Selective degradation of ARF monomers controls auxin response inMarchantia

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Abstract

The plant signaling molecule auxin controls a variety of growth and developmental processes in land plants. Auxin regulates gene expression through a nuclear auxin signaling pathway (NAP) consisting of a ubiquitin ligase auxin receptor TIR1/AFB, its Aux/IAA degradation substrate, and the DNA-binding ARF transcription factors. While extensive qualitative understanding of the pathway and its interactions has been obtained by studying the flowering plant Arabidopsis thaliana, it is so far unknown how these translate to quantitative system behaviour in vivo, a problem that is confounded by large NAP gene families in this species. Here we used the minimal NAP of the liverwort Marchantia polymorpha to quantitatively map NAP protein accumulation and dynamics in vivo through the use of knock-in fluorescent fusion proteins. Beyond revealing the native accumulation profile of the entire NAP protein network, we discovered that the two central ARFs MpARF1 and MpARF2 are proteasomally degraded. This degradation serves two functions: it tunes the stoichiometry of auxin-responsive, positively acting MpARF1 and auxin-independent, negatively acting MpARF2, thereby permitting auxin response. Secondly, through mapping a minimal degradation motif, we found that degradation is likely selective for MpARF2 monomers and favours accumulation of dimers. Interfering with MpARF1:MpARF2 stoichiometry or preventing degradation of MpARF2 monomers caused strong growth defects associated with auxin response defects. Thus, quantitative analysis of the entire Marchantia NAP, allowed to identify a novel regulatory mechanism in auxin response, built on regulated ARF degradation.