

P002 Using tomato plant as a model system to study silencing-associated RNA degradation

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Post-transcriptional gene silencing (PTGS) or co-suppression of the endogenous and trans- genes was discovered in plants in 1990 and occurs frequently among tomato transformants. The extremely abundant mRNAs of certain ripening-specific genes such as polygalacturonase (PG), whose mRNA can be as much as 4% of the total mRNAs in ripening tomato fruit, are ideal for analysis of RNA degradation. Intermediate degradation fragments of the endogenous PG mRNA accumulated in PG-silenced tomato fruits, which were related to the small interfering RNA (siRNA)-associated cleavage of the PG transcript. Inverted repeats (IRs) introduced to the 5' untranslated region of a tomato 1-aminocyclopropane-1-carboxylic acid (ACC) oxidase 1 (ACO1) transgene resulted in high frequency and strong PTGS in transgenic tomato plants. This was associated with the generation of siRNAs from the 5' region or IRs and immediate downstream region, which contrasts with the preferential production of siRNAs from the 3' region of sense transgenes without IRs. Grafting transgenic over-expressers of the ACO1 gene onto the IRs-associated ACO1 silencing tomato plants induced silencing in the scions, provided that the level of ACO1 mRNAs in the shoots (used as scions) was over a threshold before grafting.