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Poster Abstract – D.31

PLASTID PROMOTER UTILIZATION IN POTATO TUBERS AND LEAVES

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Gene expression in non green plastids, such as amyloplasts, chromoplasts etc. is known to be lower compared with expression in chloroplasts. We performed Southern blot hybridization with DNA from potato leaves and tubers of different stages of development, and the results showed in this poster indicate that the observed low expression is not regulated at the level of genome copy number.

Most plastid genes and operons are transcribed by two distinct RNA polymerases - nuclear encoded RNA polymerase (NEP) and plastid-encoded RNA polymerase (PEP). Transcription by NEP or PEP through recognition of distinct promoters is one general mechanism of gene regulation during plastid development. We investigated plastid transcript abundance and transcription initiation sites of several plastid genes and operons in both potato tubers and leaves, in order to identify plastid promoters or 5' UTRs highly active in amyloplasts and with potential use in potato plastid transformation.

Steady state transcription levels in plastids were initially determined by cDNA arrays and Northern blots (Valkov V. et al. 2005 Proc. 2nd Solanaceae Genome Workshop. Ischia, Italy, Sept. 25th-29th, 2005, pp. 204) and further verified by oligo micro arrays, as reported in this poster. Based on results of such studies, several genes were chosen for detailed transcription analyses. Transcripts of *clp*P, *rps*16, *rbc*L, *atp*I, *rpo*B and *rrn*16 genes were the most abundant in potato tubers. To study plastid promoter utilization and to identify the transcript 5' ends, primer extension analyses were also performed. In potato tubers, mRNAs of genes having both NEP and PEP promoters derived predominantly from NEP promoters. For instance, transcripts from *PclpP*-53 (NEP promoter) were abundant and the only ones detectable in tubers, whereas, in leaves, transcripts derived from both NEP (positions -53, -173) and PEP (-95) promoters were observed. Our results also show that all mRNAs from the highly transcribed *rrn* operon derived from P1 (PEP) promoter in leaves, whereas, in tubers, transcripts from both P1 (PEP) and P2 (NEP) were detected.

In conclusion, our data indicate that some plastid genes are transcribed from different promoters in different organs of potato plants. In this way, transcription together with the post-transcriptional RNA processing and editing is an important part of the highly organized process of plastid genes regulation that needs additional and more detailed investigation in potato amyloplasts. Moreover, mapping of the active promoters is valuable for organ targeting and improvement of transgene expression in non green plastids.