ABSTRACT

Plant formins define a distinct subfamily. The presence in most Arabidopsis formins of sequence motifs typical or transmembrane proteins suggests a mechanism of membrane attachment that may be specific to plant formins, and indicates an unexpected evolutionary flexibility of the conserved formin domain.

INTRODUCTION

Background Some mechanisms involved in cell morphogenesis, such as membrane vesicle transport, are conserved at least among crown eukaryotes (metazoa, fungi and plants), whereas others, such as those involving extracellular structures or the precise roles of different Rho-like GTPases, are not. Yet other cellular processes, such as cytokinesis, often recruit conserved proteins to accomplish superficially dissimilar tasks (for example, budding, cleavage or phragmoplast-based cell division of plant cells). For many morphogenetic mechanisms, the question of evolutionary conservation remains unresolved because available information is limited to one or a few model organisms. For example, this is the case for the molecular mechanisms that ensure the communication between the cytoskeleton and the surface of the cell. However, the recent increase in the data available from a number of genome projects allows wide-ranging searches for homologs of known components of signaling and morphogenetic pathways. The results of such searches can lead both to experimentally testable hypotheses and to general conclusions regarding the evolution of morphogenetic processes. Formins, also known as formin homology (FH) proteins, are proteins implicated in cellular and organismal morphogenesis of both metazoa and fungi. On the cellular level, they are involved in the establishment and maintenance of cell and/or tissue polarity, in cytokinesis and in the positioning of the mitotic spindle. They interact directly or indirectly with actin, profilin, Rho-like GTPases, the yeast Spa2 protein and septins, proteins containing SH3 or WW domains, dynein and microtubules. The yeast formin homolog encoded by BNI1 is localized to the cell periphery and participates in positioning cortical actin patches towards distinct regions of the plasma membrane. Some kind of contact with the plasmalemma (in addition to that mediated by a Rho-like GTPase) might therefore be expected, although there is no evidence as yet for such a contact. Furthermore, metazoan formins are believed to be cytoplasmic or nuclear proteins. Nothing is known about formin function in plants, although the existence of two Arabidopsis thaliana proteins containing the conserved formin-homology 2 (FH2) domain has been reported recently. Given that all known formins represent a well-defined family, this class of proteins may be a good candidate for a systematic genome sequence search. Here, I present the results of such an approach, which has led to the identification of putative plant formin genes, as well as to the finding that the evolutionarily old formin domain may be used in a number of different ways and contexts ('modules' as defined by Hartwell et al.) by recent eukaryotes.

CONCLUSION

Conclusions A systematic search of the available Arabidopsis genomic and cDNA sequences revealed the presence of eight genes encoding proteins that define a novel subfamily of the formin family. At least six out of eight Arabidopsis formins appear to be integral membrane proteins. This indicates a mechanism of membrane localization that may be specific to plants and functionally related to a possible role for formins in the communication between the plant cell and extracellular structures.