



**HAL**  
open science

# Identification of developmental zones in maize lateral roots on the basis of longitudinal epidermis cell length profiles

Yann Guédon, Beatriz Moreno-Ortega, Bertrand Muller

► **To cite this version:**

Yann Guédon, Beatriz Moreno-Ortega, Bertrand Muller. Identification of developmental zones in maize lateral roots on the basis of longitudinal epidermis cell length profiles. IEEE International Conference on Functional-Structural Plant Growth Modeling, Simulation, Visualization and Applications (FSPMA 2016), Nov 2016, Qingdao, China. pp.42. hal-01398404v2

**HAL Id: hal-01398404**

**<https://inria.hal.science/hal-01398404v2>**

Submitted on 17 Nov 2016

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

## Identification of developmental zones in maize lateral roots on the basis of longitudinal epidermis cell length profiles

Yann Guédon, Beatriz Moreno Ortega, Bertrand Muller  
yann.guedon@cirad.fr

Research focus: Cell division and elongation are key processes in root development. A growing root tip is assumed to be made of three contiguous zones: the division zone (DZ), the elongation zone (EZ) and the mature zone (MZ). Because of the concentric organization of tissues in roots, we here focus on epidermis cell length profiles for delimiting these three developmental zones. We assume that DZ is characterized by small cells, EZ by cells of gradually increasing length and MZ by rather large cells. These zones were identified on 42 maize lateral roots belonging to three genotypes and, for each genotype, to a rather large diversity in terms of development.

Methods: We built two types of Gaussian multiple change-point models for each root: heteroscedastic piecewise Gaussian linear models built on the basis of the measured epidermis cell length profiles and Gaussian change in the variance model built on the basis of the residual series deduced from the optimal piecewise linear function. The number of segments was selected using the slope heuristic, a non-asymptotic penalized likelihood criterion. The outputs of the analysis of each root using multiple change-point models (e.g. lengths of DZ and EZ, cell lengths predicted at the limits between DZ and EZ and between EZ and MZ) combined with some morphological features (first root hair position and root diameter in MZ) were then globally analyzed using principal component analysis (PCA).

Results: We identified at most three zones corresponding to DZ, EZ and MZ except in arrested roots where DZ and in some cases EZ were missing. In our modeling framework, the limit between two successive zones corresponds to a marked change in slope and in residual standard deviation. In more than 90% of cases, the limits found on the residual series on the basis of the sole change in residual standard deviation co-localized with the limit found on the original series. In most cases, the limit between EZ and MZ was consistent with the first hair position. In PCA, the first axis accounting for 49% of variance corresponds to the longitudinal variables (mainly DZ and EZ lengths but also first root hair position) while the second axis accounting for 29% of variance corresponds to the cell length variables.

Conclusions: We here provide the first pipeline of methods combining image analysis and statistical modeling for identifying developmental zones in root tips. This pipeline enabled in particular to identify emerging properties such as a jump in residual standard deviation between DZ and EZ suggesting that the distal boundary of the meristem corresponds to the onset of rapid cell expansion and a jump in residual standard deviation of high amplitude between EZ and MZ co-localized with a change in slope that could be due to the differentiation of trichoblast and atrichoblast cell files.