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Phosphate unloading in ectomycorrhizae: why is the *HcPT2* transporter of *Hebeloma cylindrosporum* a good candidate?

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It is well known that ectomycorrhizal (ECM) fungi improve the growth of their hosts by providing growth-limiting nutrients and particularly inorganic phosphate (Pi). However, the molecular players driving the Pi allocation from the fungus to the host are largely unknown thus far. In the ECM association between *Pinus pinaster* and *Hebeloma cylindrosporum*, we hypothesized that one of the three Pi transporters identified in the fungal genome (named *HcPT1.1*, *HcPT1.2* and *HcPT2*) could be more specifically involved in Pi unloading in the Hartig net. To address this hypothesis, we combined microscopy, physiology and fungal genetic approaches to unravel the role of each Pi transporter. Immuno-localization of Pi transporter proteins showed that only *HcPT1.1* and *HcPT2* are localized in the Hartig net, indicating that these two proteins could play a role in Pi efflux in the ECM. We produced transgenic lines, either down- (RNAi) or over- (OE) expressing one of the two proteins. We used them to measure *in vitro* Pi fluxes as well as P accumulation in young *P. pinaster* seedlings. Our experiments showed that only OE-PT2 lines were able to increase *in vitro* Pi effluxes and shoot P accumulation of pine seedlings whereas the OE-PT1.1 lines increased only root P accumulation. Taken as a whole, these results support that the *HcPT2* Pi transporter is a key component of the fungal Pi unloading machinery in the Hartig net of ECM.