



significantly increasing the volumes of his harvesting, uncontrollable collecting of medicinal plants in the wild nature, and also because of chemical and radiation environmental pollution.

The search of ways to compensation for a deficiency of medicinal plants has led us to development of innovative biotechnological methods of producing ecologically pure raw materials of medicinal plant *Digitalis purpurea* L. and biologically active substances of a phytogenesis on the basis of the hairy roots (HRs) technology.

Application for this purpose «hairy roots» culture of purple foxglove has a number of advantages in comparison with use of wild-growing and plantation raw materials of *Digitalis purpurea* L. There are a possibility of year-round cultivation of biomass, independence of climatic or geographical factors, lack of influence of various pests, pesticides and pollutants, the ability to fast receiving sufficient number of homogeneous biomass in aseptically controlled conditions.

HRs cultures of *Digitalis purpurea* L. were initiated by infecting the leaf explants with wild strains of soil bacterium *Agrobacterium rhizogenes* (strains 15834, A4, 8196, R-1601). For increasing of production and accumulation of roots have been applied elicitation. As elisitors we used progesteron, salicylic acid, selenium, gibberellic acid with a cyclodextrin. Productivity of culture behind indicators of wet and dry weight when using elisitors has increased by 2,5 times. Extracts obtained from hairy root of foxglove were analyzed by HPLC to determine total amount of cardiac glycosides for purple foxglove. HPLC-analysis showed that the HRs culture synthesizes all complex of the secondary metabolites typical for intact plants.

In conclusion, it is important to note that the «hairy roots» culture of *Digitalis purpurea* L. is characterized by stability, high growth rates, high level of biosynthesis of cardiac glycosides which allows to use HRs culture as an alternative source of ecologically pure raw plant materials and also biologically active compounds based on it. ❧

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GENOTYPING OF *TRITICUM AESTIVUM* L. CULTIVARS WITH IRAP MARKERS

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Genetic diversity analysis is efficiently used to select donor plants with valuable features, to obtain new cultivars and by plant breeders to protect intellectual property rights. Different types of DNA markers are utilized for this purpose. Inter-Retrotransposon Amplification Polymorphism (IRAP) markers are considered to be perspective. IRAP analysis is based on the detection of polymorphism between two retroelements with unidentified localization in the genome [1].

The purpose of the work was to compare genotypes of 16 wheat cultivars from the IPPG NAS of Ukraine and the MIW NAAS of Ukraine using multilocus IRAP markers.

The subject of the study was 16 bread wheat cultivars: Bohdana, Favorytka, Hileia, Zolotokolosa, Kryzhynka, Natalka, Pereiaslavka, Podolianka, Slavna, Smuhlianka, Sotnytsia, Spasivka, Shchedrivka Kyivska, Vesnianka, and Yatran 60. Molecular genetic analysis based on polymerase chain reaction (PCR) was performed with specific combination of primers: Sukkula / Wilma 2107, Sukkula/Nikita, Sukkula/Sabrina [2].



Table 1 illustrates the presence or absence of polymorphic fragments for 16 wheat cultivars that were received during the IRAP analysis.

Table 1. Polymorphic bands identified for 16 wheat cultivars using IRAP analysis

Cultivar of wheat	Sukkula/Wilma 2107			Sukkula/Nikita			Sukkula/Sabrina		
	179bp	214bp	469bp	439bp	400bp	361bp	605bp	81bp	138bp
Pereiaslavka	-	+	+	+	-	-	+	-	-
Podolianka	-	+	+	+	+	-	+	-	-
Yatran' 60	-	+	+	+	+	+	+	-	-
Natalka	-	+	+	+	+	+	+	-	-
Kryzhynka	-	+	+	+	+	-	-	-	-
Vesnianka	+	+	-	+	-	-	+	-	-
Bohdana	-	-	+	+	+	+	+	-	-
Slavna	-	+	+	+	-	-	-	-	-
Spasivka	-	-	+	+	-	+	+	-	-
Sotnytsia	-	-	+	+	-	-	+	+	-
Hileia	-	-	-	+	+	+	+	+	-
Shchedrivka Kyivska	-	-	+	+	+	-	+	+	-
Malynivka	-	-	+	+	+	+	+	+	-
Zolotokolosa	-	-	-	+	-	-	+	+	-
Favorytka	-	-	+	+	+	-	+	+	+
Smuhlianka	-	-	+	-	-	-	+	+	+

“+” – presence of polymorphic bands, “-” – absence of polymorphic bands...

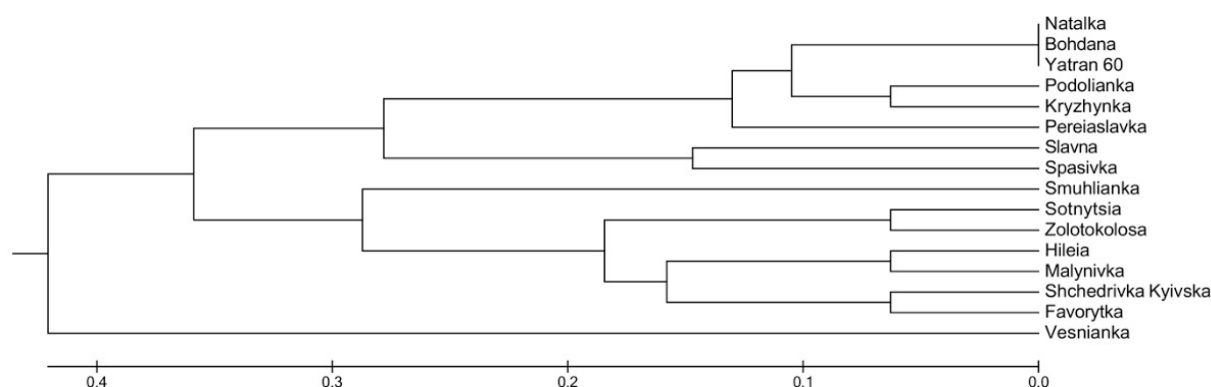


Fig. 1. Dendrogram showing similarity and clustering of 16 wheat genotypes.

The dendrogram (Figure 1) contains two main clusters. The first one consists of 15 wheat cultivars, and the only one cultivar Vesnianka formed the second cluster.

IRAP analysis made it possible to detect genetic polymorphism of cultivars. It showed varieties Natalka, Bohdana, and Yatran 60 possess very similar genotypes, whereas cultivar Vesnianka had the biggest genetic distance from the others. The proposed system of DNA markers will be useful for homogeneity and compliance verification of cultivars.

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