Poster Presentation

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Structure basis for E2-E3 interaction in the plant Atg conjugation system

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Autophagy is an intracellular degradation system conserved from yeast to mammal that isolates the cellular materials and organelles into a double membrane vesicle, termed an autophagosome, for degradation. Autophagosome formation depends on Atg8 and Atg12 conjugation systems, which produce Atg8-phosphatidylethanolamine (PE) conjugate as a final product that plays a crucial role for promoting autophagy. Another conjugate, Atg12-Atg5, functions as E3 and promotes transfer of Atg8 from Atg3 (E2) to PE. Here, we identified the minimum binding region of Atg3 for Atg12 by in vitro pull-down assay using Arabidopsis thaliana (At) homologs and crystallized the AtAtg12b-AtAtg3 peptide complex. The obtained crystal (P64, a = 128.5, b = 128.5, c = 163.2 Å) diffracted X-rays to 3.2 Å resolution, and its structure was determined by the molecular replacement method. AtAtg12b forms a swapping dimer in the crystal. The side-chain of AtAtg3 Met157 is bound deeply to the hydrophobic pocket of AtAtg12b consisting of Phe30, Val41, and Phe44. The importance of AtAtg3 Met157 for AtAtg12b binding was confirmed by mutational analysis. These data establish the basis for E2-E3 interaction in the plant Atg system.

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