Domestication genetics in the mysterious Ethiopian pea *Pisum abyssinicum*

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Studies of crop domestication provide valuable insight into the history of agriculture and the genetic basis for adaptation. In the temperate legume pea (*Pisum* spp.) two independently-domesticated forms are known: the widespread *P. sativum,* one of the world's oldest crops, and *P. abyssinicum*, a minor form restricted mainly to Ethiopia [1]. Little is known about theorigin of *P. abyssinicum,* orthe genetic control of key domestication traits such as pod indehiscence and reduced dormancy, relative to *P. sativum.* However, given that wild *Pisum elatius* does not flower under short photoperiods, the low-latitude distribution of *P.abyssinicum* implies that the ability to flower early under short photoperiods may have also been important in its domestication, unlike *P. sativum*.

Analysis of a *P. abyssinicum x* wild *P. elatius* cross identified three QTL for flowering time and four for dormancy, all of which co-located with QTL in corresponding analyses of domestication traits in *P. sativum* [2]. Initial sequence-level analysis has revealed contrasting histories of key candidate flowering time genes in *P. abyssinicum*, with *FTa3* and *TFL1c* more similar to *P. elatius* and *P. sativum* groups, but *FTa1* showing surprisingly high affinity with a second wild species *P. fulvum*. This work implies a complex origin of *P. abyssinicum* independent of *P. sativum,* and further highlightsa central role of *FT/TFL1* genes in crop legume evolution.

***References:***

[1] Kosterin O. (2017) Abyssinian pea – a problematic taxon Act. Biol. Siber. 3, 97-110

[2] Williams, O. et al. (2022) The genetic architecture of flowering time changes in pea from wild to crop. J. Exp. Bot. 10.1093/jxb/erac132