

The Frequency of Transgression Effects in F₁DH, F₂DH, SSD Barley Lines

A. KUCZYŃSKA, M. SURMA, Z. KACZMAREK and T. ADAMSKI

*Institute of Plant Genetics, Polish Academy of Sciences, 60-479 Poznań, Poland;
e-mail: akuc@igr.poznan.pl*

Abstract: The aim of the present study was to detect the transgression effects in different types of barley lines. The SSD and DH lines derived from F₁ and F₂ hybrids of the same cross combination were examined in a field experiment carried out in a complete randomised design with three replications. Grain yield per plot, 1000-grain weight, grain weight per ear, plant high and spike length were observed. Means and variances for the studied traits were evaluated and tested. Estimation of differences between each SSD or DH line and the both parents has allowed us to determine the transgression effects. Percentage of lines differing significantly (at $\alpha = 0.05$) from the better and worse scoring parents were calculated in each population. The mean values of all the traits did not differ significantly in the studied F₁DH, F₂DH and SSD populations. Additionally, the range for individual traits in the F₁DH, F₂DH and SSD populations was very similar. Moreover, no significant differences were found in the variances of all DH and SSD lines. The frequencies of transgressive lines also appeared to be similar in doubled haploid and SSD populations. Besides, the coefficient of gene dispersion (r) was calculated. The greatest number of transgressive lines was recorded in those traits for which r estimate did not differ significantly from zero. The relationship between the frequency of transgressions and gene dispersion was recorded: the greatest number of transgressive lines occurred in the grain weight per ear for which the dispersion was observed. Similar results for all the studied populations confirm the rightness of many breeding programmes in which doubled haploid lines are produced from F₁ hybrids. The use of DH lines derived from the first cycle hybrids allows breeders to shorten the time required for obtaining completely homozygous breeding lines.