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| Title: | Genome wide gene expression analyses of Arabidopsis shoot stem cell niche cell populations |
| Authors: | Malhan, D. (/jspui/browse?type=author&value=Malhan%2C+D.) Bhatia, Shivani (/jspui/browse?type=author&value=Bhatia%2C+Shivani) Yadav, R.K. (/jspui/browse?type=author&value=Yadav%2C+R.K.) |
| Keywords: | cell layer cell population epidermal subepidermal |
| Issue Date: | 2015 |
| Publisher: | Taylor and Francis |
| Citation: | Plant Signaling and Behavior, 10(4) pp. 1-3. |
| Abstract: | The shoot apical meristem (SAM) of higher plants harbors stem cells at their tips. In the SAM, stem cell niches maintain the pluripotent nature of these cell types in the central zone (CZ) and allow them to enter in to differentiation pathways either in the peripheral zone (PZ) or rib meristem (RM). Apart from functional zones, SAM is also subdivided in to distinct cell layers termed as; L1 / epidermal, L2 / subepidermal and L3 / corpus cell layer. Thus, SAM is a complex structure made up of multiple cell types having discrete cell identities. In a recent study, we employed the fluorescent activated cell sorting approach to isolate the cell population of functional zones and cell layers and identified the cell population expressed genes (CPEGs). The Gene Ontology (GO) analysis revealed cellular functions of the identified CPEGs. The cell layers of the SAM are involved in pathogen defense, cell differentiation and photosynthesis. We found many genes in SAM CEPGs that responded to hormone treatment. These observations in the future will help researchers working in the area of shoot apex biology to elucidate the gene regulatory network involved in cell and tissue specialization. |
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