

Structure of Plant ATG12, a Ubiquitin-like Modifier Essential for Autophagy

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Atg12 is a post-translational modifier that is activated and conjugated to its single target, Atg5, by a ubiquitin-like conjugation system [1]. The Atg12-Atg5 conjugate is essential for autophagy, a starvation-induced response that mediates the bulk degradation of cytoplasmic components in lysosomes/vacuoles. In autophagy, a double-membrane structure called an autophagosome sequesters cytoplasm and fuses with the lysosome/vacuole to deliver its contents into the organelle lumen. The Atg12-Atg5 conjugate plays a critical role for autophagosome formation [1], but its mechanism remains to be elucidated. In order to clarify the role of Atg12 in autophagy, we determined the crystal structure of *Arabidopsis thaliana* (At) ATG12 at 1.8 Å resolution by MIRAS phasing.

In spite of no-detectable sequence homology with ubiquitin, the structure of AtATG12 shows a ubiquitin fold, strikingly similar to those of mammalian Atg8 homologs such as LC3 [2]. Two types of hydrophobic patches are present on the surface of AtATG12: one is conserved in both Atg12 and Atg8, while the other is unique to Atg12. Considering that they share Atg7 as an E1-like enzyme, we suggest that the first hydrophobic patch is responsible for the conjugation reaction, while the latter is involved in Atg12-specific functions.

[1] Mizushima N., Noda T., Yoshimori T., Tanaka Y., Ishii T., George M.D., Klionsky D.J., Ohsumi M., Ohsumi Y., *Nature*, 1998, **395**, 395. [2] Sugawara K., Suzuki N.N., Fujioka Y., Mizushima N., Ohsumi Y., Inagaki F., *Genes Cells*, 2004, **9**, 611.

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