One of main aims of this study was to determine the phenotypic manifestation of the derived allele of *FAR5* gene which was positively selected in the course of the colonization of the alpine environment. FAR5 is a primary alcohol-forming fatty acyl-coenzyme A reductase. (Wang *et al.*, 2015) Because of its role in the fatty alcohol biosynthesis, we used the GC-MS approach to compare the variation of fatty compounds in plants with different genotypes. There was a significant difference in the proportion of C18:0-OH to C16:0-OH between plants with derived alpine allele and plants with ancestral foothill allele. The native genomic background of the plants didn’t play a significant role. Plants with the ancestral foothill allele

produced more C18:0-OH than C16:0-OH whereas plants with derived alpine allele produced more C16:0-OH when compared to C18:0-OH.

FAR5 was noted to influence production of primary alcohols of different lengths in wheat (Wang *et al.*, 2015), but data from the most closely related model organism, *Arabidopsis thaliana,* support the role in producing C18:0-OH (Domergue *et al.*, 2010; Chacón *et al.*, 2013; Vishwanath *et al.*, 2013). Moreover, by a series of domain swaps particular amino acids underlying substrate specificity of the enzyme were determined. One of the amino acids was at position 377. (Chacón *et al.*, 2013) From our data we know that this position is also altered in the derived alpine allele. Apart from this amino acid also the position 355 is mentioned to affect the substrate specificity. In particular, amino acids at both positions 355 and 377 needed to be altered to fully shift the substrate specificity of the enzyme. (Chacón *et al.*, 2013) However, our genomic data didn’t suggest any selective change at the position 355. It is possible that if this amino acid was also altered, the difference in fatty alcohol composition would be more striking.

The fatty alcohols are utilized during protection against abiotic and biotic stresses. They are part of the suberin layer in roots. (Domergue *et al.*, 2010; Vishwanath *et al.*, 2013; de Silva, Nayana D.G. *et al.*, 2021) However the method we used to extract lipidic compounds doesn’t allow us to exactly determine that the difference in composition of fatty alcohols comes from suberin. It could be from other lipidic parts of the roots. Nevertheless, it was shown that the shorter the alcohol chain, the more likely it is to be part of suberin. (Vishwanath *et al.*, 2013) Therefore we can’t rule out the possibility of different *FAR5* alleles affecting suberin composition. Apart from roots the *FAR5* expression was also shown in wounded leaves of *A. thaliana* where it probably helps with forming a healing tissue. (Domergue *et al.*, 2010) The effect of wounding was perceptible also in our samples. Five days after wounding the leaf, there was a significant induction of fatty alcohols production in all the plants. The genotypes differed only in types of fatty alcohols induced. Despite the amount of information about the specificity and stability of the enzyme, the overall effect on the plant life remains unknown.

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