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Monosomic Analysis of F_2 Poros-monos x M30 against Powdery Mildew (*Erysiphe graminis* f. sp. *Tritici marchal*)

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Abstract: Total 18 F_2-monosomic lines along with the parents Poros, M30 and control plants were examined against powdery mildew which is one of the economically important wheat diseases. Screening procedure was facilitated with the division of scale 9 to 1 into resistant (5-9) and susceptible (1-4) plants. In this research, 4 chromosomes (2B, 4D, 5A, and 6A) associated with the resistance against powdery mildew were identified.

Key words: Monosomic analysis, Poros, M30, powdery mildew (*Erysiphe graminis* f. sp. *Tritici marchal*)

Introduction

Monosomics are plants deficient for entire chromosome and they have been found in several species. Monosomics occur spontaneously and can be recognized by phenotypic observations and cytogenetic analysis. These can be used to determine gene linkage groups, especially in polyploid plants, for identification of genes on particular chromosomes and for transference of genes from one chromosome to the others. Monosomics are of great value available in Chinese Spring since 1954 (Sears, 1954) and which have now been transferred to a number of other varieties. Worland (1988) has already compiled the catalogue of 75 monosomic series in 24 countries of the world. The main source of monosomics of the Chinese Spring variety was originally obtained from two sources: haploids and asynaptics (Sears, 1954). Aneuploids have been used most extensively not only for genetic analysis but also for developing the new species.

Monosomic analysis, the use of monosomics for locating genes to chromosomes, is conducted in different ways, depending on the kind of gene concerned-dominant or recessive. There are several methods and procedures of using aneuploids in cytogenetic studies (Sears, 1953, 1954, 1972a; Law and Worland, 1973; Mc Intosh, 1978a; Khan 1991, 1994; Khan *et al.*, 1994.

Powdery mildew (*Erysiphe graminis* f. sp. *Tritici marchal*) is one of the most common and damaging wheat diseases. It is economically considered to be a very important wheat disease of the world studied intensively by different scientists over the past 40 years and several powdery mildew resistant genes have been identified. Most of them have already been incorporated into high-yielding cultivars (Heun and Friebe, 1990). The host and pathogen genetics of powdery mildew have also been studied extensively, (Moseman, 1966; Wolfe, 1972). Chae and Fischback (1979) using two sets of monosomic wheat lines showed that 14 chromosomes were involved in the resistance of wheat cultivar Diplomat. Ellingboe (1981) reported that the mildew resistance of Genesee could be traced back to one dominant gene if analysed under the controlled conditions. Hautea *et al.* (1987) presented a genetic analysis of quantitative mildew resistance of wheat and concluded that additive gene action was the most important genetical component in all crosses. No dominance occurred, epistatic effects were significant in only two crosses. Jone *et al.* (1981) analysed the genetics of quantitative powdery mildew resistance according to the methods of Hayman (1954) and Jinks (1954).

By interpreting the results of the full diallel including parents, they found that most of the genetic variability in the six barley cultivars studies was attributed to additive and dominance effects of independent genes with no evidence of non-allelic interaction. Similar results were obtained for other cultivars tested in greenhouse using five different genes isolated by Heun (1987a), when analysing a half 8 x 8 F1 diallel. Bennett (1984) described 11 loci, some with multiple alleles or closely linked genes, conferring race-specific resistance to powdery mildew.

Materials and Methods

Monosomic series in hexaploid wheat, *Triticum aestivum* L. CV. Poros-monos is actually winter wheat with 2n = 41 chromosomes-developed by Mettin (1969) at Plant Breeding Institute, Martin Luther University, Halle/Wittenberg, Federal Republic of Germany (Khan, 1991). M30 was originally introduced from USA to Sweden and then it was brought to Gatersleben-Germany under the accession number HW 2222 with group *Triticum aestivum* L. var. Lutescens (Alef) Mansf. (Sperling, 1985). Monosomic analysis in the hexaploid wheat Poros-monos x M30 was carried-out by using the F_2- monosomic lines of Poros-monos. Cytologically confirmed monosomic parents were crossed with M30 and the F_1 population was raised. Among the plants raised there were disomics, monosomics and nullisomics. Only monosomic plants that were confirmed cytologically were selfed and forwarded to F_2-generations.

The investigations were carried-out on 22 lines, including F_2-monosomics along with Poros, M30 and control plants. Plants were sown in rows. Each row had 30 plants. Distance between plants and rows were 20 x 20 cm^2. Total 22 lines having 7038 plants were arranged. In this experiment third leaf of each plant was observed critically and number of postules were counted according to the average mildew scores of scale nine to one (Stephan, 1978). Plants under observation were inoculated with WW-Strubes Dickkopf by placing diseased plants among seedlings. Infection type scale 9-1 was divided into resistant (5-9) and susceptible (1-4) groups. Each plant was examined 3 times on dates 30.5, 6.6 and 13.6 with one-week interval.

Results and Discussion

Total 22 genotypes were subjected to the attack of powdery mildew under field conditions. The F_2 monosomics were compared with parents as well as with control plants. Total 7038 F_2 plants were examined against powdery mildew. In this experiment every 3rd leaf of each plant from top to bottom was examined. The host-pathogen interaction was tested by infection type scale from 9 to 1, where 9 stand for no visible fungal growth and 1 is abundant growth and sporulation (Stephan, 1978 and Hiura, 1978). Screening of the plants was done by counting the number of resistant (5-9) and susceptible (1-4) plants. The whole procedure was repeated three times in order to combine the three observations. As a result of these observations the chromosomes 2B, 4D, 5A and 6A have shown complete resistance against this disease. A negative response was observed by the lines 1A, 2A, 3A 4B and 7B as compared to M30 and control plants (Fig. 1). The lines 1A, 1D, 2A, 3A, 3B, 3D, 4B, 5B, 5D, 7A and 7B have shown relatively identical response with control plants. While the monosomic lines 2A, 2D, 4A, 4D, 5A and 6A are similar in response to M30 against powdery mildew. Bennett and Kint (1983) have reported 17 chromosomes having complete resistance against powdery mildew. Chae and Fischback (1979) showed that

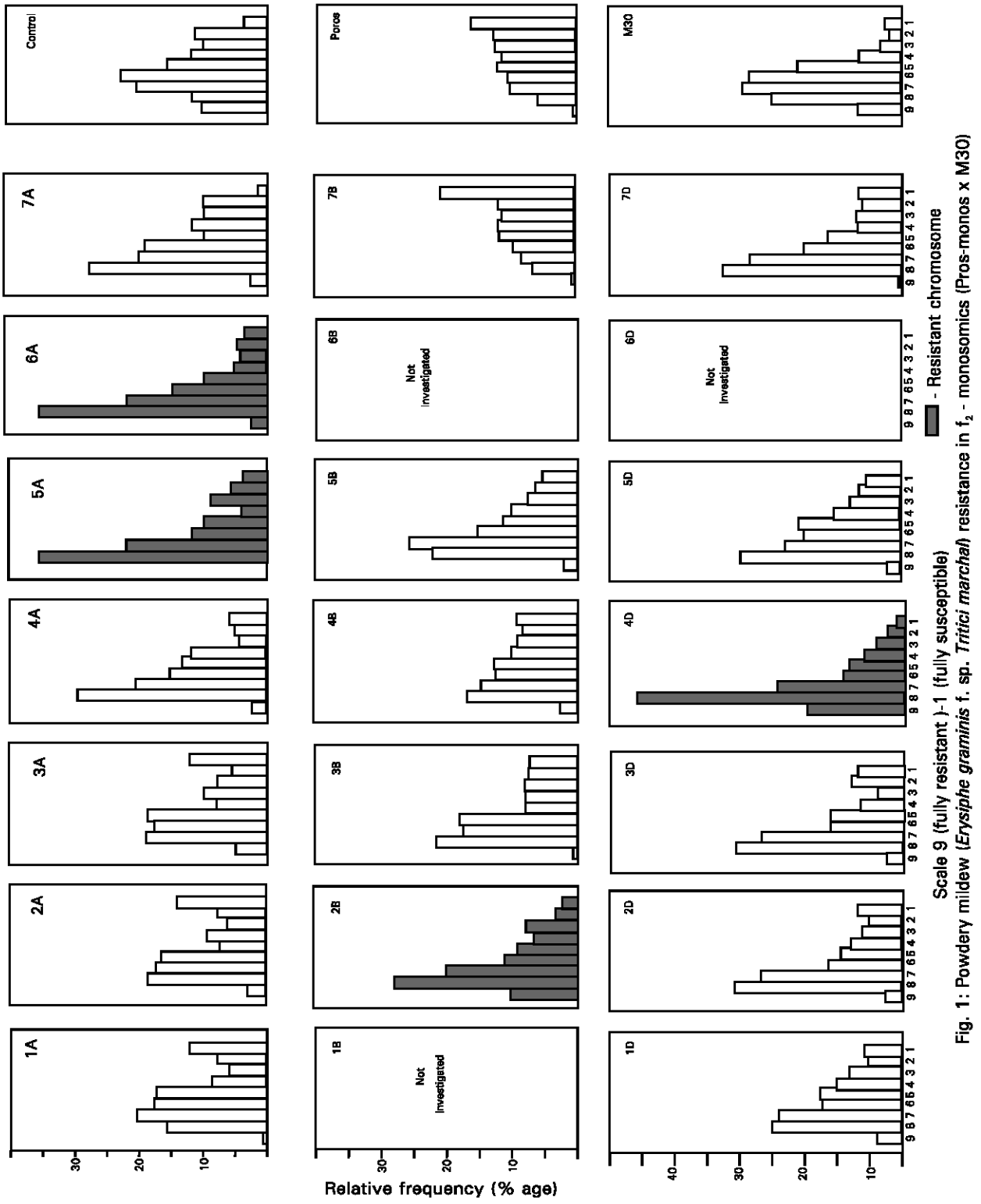

Fig. 1: Powdery mildew (*Erysiphe graminis* f. sp. *Tritici marchal*) resistance in f_2 - monosomics (Pros-monos x M30)

4 chromosomes were involved in the resistance process of variety Diplomat. Jha (1969) examined cultivar Lerma Rajo and conducted that the chromosome 6B is carrier of resistance in younger plants and 2B, 3A, 4B, 5A show resistance in adult stage. As we already know that powdery mildew is one of the most common and damaging wheat diseases and at present very effective fungicides etc. for the chemical control of mildew are in use, but for an ecological reasons and because insensitivity phenomenon with this

pathogen are reported more frequently, their employment should be confined as far as possible. Breeding efforts to improve the genetic resistance are very intensive on a worldwide basis and have already led to remarkable results.

From all these observations it was concluded that the breeding activity along with the screening experiments must be continued in order to explore and introduce new mildew resistance genes into our breeding material and to build up a broad basis of resistance by combining suitable genes in future wheat varieties.

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