DISTRIBUTION OF ALLELES OF HvITR1 GENE ENCODING CMe (BTI-CMe) TRYPSIN INHIBITOR WHICH RELATED WITH COLLOIDAL STABILITY OF BEER AMONG BARLEY VARIETIES REGISTERED IN UKRAINE

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The biotechnological analysis of modern barley varieties of national and foreign origin for the presence of valuable SE-ve genotypes was done. Identification of the allelic status of the gene was performed among 109 barley samples using the developed multiplex PCR system for SNAP molecular markers. Among the studied varieties SE+ve allele was identified in 75 barley samples and the other contained SE-ve allele. 6 samples which revealed both alleles SE+ve and SE-ve were heterogeneous (+/-).

The obtained results were compared with the data of the State register of plant varieties suitable for dissemination in Ukraine and showed that 8 samples referred to as forage, contained SE+ve allele and none of them were SE-ve allele. Of 38 varieties, which quality was identified as suitable for brewing, 19 contained SE+ve allele, the rest — allele SE-ve. The results of performed analysis of the spring barley collection for allelic composition of HvITR1 gene are of great practical importance as for the correct selection of mating pairs for malting breeding, for the selection of elite plants in breeding populations, or evaluation of barley seeds for beverage brewing purposes.

**Key words:** barley biotechnology, haze beer, CMe protein.

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