

## Editing of barley susceptibility gene for plant virus resistance

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Virus infection needs plant factors for translation, replication, systemic movement and suppression of the RNAi-based plant response. Genes encoding such factors are considered as the susceptibility (S) genes and their impairment can lead to the loss-of susceptibility. Potyviridae represents the largest family of plant viruses with ssRNA<sup>+</sup> genome. The RNA, devoid of 5'cap structure, is linked to VPg protein, which is crucial for many processes including viral translation, which is initiated by association of VPg with host eIF4E. Because of this, many virus resistance genes have been mapped to mutations of *eIF4E*.

Identification of *eIF4E* gene family in barley, characterization of the genes and constructing components for the CRISPR/Cas9-based editing will be presented. A genome-wide analysis was conducted to retrieve the putative uncharacterized *eIF4E* paralogues in *Hordeum vulgare* L. genome. The *in silico* identification and characterization revealed three paralogues of eIF4E proteins (*eIF4E1*, *eIF4E2*, *eIF4E3*) and one member of *eIF4E*-iso *eIFiso4E* in two different genome assemblies of barley i.e., MorexV3, Golden Promise V1. Interestingly, in another genome assembly (*H. vulgare* IBSC v2), we found 6 paralogues of eIF4E proteins (*eIF4E1*, *eIF4E2*, *eIF4E3*, *eIF4E4*, *eIF4E5*, *eIF4E6*) and one member of *eIF4E*-iso. The above-mentioned eIF4E proteins were characterized based on phylogeny, domain and motif analysis, protein physicochemical characteristics, gene structure prediction, chromosomal localization while using *A. thaliana eIF4E* gene family as reference proteins. Relative expression of the paralogs in leaves inoculated with BaYMV and BaMMV was analysed and discussed in relation to the putative barley *eIF4E* gene involved in virus infection.

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