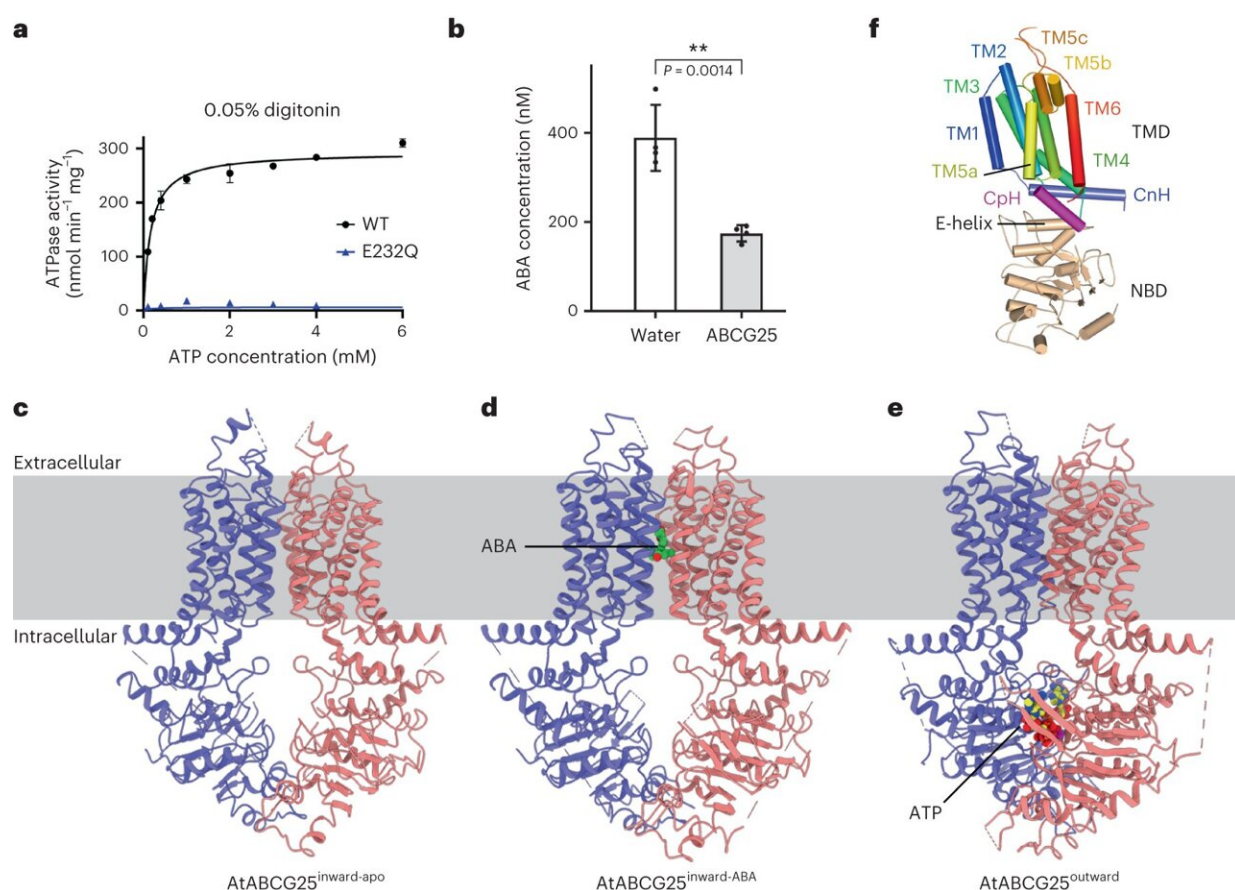


Study reveals molecular mechanism underlying cross-membrane transport of plant hormone abscisic acid

September 5 2023, by Liu Jia



Activity and overall structure. **a**, ATPase activity of AtABCG25. Error bars are mean \pm s.e.m. ($n = 4$ for wild type (WT) and EQ mutant). **b**, Transport activity of AtABCG25. The y axis is the ABA concentration in the final 50 μ l extract of *Xenopus* oocytes for mass spectrometry analysis. Bars are mean \pm s.d. Points represent biologically independent experiments ($n = 4$ for H₂O and ABCG25).

Two-tailed t -test was performed. $**P = 0.0014$. **c–e**, Overall structures of AtABCG25 in inward-facing apo conformation (AtABCG25^{inward-apo}) (**c**), ABA-bound pre-translocation conformation (AtABCG25^{inward-ABA}) (**d**) and outward-facing post-translocation (occluded) conformation (AtABCG25^{outward}) (**e**). The two protomers of AtABCG25 are colored in purple and pink, respectively. **f**, The structure of AtABCG25 protomer is represented as cylinders. The TMD helices are shown with cylinders colored in rainbow, and the CpH and CnH are shown as cylinders colored in magenta and light-blue, respectively; the secondary structures of the NBD are colored in gold. Credit: *Nature Plants* (2023). DOI: 10.1038/s41477-023-01509-7

Abscisic acid (ABA) is a key plant hormone produced in response to abiotic stress such as drought and salt. It is mainly synthesized in roots and vascular tissues and transported to specific sites to exert physiological functions. Several ABA transporters have been identified; however, the molecular mechanism underlying specific binding and cross-membrane transport of ABA remains unknown.

In a study published in *Nature Plants*, researchers reported the structural study of the [abscisic acid](#) transporter ABCG25 from Arabidopsis (AtABCG25). The study was mainly conducted by Prof. Zhang Peng's group from Center for Excellence in Molecular Plant Sciences of the Chinese Academy of Sciences, collaborating with Prof. Chen Zhenguo's group from Fudan University.

AtABCG25 protein was expressed and purified through heterologous expression, and different 3D structural conformations of AtABCG25, including inward-facing apo conformation (AtABCG25^{inward-apo}), ABA-bound pre-translocation conformation (AtABCG25^{inward-ABA}) and outward-facing occluded conformation with ATP bound (AtABCG25^{outward}), were captured by single-particle cryo-electron microscopy.

Structural analysis revealed the homodimeric structure of AtABCG25, the binding site of ABA, and that the key residues dictate the ABA specific binding. Structural based transport assay and binding analysis further confirmed the structural data.

Based on the structure analysis, a "gate-flipper" model was proposed to summarize the dynamic process of AtABCG25-mediated ABA cross-membrane transport.

This study represents the first 3D structure of ABA transporter, which not only reveals the [molecular mechanism](#) of specific binding and cross-membrane transport of plant hormone ABA, but also provides new insights for the study of plant ABC transporters.

More information: Xiaowei Huang et al, Cryo-EM structure and molecular mechanism of abscisic acid transporter ABCG25, *Nature Plants* (2023). [DOI: 10.1038/s41477-023-01509-7](https://doi.org/10.1038/s41477-023-01509-7)

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