PYRAMIDING MAJOR GENES FOR RESISTANCE TO LEAF RUST PATHOGEN OF WHEAT

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The individual use of single race-specific resistence genes with major phenotypic effects has rarely provided lasting resistence. However, breeding and combining or pyramiding of resistence genes into individual cultivars has had considerable success, particulary in situation where the pathogen does not reproduce sexually, as in the case of wheat lwaf rust phatogen. Within international leaf rust of wheat investigations it was necessary, to create by breeding new resistant wheat lines to Puccinia recondita tritic ifor differentiation of pathogen population, as well as for sources of resistance in European-Mediterranean regions. In the beginning 18 donors of resistance had been selcted after an extensive screening test of several International Rust Nurseries, to be crosses with recurente parents variates Princ and Starke. These testing proved that in those lines were present new resitant genes. Eighth geneticll different hybrids of the first backcross had been selected and tested in the seedling stage with three international pathogen cultures (YU-13-19-1; H-13-9-1 and C2-13-Ar-3). Considerable influence of recurente parent to the number of resistant genes in donors used were demonstrated. On the other side, it was established considerable influence of the pathogen culture to the number of resisrance genes in donors used. The same crossing combinations tested with one pathogen culture results in presence of two resistance genes, but with another culture three or one resistence gene. in order to enhancement resistence and pyramiding genes in these hybrids, eight select the most interesting lines have been crossed with only effective isogenic containing the strong genes Lr9, Lr19 and Lr24. the genetic analysis of twenty two crossing combinations have been realized by testing with three pathotypes of Puccinia recondita tritici (Bg.s. 12/89; Is.w 8/89 and Chl.w. 14/89). On the base of different segragation ratios of all crossing combinations it was proved that no one of the resistant donors did not contained the strong resistant genes used. It means, that our hybrid lines contained resistent genes from the donors and in addition three strong resistant genes Lr9, Lr19 and Lr24. Key words: hybrids wheat, acumulations genes resistance, leaf rust pathogen