# Differential Expression and Roles of the Vacuolar $H^+$-ATPase subunit c1 and c3 in Plant Growth

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The vacuolar $H^+$-ATPase (VHA) acidifies intracellular compartments and generates a proton electrochemical gradient to transport ion and metabolite across vacuolar and other membranes; although the potentially diverse functions of this complex pump in plant growth, development and adaptation are not understood. The multiple subunits that form a peripheral $V_1$ complex and an integral $V_o$ complex are encoded by a single gene or by multiple genes in Arabidopsis. Of these, the 16kda subunit c of the $V_o$ sector is encoded by the largest gene family with 5 members, Vha-c1 to Vha-c5. Analysis of promoter-Gus reporter gene showed c1 and c3 are differentially expressed. c1 is highly expressed in most tissues of the root and leaf, whereas c3 is expressed only in the root tip. In the flower, c1 is expressed in all flower parts including sepal, stamen, anther and stigma but not in the petal. In contrast, c3 is expressed only in pollen. In dark-grown etiolated seedlings, c1 is highly expressed in hypocotyls, but not in the cotyledons. In light-grown (blue or far red) seedlings, expression of c1 is high in cotyledons but not in hypocotyl. Thus c1 expression accompanies cell expansion, and its promoter activity is tissue-specific and developmentally regulated. To test in vivo function of each subunit c, homozygous plant containing ds-RNA constructs of c1 or c3 were analyzed. RT-PCR confirmed that 6 out of 10 independent transformants showed reduced levels of native RNA. Relative to wild type, roots of 7 d etiolated seedlings with dsRNA-c1 were shorter by 40%; surprisingly, the hypocotyls were only 15% shorter. Roots of plants with ds-RNA c3 were also inhibited though by only 20%. These results demonstrate that c1 and c3 subunits are differentially expressed, and that the $V_1V_o$-ATPase complexes formed by c1 or by c3 play differential roles in plant growth.

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Reference:

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