

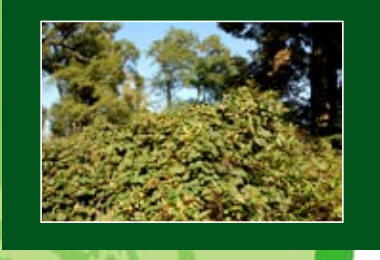
Variability of wild hops (Humulus lupulus L.) in Czech Republic



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The aim of the wild hops study is to obtain some new genetic resources suitable for hop breeding, which will be resistant to mycosis and dryness. It is supposed that natural selection has selected resistant plants and susceptible ones did not go through this natural process. Wild hops can be divided into the following three groups with regard to their origin:

1. Original wild hops, which have not been used for commercial hop growing yet.
2. Escaped original domestic hops, which used to be cultivated in the vicinity of towns and monasteries where beer was brewed.
3. New genotypes of wild hops, which arise due to mutual pollination. New genotypes arise due to high degree of heterozygosity

Materials and methods

During 2005 - 2006, we realized successful expeditions for wild hops in different Czech regions. Collected samples were transferred as rootstock or dry cones. Dry cones were used for chemical analyses of hop resins. Hop resins were determined according to EBC 7.7. method by HPLC on SHIMADZU LC 10A (Shimadzu, Japan). Wild hop rootstocks were multipropagated in glasshouse and transferred to field condition. DNAs were isolated from young leaves according to Patzak (2001). For molecular analyses, we used nine SSR (Haddon et al., 2004; Jakše et al., 2002) and three STS (Patzak et al., 2007) loci. PCR reactions were performed in TGradient thermocycler (Biometra, FRG). The genetic diversity analysis was evaluated by cluster analysis, which was revealed by NTSYS-pc v. 2.11V for WINDOWS (Exeter Software, USA)

Results

Assessment of wild hops includes the following parts:

1. Spring investigation of the occurrence of wild hops. Each year we choose a part of Czech Republic territory where exploration of wild hops is carried out. In each found wild hop its GPS is determined and samples of young leaves are taken to a laboratory to do DNA analysis.
2. Summer assessment of wild hops. During its growth each genotype is evaluated in its own habitat. Attack by mycosis is monitored at first in this phase.
3. Autumn collection of hops. In female genotypes cones are sampled. After drying they are analyzed in a chemical laboratory and aroma is evaluated.

Table 1: Variability of hop resins contents

Statistical value	Alpha acids (% w/w)	Beta acids (% w/w)	alpha/beta ratio	Cohumulone (%rel.)	Colupulone (%rel.)
Maximum value	6,77	7,72	2,01	31,9	53,6
Minimum value	0,73	1,21	0,33	18,8	38,5
Average	2,93	3,57	0,91	24,83	45,78
Statis. deviation	1,257	1,274	0,422	3,058	3,688
Variation coef. (%)	42,97	35,71	46,50	12,32	8,06

Perspective genotypes are multiplied and planted in field conditions where characteristics, due to them each genotype was selected, are researched. Wild hops have been collected since 2003. Since the end of 2006 a considerable part of Czech Republic has been investigated as well. In table 1 you can see variability of hop resins contents.

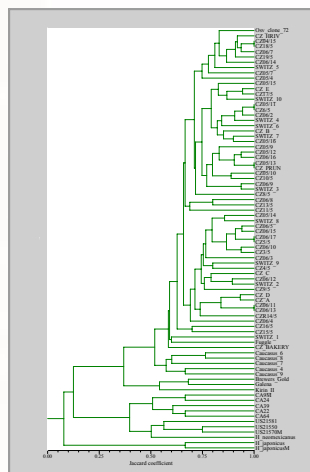


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The molecular DNA technology is a useful method for the study of genetic diversity, individual genotyping, population structure and phylogeny. Therefore, we used it for the study of wild hop genetic variability. In our experiment, we tested fifty wild genotypes in comparison to European and American wild hops (totally 80 genotypes). We found that Czech wild hops were clustered to European hop germplasm (Figure 1), which is evidently separated from wild American germplasm and *H. japonicus*. Caucasian wild hops and cultivated hops with mixed Euro-American germplasm were divided to two groups separately from Czech and Swiss wild hops. From this analysis is evident that Czech wild hops belong to fine aroma hops closely related to Saazer and Fuggle. It was not found any dependence between origin locality and genotype.

Figure: Dendrogram of individual wild hops revealed by UPGMA cluster analysis based on Jaccard's similarity coefficient determined using 22 STS and 46 SSR markers. CZ - Czech, CA - Canada



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