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Linkage of two mutant allozymes for *Amp2* and *Aat2* with marker loci on barley (*Hordeum vulgare* L.) chromosomes 1 and 6

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Abstract. To saturate barley (*Hordeum vulgare* L.) genetic maps the linkage relationships of two isoenzyme loci *Amp2* (aminopeptydase) and *Aat2* (aspartate aminotransferase) with known genetic markers were investigated. Results of the genetic analysis support previous information on the localization of these loci on chromosome 1 and 6, respectively. The following recombination values were estimated: between locus *Amp2* and T1-3b translocation break point 13.8 ± 2.1%, between locus *Aat2* and translocation T6-7i, 17 ± 3.0% and between locus *Aat2* and marker *o* 24.1 ± 3.0%.

Key words: *Hordeum vulgare*, isozymes, linkage.

Introduction

Most of barley *Hordeum vulgare* L. isozyme loci were localized to particular chromosomes with the use either addition lines or trisomics (BROWN 1983). There is very limited information on the relationship between these loci and other chromosome markers. The low level of variability for some isozymes among barley cultivars and genetic stocks utilized in genetic analysis makes it difficult to localize respective genes within particular chromosomes. The use of induced mutants may act as an additional source of isozyme diversity to help to solve this problem (KUCHARSKA, MALUSZYNSKI 1991a). The present study was designed to estimate the linkage relationships between two isoenzymatic loci, *Amp2* and *Aat2*, and genetic markers of chromosome 1 and 6, respectively.

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Material and methods

Plant material consisted of 7 populations of F_2 plants derived from crosses between isozyme mutants and selected genetic markers. Two mutants derived from variety Karat, 843Q and 673Q, were selected from a collection of dwarf and semi-dwarf spring barley chemomutants described earlier (KUCHARSKA, MALUSZYNSKI 1991b). Mutant 843Q contains the unique allozyme of *Amp2*, and mutant 673Q contains the unique allozyme of *Aat2*. Two types of genetic markers were used. One was Multiple Recessive Stock (MRS), containing two morphological markers of chromosome 1 (*lk*, *n*) and two of chromosome 6 (*rb*, *o*), provided by Dr. Franckowiak from North Dakota University, USA. The other was a set of translocation lines involving chromosomes 1, 3 and 6, obtained from Svalöf AB, Sweden. Localization of markers on barley chromosomes was described by PERSSON (1969) and SØGAARD and von WETTSTEIN-KNOWLES (1987).

F_2 plants were harvested and classified in respect of morphological characters or in respect of plant fertility, depending on the marker type involved. At least 5 progeny seedlings of each F_2 plant were subjected to starch gel electrophoresis in order to determine the isoenzymatic genotype. Electrophoresis in lithium-borate system (pH 8.2) and staining procedures for leucine aminopeptidase and aspartate aminotransferase followed those of SOLTIS et al. (1983). Recombination values were estimated by the MLH method (HANSON, KRAMER 1950, ALLARD 1956).

Results and discussion

The F_2 data established the linkage relationship between *Aat2* and *o*, 'orange lemma', marker of the long arm of chromosome 6 (Table 1.) Linkage between *Aat2* and translocation break point T6-7i reconfirms the localization of *Aat2* on the long arm of chromosome 6 (Table 2). These data are in agreement with HART et al. (1980) who reported on the localization of *Aat2* locus on chromosome 6 with the use of wheat-barley addition lines.

The *Amp2* locus data revealed the linkage relationship with translocation break point T1-3b (Table 2), which involves chromosome 1 and 3. The results of testing other translocation lines of chromosome 3 showed independent segregation with two translocation break points: T3-7c involving the long arm of chromosome 3 and T3-7d involving the short arm of chromosome 3. Free recombination was also found between locus *Amp2* and another tested trans-

Table 1. F_2 data for linkage involving marker loci in barley chromosomes 6, 1 and *Aat2*, *Amp1*, respectively, obtained from crosses between mutants and MRS

Loci involved	Total	No. of F_2 families*						χ^2	Recombination value ± S.E. (%)
		e+f	g+h+i	j+k	l	m	n		
Aat2/o	83	11	34	18	15	2	3	14.85	24.1 ± 3.0
Aat2/rb	83	40	15	8	14	3	3	0.01	independent
Amp2/lk2	123	22	56	17	4	15	9	5.76	independent
Amp2/n	123	23	56	17	3	15	9	6.80	independent

e+f – A_1A_1B, g+h+i – A_1A_2B, j+k – A_2A_2B, l – A_1A_1bb, m – A_1A_2bb, n – A_2A_2bb, A_1A_1bb – MRS, A_2A_2BB – mutant,
*designation after ALLARD (1956)

location line of chromosome 1 (T1-7f), and between *Amp2* and two morphological markers located on the long arm of chromosome 1, *lk* and *n*. The preliminary results (data not shown) excluded the linkage between *Amp2* and *br*, a marker of the short arm of chromosome 1. The present results showing linkage between *Amp2* and translocation break point T1-3b in chromosome 1 support the report of SOLIMAN and ALLARD (1989) on localization of one of barley aminopeptidase loci in chromosome 1 (data obtained with the use of wheat-barley addition lines). However, the present data are not in agreement with the results of DIAS (1978), as the present study found no recombination between *Amp2* and marker *n*. On the basis of these results we can conclude that locus *Amp2* is located on chromosome 1, but further linkage relationship needs to be studied.

Table 2. F_2 data for linkage between two barley isoenzyme loci and translocation break points

Locus/ translocation involved	Total	No. of F_2 families*						χ^2	Recombination value ± S.E. (%)
		d	h	g	c	f	e		
Amp2/T1-7f	91	17	11	11	15	21	14	0.89	independent
Amp2/T1-3b	197	38	14	50	18	62	15	53.85	13.8 ± 2.1
Amp2/T3-7c	151	19	35	23	20	26	28	1.49	independent
Amp2/T3-7d	147	22	29	17	25	28	26	1.15	independent
Aat2/T6-7i	136	27	19	13	8	56	13	23.06	17.8 ± 3.0

d – A_2A_2F, h – A_1A_2F, g – A_1A_1F, c – A_2A_2PS, f – A_1A_2PS, e – A_1A_1PS,
A_1A_1 – translocation line, A_2A_2 – mutant,
*designation after HANSON and KRAMER (1950)

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