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Transcriptomic analysis of senescence in maize inbred lines with different rate of senescence

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Behind the physiological and metabolic changes occurring at maize senescence there are changes in the expression of thousands of genes. We carried out a genomewide analysis of the changes in gene expression during leaf senescence in seven inbred lines of maize which differed in the rate of senescence. The lines were planted in a randomized completely block design with 2 replications in a single environment. Chlorophyll content and CO2 exchange were measured from flowering to complete senescence each 15 days in the middle part of the ear leaf of three plants per plot. Samples of the middle part of the ear leaf of three plants per plot were taken and mixed each 15 days from flowering to complete senescence. RNA library construction and sequencing were performed with TruSeq Stranded mRNA Library Prep Kit and HiSeq 4000 PE100 platform (Illumina Inc). Following reads alignment, annotation, and a differential expression analysis we detected 1083 and 588 genes that were up and down regulated, respectively, during the senescence in all seven lines. Because the genes were consistently detected in different lines we are confident in their involvement in senescence. However, some genes were detected in some lines, but not in others. For example, 1747 genes were detected only in 3 of the lines, indicating that the genes expressed at senescence partially depend on the specific lines. The genes that were down regulated were mainly involved in photosynthesis, while the genes up regulated were related to catabolic processes. 196 of the differentially expressed genes codified for transcription factors; some of them are homologous to transcription factors found in Arabidopsis in different signaling pathways, for example, ATAF1, GLK1, PIF5, JUB1, or AtNAP.

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