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GENETIC DISSECTION OF THE DIFFERENCES BETWEEN WILD EMMER WHEAT, TRITICUM DICOCCOIDES, AND CULTIVATED WHEAT, T. DURUM, FOR AGRONOMICALLY IMPORTANT TRAITS

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The experiment was performed on an F2/F3 mapping population derived from a cross between a highly stripe-rust resistant wild emmer wheat Triticum dicoccoides (accession H52, from the Mt. Hermon, Israel) and a T. durum cultivar, Langdon released in North Dakota, USA. The tetraploid wild emmer, T. dicoccoides, is the progenitor of cultivated wheat; hence, the genetic dissection of quantitative trait differences between the wild species and the cultivated crop is of great interest from the viewpoint of domestication evolution. It is also important for the ever-increasing utilization of T. dicoccoides as a rich genetic resource for wheat improvement. The quantitative traits were scored on the selfed progeny in field trials. Eleven quantitative traits were scored on F3 progeny: plant height, plant heading date, spike number/plant, spike weight/plant, single spike weight, kernel number/plant, kernel number/spike, kernel number/spikelet, 100-grain weight, grain yield/plant, and spikelet number/spike. For most of the traits, the number of detected QTLs on the A genome was equal or exceeded that of the B genome. The number of QTLs located on chromosome 1B, 2A, 3A and 5A accounted for about 70% of the QTLs detected. There were a few QTLs on chromosomes 1A, 4A, 6A, 2B, 4B and 7B. On specific chromosomes, QTLs clustered in a few regions (especially in 1B, 2A, 3A, 5A and 5B). Most of the major QTLs (significant at $p<0.001$-0.0001) were located on chromosomes 2A and 5A.

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MASSIVE NEGATIVE INTERFERENCE, AND PUTATIVE QUASI-LINKAGE UPON HYBRIDIZATION OF WILD EMMER WHEAT, TRITICUM DICOCCOIDES , WITH CULTIVATED WHEAT, T. DURUM

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A genetic map of a cross between wild emmer wheat, Triticum dicoccoides, and cultivated wheat, T. durum was constructed spanning more than 3000 cM (see companion abstract). The main objective of this study was to characterize the recombination patterns upon crossing of T. dicoccoides with its domesticated descendant, T. durum (cultivar Langdon). Massive negative interference (an excess of double crossovers in adjacent intervals relative to the expected rate on the assumption of no interference) was observed in most of the chromosomes in both genomes, A and B, of our T. durum x T. dicoccoides hybrid, and confirmed also for chromosome 1B in another independent cross of different parental lines. The general pattern of distribution of the island of negative interference included near-centromeric location, spanning the centromere and median/subterminal location. A departure from random segregation of markers on non-homologous chromosomes is termed quasi-linkage. This phenomenon was observed earlier both in plants and animals, especially in interspecific hybrids. In our F2 mapping population (T. durum x T. dicoccoides) several pairs of non-homologues chromosomes manifested a highly significant deviation of recombination of their markers from the expected r=50% level. These included either excess or deficit of recombinant genotypes. Following these results, we conducted a few other tests of quasi-linkage, with hexaploid wheat, maize, and Arabidopsis. It appeared that quasi-linkage might indeed be a significant phenomenon in wheat, as well as in other plants.