ARRAY ANALYSIS THE GENE EXPRESSION ASSOCIATED WITH CHLOROPLAST DEVELOPMENT IN BARLEY ALBINA MUTANTS


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We investigated four albina and xantha barley mutants representing successive steps in chloroplast biogenesis and the corresponding wild type (WT) with the Affymetrix Barley1 GeneChip® (about 22,000 probe sets) to assess the variation of gene expression associated with chloroplast development. Chloroplast defective mutants display a large number of genes with altered steady state levels with respect to the corresponding WT. When mRNA isolated from leaves of mutant plants grown at 20°C were compared with mRNA extracted from green leaves of WT plants grown under the same conditions, a number of probe sets were found more than 3 fold up- or down-regulated. Since the mutants analyzed represent successive steps in the chloroplast biogenesis, the number of probe sets up- or down-regulated decreased according to progress in chloroplast development. Moving from alb-e16 (the most extreme mutant) to xan-b12 (the genotype closest to WT) the number of genes up- or down-regulated during growth at 20°C dropped from 1482 to 410 (from 12.6 to 4.7% of the probe sets detected as present in each comparison) suggesting a progressive normalization of the transcriptome as chloroplast development proceed. Genes caracterised by induction orn repression in the mutants respect to WT, were found to encode for protein localized in the chloroplast as well as for non chloroplast localized polypeptides, demonstrating the effetc of the chloroplast on the whole cell metabolism. The comparative analysis of gene expression in the four mutants allowed the identification of class of genes as well as of metabolic process whose normal expression is dependent from single steps of the chloroplast development. Beside the genes coding for photosynthetic related protein (down regulated in the mutants) our analysis has found a tight control of the chloroplast on the expression of the genes coding for the component of the protein synthesis machinery (ribosomal protein, tRNA ligase, elongation/initiation factors).