THE NICOTIANA PLUMBAGINIFOLIA PLASMA MEMBRANE H+-ATPase GENES ARE DIFFERENTIALLY REGULATED BY ENVIRONMENTAL SIGNALS

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The plasma membrane H^+ -ATPase represents the major cation-translocating P-type ATPase involved in activating various secondary ion and metabolites transport systems. In Nicotiana plumbaginifolia, this enzyme is encoded by nine pma (plasma membrane H^+ -ATPase) genes (pma 1-9). Eight of these have been shown, by means of the $\beta\beta$ -glucuronidase reporter gene, to be differentially expressed according to the cell type and developmental stage (Michelet et al., 1994; Moriau et al., 1999; Oufattole et al., 1999).

During the current work, we have analyzed the response of the *pma* genes to environmental factors. Salt and low pH stress tests were performed on young plantlets grown *in vitro*. When controlled by the *pma2* and *pma4* transcription promoters, expression of *gusA* was found to be enhanced in root tissues in the presence of 50 mM NaCl. However, under the control of the *pma3* and *pma5* promoters, an induction was only seen at a higher concentration (150 mM). In the shoots, 150 mM NaCl induced the expression of *pma1*- and *pma5-gusA* in the guard cells and the cotyledons, respectively; increasing NaCl to 200 mM allowed strong *gusA* expression, driven by the *pma6* promoter in the very young leaves. At low external pH (4.5 and 4.0), expression of *pma2*- and *pma4-gusA* genes was found to be increased in root tissues only.

Plant parasitic nematodes induce the formation of permanent feeding sites consisting of large transfer cells where intense nutrient transport is expected to take place. Infection of the transgenic tobacco with the root-knot nematode *Meloidogyne incognita* showed strong GUS staining in the *pma4* transformant and lower GUS activity with *pma1*, 2 and 3. On the other hand, infection by the cyst-forming *Globodera tabacum* induced GUS expression only in the *pma4* transformant.

These data therefore indicate that *pma* genes are activated by various abiotic as well as biotic environmental factors and open the way forward to a detailed analysis of cissequences involved in this response.

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