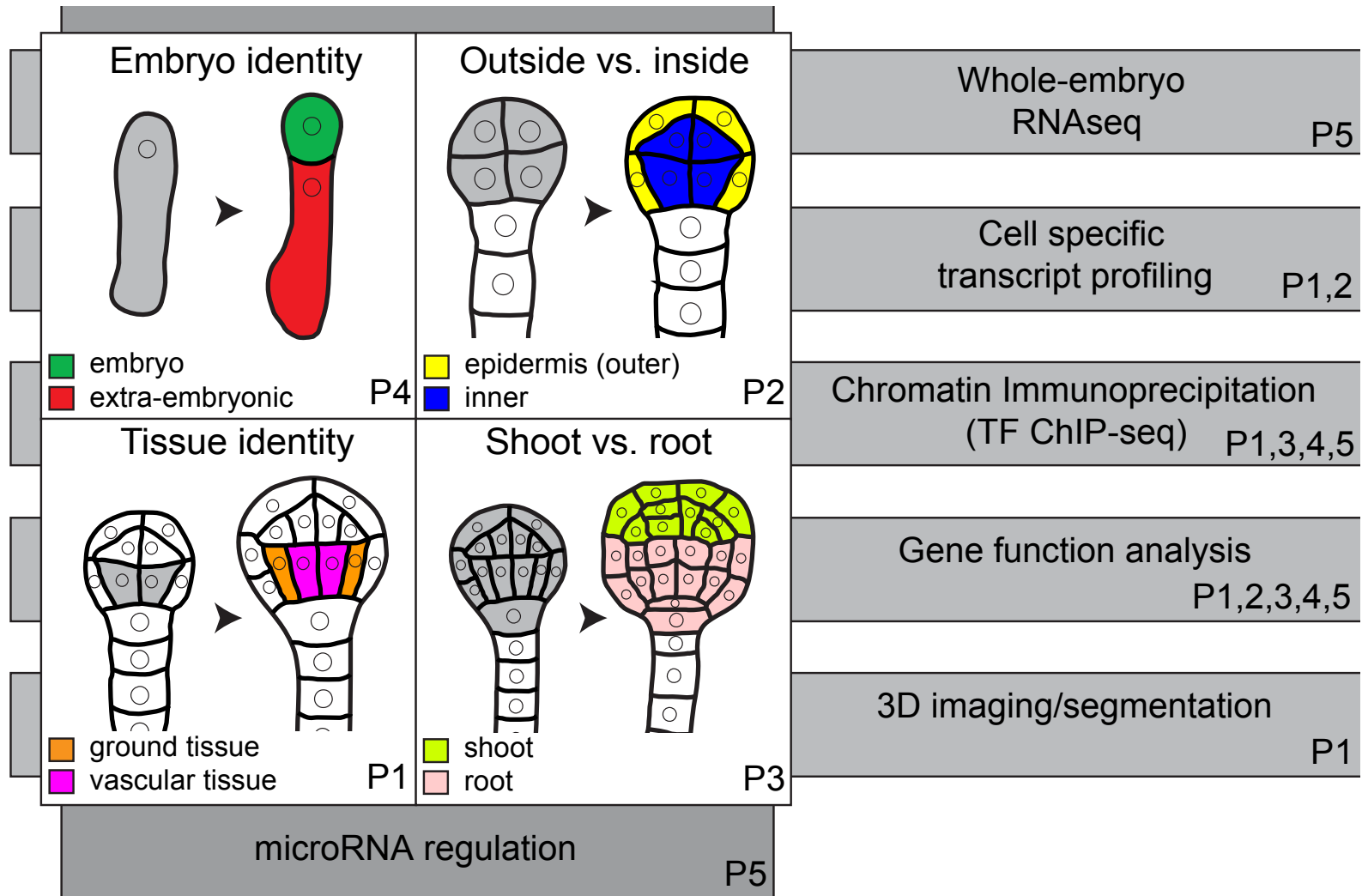
Gene function analysis
P1,2,3,4,5

3D imaging/segmentation

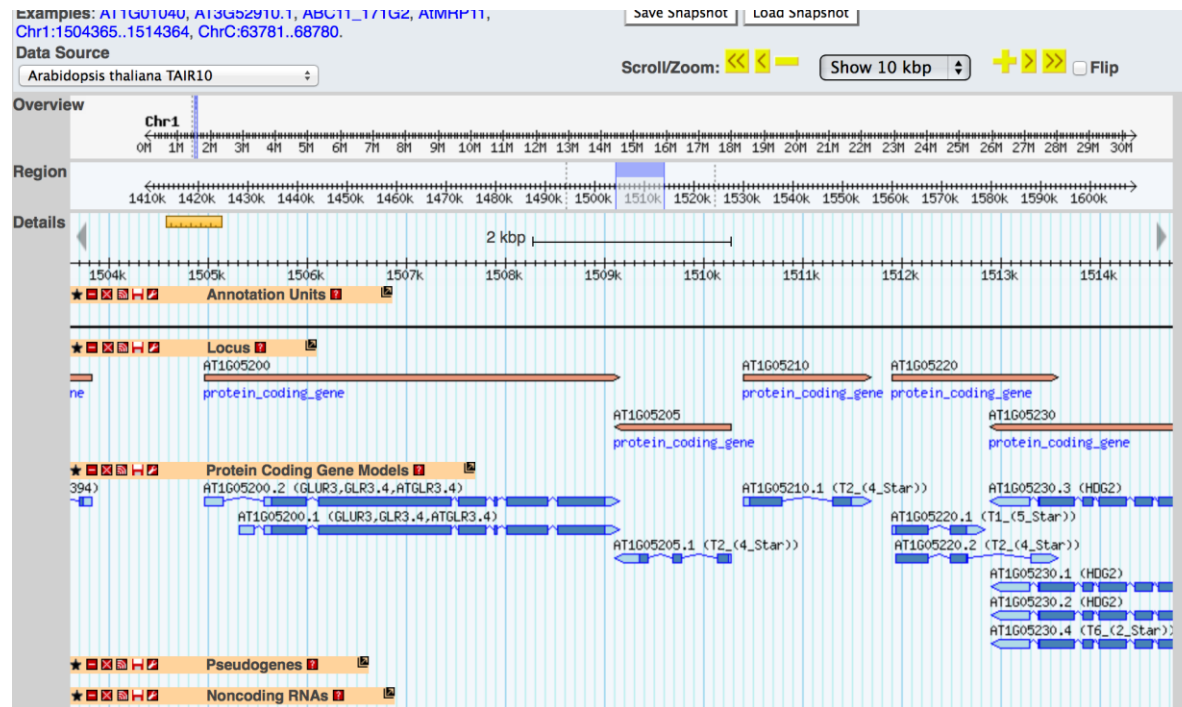
P1



EURO-PEC strategy



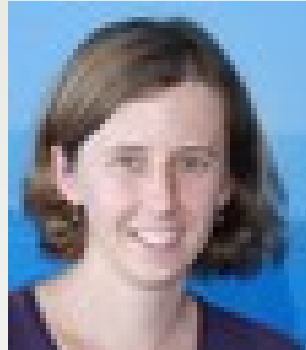
A dedicated genome browser



- All RNAseq and ChIP-seq data will be entered in a genome browser
- Data curation by Nodine (Vienna)
- Standardized sequencing protocol

Outcomes

1. Knowledge on regulatory context of key cell fate regulators (upstream regulators / targets)
2. Atlas of transcriptional reprogramming during embryo development
1. Network connecting key cell fate regulators



Thank you!



ERA-NET for Coordinating
Action in Plant Sciences



Management

1. Quarterly online PI meetings
2. Annual meeting with PI's, fellows and other partner lab members

1. Lab-Wiki (closed)

