# SYNOPSIS

Four hybrid crosses which were identified as the highest yielding in a previous diallel trial were evaluated along with their basic generations and $F_3$ families under spaced plant conditions to study the underlying causes of heterosis and to compare the performance of these hybrids with commercial control varieties. Overall, these hybrids showed greater vigour compared with the selfed generations produced from the crosses. One hybrid cross ($F_1$) out-performed the control varieties. Considerable non additive genetic variance (dominance) was shown to be present in the crosses and a reasonable proportion of second cycle hybrids are predicted to out-perform the $F_1$. A very small percentage of recombinant inbreds are predicted to exceed the performance of $F_1$ thus confirming the fact that overdominance may not be the cause of the heterosis manifested by the crosses.

Genetic differentiation of perennial ryegrass populations collected in different parts of Europe was studied using both quantitative characters and isozyme polymorphisms. Early heading populations showed less vigour for yield and reproductive ability compared with the late heading populations. When assessed in two locations the mean performance of populations showed a very high similarity especially for heading date and yield, but the intraclonal variance of individual genotypes differed considerably among genotypes, populations and at the two locations. Multivariate analyses produced 4 groups of populations separated by Mahalanobis distances ranging from 5.9 to 30.9. The results indicated that populations within a group were more similar in their management rating rather than the geographical origin.

Isozyme polymorphisms were ubiquitous in all populations and populations differed in the allele frequencies at all loci analysed. A high percentage of loci were

polymorphic in the populations ranging from 71-100% and the expected heterozygosity varied from 0.234- 0.410. The within population component of the total gene diversity was very high ($H_S$ = 0.94) indicating the highly outbreeding nature of these populations. Both quantitative variation and isozyme polymorphisms showed that German accession BA 10998 as distinct from the others.