Analysis of Gene Expression Patterns during Seed Coat Development in Arabidopsis

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ABSTRACT The seed coat is important for embryo protection, seed hydration, and dispersal. Seed coat composition is also of interest to the agricultural sector, since it impacts the nutritional value for humans and livestock alike. Although some seed coat genes have been identified, the developmental pathways controlling seed coat development are not completely elucidated, and a global genetic program associated with seed coat development has not been reported. This study uses a combination of genetic and genomic approaches in Arabidopsis thaliana to begin to address these knowledge gaps. Seed coat development is a complex process whereby the integuments of the ovule differentiate into specialized cell types. In Arabidopsis, the outermost layer of cells secretes mucilage into the apoplast and develops a secondary cell wall known as a columella. The layer beneath the epidermis, the palisade, synthesizes a secondary cell wall on its inner tangential side. The innermost layer (the pigmented layer or endothelium) produces proanthocyanidins that condense into tannins and oxidize, giving a brown color to mature seeds. Genetic separation of these cell layers was achieved using the ap2-7 and tt16-1 mutants, where the epidermis/palisade and the endothelium do not develop respectively. This genetic ablation was exploited to examine the developmental programs of these cell types by isolating and collecting seed coats at key transitions during development and performing global gene expression analysis. The data indicate that the developmental programs of the epidermis and the pigmented layer proceed relatively independently. Global expression datasets that can be used for identification of new gene candidates for seed coat development were generated. These dataset provide a comprehensive expression profile for developing seed coats in Arabidopsis, and should provide a useful resource and reference for other seed systems.