BIOINFORMATIC SEARCH FOR PLANT HOMOLOGUES
OF ANIMAL STRUCTURAL MAPs IN THE ARABIDOPSIS
THALIANA GENOME

PAVEL A. KARPOV* AND YAROSLAV B. BLUME
Institute of Cell Biology and Genetic Engineering, Natl
Academy of Sciences of Ukraine, acad. Zabolotnogo str., 148,
Kiev, 03680 Ukraine

Abstract. Although various plant microtubule-associated proteins (MAPs) have been described because of their role in modulating microtubule functions, the full complement of these important sequences has not yet been described. Taking into account the high level of homology between animal and plant tubulins, and the potential conservation of their MAP binding domains, we carried out a bioinformatic investigation of the MAP1, MAP2, tau protein, and MAP4 families from animals and humans. The gene-identification strategy, utilizing site-based and comparative methods, allowed us to identify amino acid motifs that are conserved within each MAP family. According to these amino acid motifs we designed corresponding nucleotide motifs in IUPAC code, accommodating potential codon polymorphism by applying the universal symbols representing all possible substitutions. Scanning the complete sequences of all five Arabidopsis thaliana chromosomes, we identified candidate coding sequences for plant homologues of animal structural MAPs. Furthermore, we identified 200 loci (i.e., 178 of MAP1 and 22 of MAP2 and tau) that are of interest as potential chromosomal regions for plant structural MAPs. Interestingly, consensus regions for MAP4 were not identified in A. thaliana. Chromosomal locations for three previously known plant homologues of MAP1 (i.e., AtEB1a, AtEB1b and AtEB1c) were also identified in the A. thaliana genome.

*Author to whom correspondence should be addressed: P. Karpov, Institute of Cell Biology and Genetic Engineering, National Academy of Sciences of Ukraine, acad. Zabolotnogo str., 148, Kiev, 03680 Ukraine; e-mails: Karpov_Pavel@univ.kiev.ua, Karpov.P.A@gmail.com
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1. Introduction

Structural microtubule-associated proteins (MAPs) are the fibrillar proteins, which play an important role in the regulation of microtubule functions. They increase the rate of polymerization and assembly, and stabilize microtubules.\(^1,2\) MAPs, binding reversibly to microtubules, promote both their polymerization, organization into bundles, as well as their resistance to depolymerizing factors.\(^3-5\). Thus structural MAPs stabilize microtubules and support their interactions with other cell components.\(^6,7\) Numerous specific families of plant MAPs, such as MAP18\(^2\) in *A. thaliana*; MAP60 in *Daucus carota*\(^8\); MAP65 in *A. thaliana*,\(^9-12\) *Nicotiana tabacum*\(^13\) and *D. carota*\(^14\); MAP70 in *A. thaliana*\(^15\); MAP120 in *D. carota*\(^16\); MAP190 in *A. thaliana*\(^9\) and *N. tabacum*,\(^17,18\) etc. have been identified. Most of the plant MAPs discovered so far have homologs in eukaryotes, but not all animal or fungal MAPs are present in plants.\(^6,11,19\)

The identified animal and human structural MAPs can be divided into two groups: Type I includes MAP1 proteins and Type II includes MAP2, tau and MAP4 proteins (Figure 1). MAP1a, MAP1b and MAP1c, which make up the MAP1 family, bind to microtubules differently than other MAPs, namely, by the force of charge interactions. Microtubule binding by MAP1 is closely associated with EB1 domain, which interacts directly with tubulin.\(^20\) While the COOH-termini of these MAPs binds the microtubules, the NH\(_2\)-termini bind other components of the cytoskeleton or the plasma membrane to control the distribution of microtubules within the cell. As a rule animal analogs of the MAP1 are observed mainly in axons and dendrites of neurons.\(^21\) It was shown previously, that the *A. thaliana* genome contained three EB1 genes designated AtEB1a, AtEB1b, and AtEB1c. Each of the predicted proteins contains conserved domains and shares significant sequence similarity with EB1 proteins from others eukaryotes. It was predicted that all three AtEB1 proteins would contain a conserved amino-terminal calponin homology domain required for MT binding in addition to a conserved coiled-coil (EB1) domain, which is thought to mediate protein-protein interactions.\(^20,22\) So, among hypothetical plant homologues, they seem to be the most similar to animal structural MAPs.\(^23,24\)

All Type II proteins have microtubule-binding repeats near their carboxyl ends (Figure 1),\(^25\) each containing a conserved KXGS motif, which can be phosphorylated.\(^26,27\) Reversible phosphorylation of the KXGS motif induces its association/dissociation with microtubules.\(^26,28,29\) Also,