

CLOSE LINKAGE BETWEEN GLUTAMATE OXALOACETIC TRANSAMINASE AND PHOSPHOGLUCOSE ISOMERASE ALLOZYME LOCI IN *LARIX DECIDUA* MILL.

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ABSTRACT

Presented data confirmed that the close linkage between loci of aspartate aminotransferase and phosphoglucose isomerase reported for many conifer species also holds in European larch ($R = 0.026$). However contrary to the members of the *Pinus* and *Picea* group a close linkage exists between *Got-2* and *Pgi-2* loci.

Key words: *Larix decidua* Mill, allozyme, inheritance, linkage.

INTRODUCTION

Despite advances in molecular biology techniques, allozymes are still useful tools in population genetics. Various analyses in population genetics, e.g. estimation of mating systems parameters and genetic distances, require information from a number of independent loci (SHAW *et al.* 1981; NEI 1975). Conifers are especially convenient for linkage analysis. Linkage can be detected without making crosses by testing independence of single-loci segregation in the haploid macrogametophyte tissue of seed from trees heterozygous for at least two loci.

In the genus *Larix* a few linkage studies have been performed and some more or less closely linked loci have been established (CHELIAK & PITEL 1985; YING & MORGENSTERN 1990; LEWANDOWSKI & MEJNARTOWICZ 1991).

In this paper, results indicating close linkage between the *Got-2* and *Pgi-2* loci in *Larix decidua* are presented.

MATERIALS AND METHODS

Among the analysed trees of European larch (*Larix decidua* Mill.) from Poland one rare tree heterozygous for both the *Got-2* and *Pgi-2* loci were found. A total of 76 macrogametophytes were analysed. Macrogametophyte tissue was homogenized in 30 μ l of Tris-HCL buffer pH 7.2 with the addition of 15% 2-mercaptoethanol. Electrophoretic separation was carried out in 12% starch gel by applying a buffer system according to RIDGEWAY *et al.* 1970. Gel slices were stained for activity of glutamate oxaloacetic transami-

nase (GOT, E.C. 2.6.1.1) and phosphoglucose isomerase (PGI, E.C. 5.3.1.9), using recipes described by CHELIAK and PITEL (1984).

The statistical evaluation of linkage relationships was conducted using χ^2 -tests as described by MATHER (1951). Recombination fractions (R) were calculated by the binominal estimator: $R = r/n$, where r is the number of recombinant types observed and n is the total number of observations. The standard error of this estimate is given by $[R(1-R)/n]^{1/2}$ RUDIN & EKBERG 1978).

RESULTS AND DISCUSSION

Three zones of activity for GOT were observed. However, inheritance of GOT in *Larix decidua* has not been tested so far, it seems that these three zones are coded by three loci. Similarly to European larch, three zones coded by three independent loci have been observed for GOT in *Larix laricina* (CHELIAK & PITEL 1985) and *Larix sukaczewii* (TIMERJANOV *et al.* 1994). According to earlier studies (LEWANDOWSKI 1995) two zones of activity for PGI were detected. Variants (S = slow migrating, and F = fast migrating) in both *Pgi-2* and second zone of GOT (designated as *Got-2*) showed agreements with a 1 : 1 segregation (Table 1). The observed pattern of segregation of these two loci together deviated significantly from the expectation for unlinked loci (Table 1). *Got-2* and *Pgi-2* are closely linked in the investigated tree, with an estimated recombination frequency (R) of 0.026 ± 0.018 . Almost the same value of R has been detected in *Larix laricina* ($R = 0.030 \pm 0.017$) by CHELIAK & PITEL (1985). Because of the small recombination values, this is one

Table 1. Test for linkage of the *Got-2* and *Pgi-2* allozyme loci in European larch, with recombination frequency (R) and its standard deviation (SD).

Locus pair	Number of macrogametophytes				Chi-square tests			Recombination frequency	
	FF	FS	SF	SS	a	b	c	(R)	(SD)
<i>Got-2/Pgi-2</i>	38	2	0	36	0.21	0	68.21***	0.026	0.018

*** $p < 0.1\%$; a = deviation from a 1:1 segregation at *Got-2*; b = deviation from a 1:1 segregation at *Pgi-2*; c = deviation from a free segregation of *Got-2* and *Pgi-2*.

of the most highly conserved gene blocks that is known in conifer karyology.

In studies where different species of the genera *Abies*, *Larix* and *Pseudotsuga* are involved, linkage has been observed to exist between *Got-2* and *Pgi-2*. (NEALE & ADAMS 1981; CHELIAK & PITEL 1985; EL-KASSABY *et al.* 1982) In contrast, in species from the genera *Pinus* and *Picea* linkage exists between *Got-1* and *Pgi-2* (GURIES & LEDIG 1978; ADAMS & JOLY 1980; CONKLE 1981; STRAUSS & CONKLE 1986; GONCHARENKO *et al.* 1998; KING & DANCİK 1983; MUONA *et al.* 1987). CHELIAK & PITEL (1985) suggested that evolution from the last common ancestor between the *Pinus* – *Picea* group, and the other genera has progressed to the point where accumulated mutations can now be observed as electrophoretic mobility differences. Thus, *Got-1* in the *Pinus-Picea* group is functionally *Got-2* in the other genera and similar *Got-1* in *Abies*, *Larix* and *Pseudotsuga* is functionally *Got-2* in the *Pinus* – *Picea* group. Results reported in this paper fully agree with this suggestions.

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