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Title:	A high-resolution gene expression map of the arabidopsis shoot meristem stem cell niche
Authors:	Yadav, R.K. (/jspui/browse?type=author&value=Yadav%2C+R.K.)
Keywords:	Central zone WUSCHEL CLAVATA
Issue Date:	2014
Publisher:	Company of Biologists Ltd
Citation:	Development (Cambridge), 141(13), pp. 2735-2744.
Abstract:	The shoot apical meristem (SAM) acts as a reservoir for stem cells. The central zone (CZ) harbors stem cells. The stem cell progenitors differentiate in the adjacent peripheral zone and in the rib meristem located just beneath the CZ. The SAM is further divided into distinct clonal layers: the L1 epidermal, L2 sub-epidermal and L3 layers. Collectively, SAMs are complex structures that consist of cells of different clonal origins that are organized into functional domains. By employing fluorescence-activated cell sorting, we have generated gene expression profiles of ten cell populations that belong to different clonal layers as well as domains along the central and peripheral axis. Our work reveals that cells in distinct clonal layers exhibit greater diversity in gene expression and greater transcriptional complexity than clonally related cell types in the central and peripheral axis. Assessment of molecular functions and biological processes reveals that epidermal cells express genes involved in pathogen defense: the L2 layer cells express genes involved in DNA repair pathways and telomere maintenance, and the L3 layers express transcripts involved in ion balance and salt tolerance besides photosynthesis. Strikingly, the stem cell-enriched transcriptome comprises very few hormone-responsive transcripts. In addition to providing insights into the expression profiles of hundreds of transcripts, the data presented here will act as a resource for reverse genetic analysis and will be useful in deciphering molecular pathways involved in cell type specification and their functions.
Description:	Only IISERM authors are available in the record.
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