TRANSCRIPTOME ANALYSIS OF WHEAT UNDER DROUGHT

Poersch-Bortolon, LB[1*]; Pereira, JF[2]; Nhani-Junior, A[2];Soto Gonzáles, HHS[2]; Patricio, DI[2]; Torres, GAM[2]; Consoli, L[2]; Margis-Pinheiro, M[1]and Bodanese-Zanettini, MH[1].

[1]Dep. de Genética/PPGBM, Univ. Fed. do Rio Grande do Sul, Porto Alegre, RS, 91501-970. [2]Embrapa Trigo,Passo Fundo, RS, 99001-970.

*E-mail: lianebpoersch@yahoo.com.br

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Drought is a significant constraint for the increase of wheat production in Brazilian Cerrado. That abiotic stress causes dramatic reductions in crop productivity and the plant response is known to be a complex mechanism with several different pathways components being up or down regulated. A large number of genes related to drought tolerance mechanisms can be effectively identified in plants using next-generation sequencing (NGS) technology and such information can be useful to plant breeders. In this context, the aim of this work was to analyze the transcriptional profiling, obtained through NGS, in one Brazilian wheat genotype submitted to drought. Seeds of wheat cultivar MGS1 Aliança were grown in glasshouse using pots containing 6.5 kg of soil. Control plants were grown for 5 weeks at 100% of field capacity while, in the drought treatment, plants were watered for 2 weeks at 75 % of field capacity following 3 weeks of water deprivation. RNA extraction of pooled leaves or root tissues was carried out with Trizol (Invitrogen). The cDNAs were sequenced using Roche 454 FLX and the data was analyzed using GS De Novo Assembler v2.6. Similarity analysis was obtained using BlastX program and GO (http://www.geneontology.org/) database to obtain sequence annotation. Statistical analyses including control and treatment assembled (isotig) sequences for each set of samples were performed using the DEGseq R method. For leaf samples a total of 619.629 sequences was obtained originating 19.899 isotigs and 31.374 singletons. BLAST results showed that 27% of isotigs sequences are involved in biological processes (most represented by metabolic process), 27% in molecular function (catalytic activity), 22% are cellular components (cell part) and 24% are no hits. For root samples a total of 606.309 sequences was obtained originating32.085 isotigs and 40.377 singletons. BLAST results showed that 27% of isotigs sequences are involved in biological process (most represented by unclassified sequences); 28% in molecular function (binding); 21% are cellular components (cell part), and 24% are no hits. Statistical analysis showed that 1664 (being 1017 up-regulated) out of 19.899 isotigs in leaves and 2808 (being 1102 up-regulated) out of 32.085 isotigs in roots have statical significance at a p-value <0.001. In leaves 170 out of 1017 isotigs and, in roots, 592 out of 1102 isotigs showed a fold-changed greater than 5.The isotig with lower p-value in leaves was identified as a "photosystem Q(B) protein 2" and in roots was a protein with hydrolase activity, both being up-regulated. The information generated in this study is a valuable resource to identify genes from a Brazilian wheat cultivar, adapted to the Cerrado region, related to drought tolerance. To the best of our knowledge, this is the first report on NGS technology use to study wheat transcriptome in Brazil.

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