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UNRAVELING THE ROLE OF MDGPAT6 IN APPLE SCAB RESISTANCE: LOCALIZATION AND FUNCTION ANALYSIS

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Apple scab, caused by the devastating fungal pathogen *Venturia inaequalis*, is a significant and widespread disease that poses a significant threat to apple-growing regions worldwide. This fungal pathogen specifically targets apple trees, leading to detrimental effects on both fruit quality and tree health. The disease manifests as distinct scab-like lesions on leaves, fruits, and even twigs, significantly impacting the overall yield and market value of apple crops. The ascomycete *V. inaequalis* thrives in mild and moist conditions, making it particularly problematic in regions with temperate climates. The pathogen has a complex life cycle, involving both sexual and asexual reproduction, allowing it to adapt and persist in various environments. It produces abundant conidia that are readily dispersed by wind, rain, and other means, facilitating the rapid spread of the disease within and between orchards. The *Vf2* gene, derived from a wild *Malus* species, has emerged as a crucial genetic factor conferring resistance to apple scab in Gala cv. apple plants. This resistance mechanism involves a sophisticated recognition system, following the gene-for-gene concept, wherein the *Vf2* gene product recognizes specific avirulence (*Avr*) factors produced by *V. inaequalis*. This recognition triggers a robust defense response, effectively halting the progression of the disease and conferring resistance. Previous research using yeast two-hybrid (Y2H) screening identified an interaction between *MdGPAT6* and a specific *Avr* gene from *V. inaequalis* in Golden Delicious cv. apples. Additionally, bimolecular fluorescence complementation (BiFC) screening in *Nicotiana benthamiana*

was conducted to localize the interactions between Avr-Vf2 and Avr-GPAT6, showing a plausible interaction at the plasma membrane level. GPATs (Glycerol-3-Phosphate Acyltransferases), including endoplasmic reticulum (ER) and mitochondrial GPATs, are membrane-bound enzymes involved in cutin, suberin, and storage lipid synthesis. In particular, GPAT6 is predicted to be a membrane-bound protein in the ER or plasma membrane and plays a crucial role in the accumulation of C16 cutin monomers. It has been observed that *GPAT6* expression is induced by P*hytophthora infestans* and, interestingly, *N. benthamiana* and tomato plants with mutated *gpat6* gene exhibit increased susceptibility to *Phytophthora* but enhanced resistance to *Botrytis cinerea*. This suggests a dual functionality of GPAT6 in influencing epidermal cell properties important for microbe interactions. In this study, our objective is to determine the localization of MdGPAT6 by expressing it with yellow fluorescent protein (YFP) in the heterologous system *Nicotiana tabacum*. By examining the subcellular localization of GPAT6, we aim to gain insights into its role and function in apple scab resistance.