

Migration Features of *Ips typographus* in the Tatra Mountains: Using a Genetic Method

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The genetic structure of *Ips typographus* populations in the Tatra Mountains was studied based on the observed differences of gene flow and migration rate. It was a highlighted question as to what extent different natural barriers influence the migration potential of the species.

Material and Methods

Samples of *Ips typographus* adults were collected from attacked trees (first generation) in the following valleys of Tatra: *Southern part*, Ticha dolina (TI), Koprova dolina (KO), Mengusovska dolina (ME), Velka Studena dolina (VS), *Northern part*: Javorova dolina (JA), and Bielovoda dolina (BI). Within the Bielovoda dolina samples were taken at different altitudes: 900m (BI9), 1100m (BI11), 1300m (BI13 and BI13B), and 1400m (BI14) respectively. Only parental beetles were taken to avoid the effects of the homogeneity of the “one-family” beetles. Isoenzyme analyses were carried out using the NATIVE PAGE method.

Statistical analyses of the results were made applying different genetic structure describing statistics (FStat, Biosys, Popgene, and Slatkin's). Allele frequency and genetic distance values were calculated. Dendrograms were constructed to demonstrate the relationships among the locations. Gene flow and migration rate was estimated using graphical (Slatkin's method) and statistical (F statistics) methods. All analyses were made over all populations and loci.

Results and Discussion

The proteins of 12 enzymes (22 loci) were stained and five of them were polymorph. The five polymorph loci (*Aat-2*, *Amy-1*, *Est-2*, *Est-3*, *Est-4*) had 8, 10, 15, 9, and 4 alleles (Table 1.).

All investigated loci were in the Hardy-Weinberg equilibrium at the significance level of $p=0.001$. The effective number of alleles varied strongly from 1.054 (*Est-4*) to 5.152 (*Est-2*), with an average of 2.319. The observed heterozygosity ($H_{Obs.}$) was high, with heterozygote deficiencies on two loci (*Est-2*, *Est-3*).

Table 1.—Observed number of alleles

Locus	Population										All Populations
	BI9	BI1	BI13	BI13B	BI14	TI	JA	ME	KO	VS	
<i>Aat-2</i>	7	5	5	5	5	3	3	4	4	4	8
<i>Amy-1</i>	5	6	7	8	7	7	6	9	9	6	10
<i>Est-2</i>	14	13	12	12	11	12	11	13	12	12	15
<i>Est-3</i>	9	8	8	5	7	4	6	7	6	7	9
<i>Est-4</i>	4	1	3	2	2	3	1	2	2	1	4
Mean	7.8	6.6	7.0	6.4	6.4	5.8	5.4	7.0	6.6	6.0	9.2
St. Error	1.8912	2.1966	1.6956	1.8908	1.6432	1.9171	1.8908	2.1506	1.9875	2.0310	1.9812

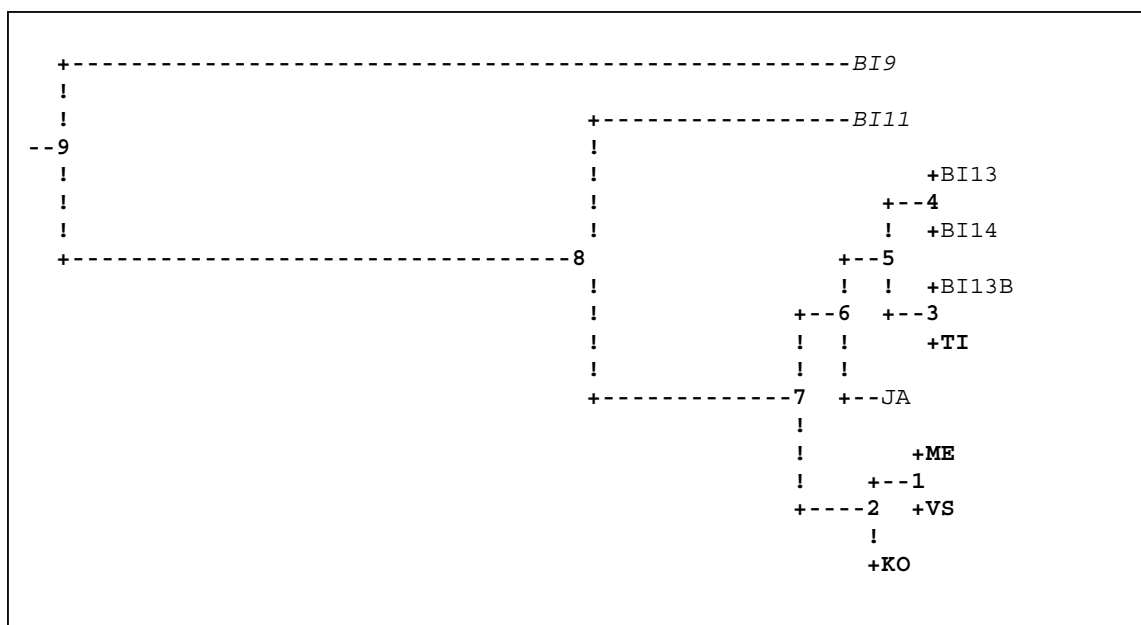


Figure 1.—Dendrogram based on Nei's genetic distance values (1972), neighbour joining method (populations in *italics* are from lower /1100m and below/ elevation, populations in **bold** are from the southern part, all the others from the northern part of the Tatra Mountains)

Nei's genetic distance values ($D = 0.0067$ to 0.0167) in the investigated area were rather close to the values found in an area of similar size in Hungary ($D = 0.0018$ to 0.0289). All populations showed high genetic variation. Most of the genetic differences were found within the individual populations; only 1.6% of the differences could be attributed to differences between populations ($F_{ST}=0.016$).

Using Nei's genetic distance values for constructing a dendrogram for the locus *Aat-2* with the "neighbor joining" procedure (Fig. 1.), the investigated populations were grouped into three main groups: (a): the populations from Bielovoda dolina lower elevations (BI9 and BI11), (b): the populations from Bielovoda dolina higher elevations (BI13, BI13B and BI14) with the neighbouring Javorova dolina (JA) and (c): the populations from the southern valleys (ME, KO, VS). Only the population from Ticha dolina (TI) did not group with its geographical origin (group c), but with northern populations (group b).

The migration rates (N_m) are high among all investigated *Ips typographus* populations. These results support previous observations that imagines fly greater distances and cover significant distances in areas where there are no host plants, and that they can disperse over higher mountain peaks.

Comparative studies showed migrational potentials in the Tatra ($N_m = 19.70$ to 51.16) were similar those in Hungary ($N_m = 10.96$ to 63.37 ; Lakatos, 1998) and in Southern Germany ($N_m = 22.96$ to 64.35 ; Gruppe, 1997).

References Cited

- Gruppe, A. 1997. Isoenzymatische Variation beim Buchdrucker *Ips typographus*. Mitt. Dtsch. Ges. Allg. Angew. Ent. 11: 659-662.
- Lakatos, F. 1998. Genetic variation of *Ips typographus* L. populations from in and outside of the native range of its host *Picea abies* (L.) Karsten. In: J. Hayes and K. Raffa ed.: Proceedings of a Workshop on Bark Beetle Genetics: Current Status of Research. Madison, Wisconsin, USA: 12-14.