C-banding pattern and powdery mildew resistance
of *Triticum ovatum* and four *T. aestivum—T. ovatum* chromosome addition lines

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Summary. C-banding patterns of *T. ovatum* (*Ae. ovata*) and four *T. aestivum* cv ‘Poros’-*T. ovatum* chromosome addition lines are presented, and the added chromosomes of *T. ovatum* have been identified. Furthermore, nucleolar activity and powdery mildew resistance were analyzed in the ‘Poros’-ovatum addition lines and compared to that of *T. ovatum* and *T. aestivum* cv ‘Poros’. The addition lines II, III and IV and ‘Poros’ were highly susceptible to powdery mildew isolates nos. 8 and 9, whereas the addition lines VI1 and VI2 showed high resistance. Even for an Ml-k virulent isolate, these two lines were highly resistant. By combining the cytological results and those of the powdery mildew analysis, the added chromosomes of *T. ovatum* can be excluded from responsibility for the high powdery mildew resistance of the addition lines VI1 and VI2. The same is true for a modified chromosome 6B, which is present in the ‘Poros’-ovatum addition lines II, III and VI. The high variation in C-banding pattern observed in the A-, B- and D-genome complement of the addition lines is believed to be the result of crossing different lines of *T. aestivum* instead of ‘Poros’ alone. Thus, we cannot trace the powdery mildew resistance back to a specific chromosome.

Key words: Common wheat — *T. ovatum* — C-banding — Nucleolar activity — Powdery mildew resistance

Introduction

Many wild relatives of hexaploid wheat, *Triticum aestivum* (genomically AABBDD), are known to carry interesting genes, such as powdery mildew resistance (Gill et al. 1985), which might be useful in broadening the genetic variability of cultivated wheats. Due to the close evolutionary relationship of the genus *Aegilops*, which is now included in the genus *Triticum* (Bowden 1959), many of these wild *Triticum* species can be crossed quite easily with cultivated wheat. The obtained amphiploids and, later on, the derived chromosome addition lines are the first steps toward the incorporation of such new genes into cultivated backgrounds; exactly this is our intention in analyzing new possible sources for powdery mildew resistance.

This paper describes the C-banding pattern of the allotetraploid species *T. ovatum* (formerly *Aegilops ovata*, genomically UUMM, after Kimber and Sears 1987) and four *T. aestivum — T. ovatum* chromosome addition lines. In addition, the disease reaction of these lines against *Erysiphe graminis* f. sp. *tritici* is analyzed.

Materials and methods

The material analyzed consists of the hexaploid winter wheat cultivar ‘Poros’ (kindly provided by the gene bank of Braunschweig, FRG), *Triticum ovatum* (from Gatersleben, GDR) and the *T. aestivum* cv ‘Poros’-*T. ovatum* addition lines II, III, IV and VI. These addition lines originated from D. Mettin, GDR, who attempted to increase the protein content by crossing *T. aestivum* with *T. ovatum* (Mettin et al. 1977).

Chromosome identification was carried out in 20—30 plants per line by phase contrast analysis and Giemsa C-banding, according to Giraldez et al. (1979). Nucleolar activity was analyzed by using the silver staining technique described by Lacadena et al. (1984). The methods used for testing powdery mildew resistance are described in detail by Heun and Fischbeck (1987a, b); leaf segments placed on agar containing 50 ppm bza were inoculated homogeneously and stored for 10 days at 17°C ± 1°C at low light intensity. Then, disease assessments were carried out by visual estimation of the infection grade (scale 0—9) and the infection type (scale 0—4). The pustule sizes were also recorded. These data were combined to form three classes: r = resistant, i = intermediate and s = susceptible. The powdery mildew isolates nos. 8 and 9 described by Heun and Fischbeck (1987b) and powdery mildew isolate no. 4a, possessing Ml-k virulence, were used.
Results and discussion

C-banding pattern of T. ovatum

Figure 1 b shows C-banded mitotic metaphase of T. ovatum. A detailed karyogram of this line is given in Fig. 2. The arrangement of chromosomes according to size and arm ratios follows the study of Chennaveeraiah (1960). Since data on the relationship to the homoeologous groups of Triticeae do not yet exist, the chromosomes are lettered A to N.

Two chromosome pairs of T. ovatum show a secondary constriction in phase contrast, which were identified as chromosomes A and I after C-banding. Characteristic C-bands are also present in all the other chromosomes, allowing the identification of each chromosome pair. Only minor variation in C-banding pattern was observed within and between different plants of the T. ovatum line analyzed.

It is generally accepted that the U-genome of T. ovatum is closely related to that of the diploid ancestor T. umbellulatum (formerly Aegilops umbellulata), whereas the M-genome of T. ovatum corresponds to that of the diploid progenitor T. comosum (formerly Aegilops comosa) (Kihara 1937, 1946). Kimber and Sears (1983) proposed the genome symbols UUMM for T. ovatum to indicate that the M-genome of T. ovatum is modified compared with the M-genome present in T. comosum. By analyzing meiotic chromosome pairing in different hybrid combinations, Kimber et al. (1983) were able to show that the M-genome of T. ovatum has undergone