

GenomiX, Montpellier, France 4 ICRISAT, Niger 5 LMI LAPSE, Dakar, Senegal § Present address: UCL, Louvain-la-neuve, Belgium; IRD

Abstract

Early root growth plays a pivotal role for crop establishment and adaptation in low-input agricultural systems where water and nutrients are scarce. We studied primary root growth in pearl millet, a key staple crop for food security in arid region of sub Saharan Africa and India. We evaluated primary root length using a 2D pouch system in a large panel of 173 inbred lines representing the crop genetic diversity. Genome Wide Association Scan (GWAS) using 392.493 SNP markers revealed nine significant marker-trait associations for primary root growth. These markers were mapped to the newly released pearl millet genome (Varshney et al. , 2017). In parallel, we compared gene expression in the root tip of two inbred lines with very contrasted root growth phenotype using RNAseq. The combination of GWAS and gene expression data revealed some interesting candidate gene for the regulation of root growth in pearl millet. These candidates were assessed further in a new evaluation of primary root growth conducted in two large segregating F2 populations derived from crosses between contrasted inbred lines. Variations of allele frequency at the targeted genes in bulked pools of lines with extreme phenotypes provided the means for a cost-effective validation of our results.

Diversity and Genetic Basis of Complex Traits
Concurrent Speaker - Luis Fernando Revers

Abstract Title: APPLE FLC AND TBRR GENES REGULATE DORMANCY INTEGRATING HORMONAL STIMULUS AND MOLECULAR RESPONSES

Primary Author(s) and Institution(s): REVERS LF 1,2 , CATTANI AM 1,2 , SARTOR T 1,2 , SILVEIRA CP 1 , PASQUALI G 2 . 1 Centro Nacional de Pesquisa de Uva e Vinho, Empresa Brasileira de Pesquisa Agropecuária, Bento Gonçalves, RS, 95701-008, Brazil 2 Graduate Program in Cell and Molecular Biology, Centro de Biotecnologia, Federal University of Rio Grande do Sul, Porto Alegre, RS, 91501-970, Brazil Embrapa

Abstract

Type-B response regulators (TBRRs) act in the final steps of the cytokinin-signaling pathway. Previous studies revealed the presence of TBRR binding sites at the promoter region of MdoDAM1 and MdoFLC , important genes for apple dormancy regulation. The aim of this study is to understand the MdoDAM1/MdoFLC gene expression regulation through TBRRs in response to cytokinin stimulus. The transcript levels of the TBRR s, MdoFLC and MdoDAM1 genes were measured by RT-qPCR in 'Royal Gala' apple buds exposed to controlled chilling (3°C) and growth-promoting conditions (25°C). Results indicated that MdoFLC expression increases during chilling exposure, which contrasts with a drop in MdoDAM1 transcript levels. Two TBRR s have a peak expression during chilling accumulation, also contrasting with a decrease in MdoDAM1 expression. When buds were exposed to growth-promoting conditions, transcripts of other TBRR s increased, while at the same time MdoFLC expression dropped. The ability of TBRRs and MdoFLC to bind the MdoDAM1 promoter was evaluated by a transactivation assay using Arabidopsis thaliana protoplasts. Results showed that TBRRs and MdoFLC bind to the MdoDAM1 promoter, acting as repressor transcription factors. These findings suggest an important link

between cold exposure, hormonal stimulus, and molecular responses regulating dormancy and budbreak in apple.
