

T7: Role of Ancient Tubulin FtsZ in Moss Division Processes

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Integral part of bacterial division machineries is the protein FtsZ (*filamentous temperature sensitive Z*). Despite only weak sequence similarities between FtsZ and tubulin, both protein families share convincing structural and biochemical similarity, suggesting FtsZ as the evolutionary ancestor of tubulin.

In plants, several FtsZ proteins are encoded by two small nuclear gene families designated FtsZ1 and FtsZ2. For some of these homologues it has been proven experimentally that they are essential for chloroplast division. Furthermore, certain FtsZ proteins polymerise to a ring-like structure at the division site of plastids. Therefore, bacterial cell division and eukaryotic plastid division share at least the essential role of FtsZ in the division process. However, while most eubacteria possess only one *ftsZ* gene, plants harbour several different *ftsZ* homologues encoded by two different gene families, indicating a more complex role of FtsZ in plants when compared to bacteria.

In transiently transfected moss (*Physcomitrella*) protoplasts, FtsZ2::GFP fusion proteins polymerised to highly organised networks within the plastids. Strikingly, models drawn from TEM results demonstrating microtubule-like structures within plastids match with the FtsZ networks found in chloroplasts. Thus, we suggested the term ‘plastoskeleton’ for these filamentous networks. This plastoskeleton could help the chloroplasts to keep or change their shape in different tissues.

We will present a phylogenetic analysis of the FtsZ-families in plants as well as a detailed analysis of the sub-cellular localisation of each single member in the moss *Physcomitrella* utilising *ftsZ::gfp* fusion constructs and transient transformation techniques. These transient assays provide –beside classical knockout approaches- functional evidence for the role of FtsZ in division processes. Furthermore, co-transfection and fluorescence resonance energy transfer (FRET) provide the first evidence for the in-vivo interaction of different FtsZ isoforms. Proteomic approaches will be described to unravel the dynamic interaction of the FtsZ isoforms as well as to isolate novel FtsZ-interacting proteins.

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