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Study of transferability of *H. vulgare* EST markers for characterization of introgression bread wheat – *H. marinum* subsp. *gussoneanum* lines

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H. marinum subsp. *gussoneanum* (2*n* = 28) is a valuable source of genes that determine resistance to abiotic stresses (salinization, flooding, waterlogging, temperature severe changes). In addition, accessions of this barley with a high content of protein in seeds have been isolated. These traits may be transferred to wheat, since *H. marinum* subsp. *gussoneanum* is able to cross with bread wheat. To efficiently obtain introgression genotypes of wheat with the genetic material of barley, it is necessary to use methods for reliable and quick identification of its chromosomes in the *T. aestivum* background. For this purpose, we evaluated the possibility of using *H. vulgare* EST markers for studying wheat – *H. marinum* subsp. *gussoneanum* substitution and addition lines of bread wheat. The work included the developed lines of bread wheat, carrying the chromosomes of *H. marinum* subsp. *gussoneanum*. The presence of wild barley chromosomes was detected using GISH and C-banding. The applicability of 78 EST markers localized in different chromosomes of *H. vulgare* barley for analysis of *H. marinum* ssp. *gussoneanum*. Of all the markers studied, 35 were suitable for the analysis of lines carrying the chromosomes of *H. marinum* ssp. *gussoneanum*. At the same time, for 20 EST markers out of these 35, localization in the short or long arm of *H. vulgare* chromosomes is known. The identified EST markers specific for *H. marinum* ssp. *gussoneanum* were amplified in the lines obtained in our work with the chromosomes of wild barley. It was shown that the results of the identification of chromosomes of barley using EST markers confirmed the C-banding data. Thus, it has been established that the *H. vulgare* EST markers can be successfully used to identify the chromosomes of the *H. marinum* subsp. *gussoneanum*.
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