KARYOTYPE ANALYSIS OF HEXAPLOID WHEAT, *TRITICUM AESTIVUM* L. CV. 'SARSABZ'

QAMAR JAHAN*
AHSAN A. VAHIDY*

SUMMARY: Karyotype analysis of several cultivars of hexaploid wheat have been done by many different workers in past. Earlier the parameters employed were the chromosomal length and the arm ratio. After the invent of the Giemsa banding technique, C and N bands were recognized that were specific for different chromosomes. However, the inconsistencies in the banding pattern are quite common, which are due to inter and intra specific banding polymorphism and lack of standardization of banding techniques. As no karyotype analysis in any Pakistani cultivar of hexaploid wheat has been reported in the literature, the present study was undertaken to perform karyotype analysis by the conventional method in the cultivar Sarsabz. The cytological technique employed was a simplified version of the one described by Mujeeb-Kazi and Miranda (8). Chromosomes were identified on the basis of total length, arm ratio and satellites. A comparison was made with the corresponding values of cv. Chinese Spring reported by Gill (2).

Key Words: Hexaploid wheat, Triticum Aestivum. CV. Sarsabz. Karyotype analysis.

INTRODUCTION

The earliest work on wheat chromosomes relied on reconstructions made from microtomal serial sectioning of root tips. The development of squash technique reduced the possibilities of misinterpretations. Studies of the morphology of choromosomes in hexaploid wheat; *Triticum aestivum* L (2n=6x=42) have been made by many workerk, including Schulz-Schaeffer and Haun (9), Khan (4) and Kimber (5). Since 1970 exciting developments have been made in chromosome identification by specialized Giemsa banding methods. Two such techniques viz., C-banding and N-banding have been most useful in cytogenetic studies of wheat and other cereals (1,2,3). However, the banding pattern reported by different workers showed inconsistencies due to intra and inter banding polymorphism, and due to lack of standardization of banding techniques used in different laboratories. Because of these reasons, the standard karyotype analysis based on chromosome length and arm ratio still holds its merit. Since no reference in the literature was found about the karyotype analysis of any Pakistani cultivar of hexaploid wheat, the present study was undertaken with the cultivar 'Sarsabz'.

* Department of Genetics, University of Karachi, Karachi-75270 Pakistan.

MATERIALS AND METHODS

Seeds of cultivar Sarsabz were obtained from the Atomic Energy Agricultural Research Centre (AEARC), Tandojam for this study. The technique developed by Mujeeb-Kazi and Miranda (8) was modified and employed in this work. Seeds were treated with fungicide 'Topsin' and were germinated in the Petri plated, lined with moist filter paper, kept in the dark at a constant temperature of 20 degrees celsius for about 72 hours. The root tips were harvested in late mornings to obtain good mitotic index and were transferred to another Petri plate for the pretreatment of 2.5 hours in dark at 25 degrees celsius. The pretreatment solution used was a mixture colchicine, 8-hydroxyquinoline and DMSO. The root tips were then transferred to 1.8% acetoorcein stain in which a few drops of 1N HCI were also added and stored in a refrigerator for at least 7 days. Before squashing the root tpis were treated with 45%

acetic acid to remove excess of stain and to further soften the tissues. Squashing was done in a drop of 45% acetic acid without using any high temperature or flame treatment. The slides were permanized in euparal after remving the cover slips in liquid nitrogen and treating the slides in absolute ethyl alcohol for about two minutes. The selected cells were photographed. Individual chromosomes from the enlarged photograph were measured, cut and rearranged according to homoeologous groups and genomes.

RESULTS AND DISCUSSION

The common hexaploid wheat with a genomic formula of 2n=6x=42, AABBDD is believed to have arisen as a result of amphiploidy between an AABB tetraploid, *Triticum turgidum* and the DD genome diploid, *Aegilops squarrosa (Triticum tauschii)*. It is generally believed

Figure 1: A representative cell showing well spread 42 chromosomes in the root tip of *T. aestivum* cv. Sarsabz.

that the AA genome of hexaploid wheat has its origin from *Triticum urartu*, but the opinions about the origin of B genome differ (7). The chromosomes in each of the three genomes are further classified into seven homoeologous groups. Chromosomes 1B and 6B carry nucleolar organizers on their short arms. These secondary constrictions are proximal to the satellites and are fairly conspicuous in good preparations (Figure 1). Less conspicuous secondary constrictions and satellites are some times observed on the short arms of 1A and 5D (6). However in our preparations these satellites were not observed. In general the chromosomes of D

Figure 2: A karyogram developed from the cell shown in Figure 1.

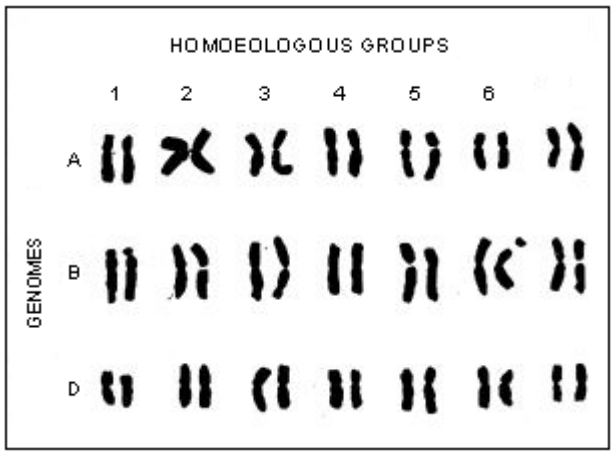

Table 1: Somatic metaphase chromosome size and arm ratio of chromosomes of *T. aestivum* cv. Sarsabz and a comparison of the corresponding readings reported by Gill, 1987 for cv. Chinese Spring.

Homoeologous group, Genome	cv. Sarsabz		cv. Chinese Spring (Gill, 1987)	
	Size	arm ratio	size	arm ratio
1A	7.70	1.9	11.1	1.9
2A	8.93	1.3	12.5	1.3
3A	8.40	1.3	11.5	1.3
4A	7.95	1.7	11.9*	1.7*
5A	8.11	1.9	11.5	1.8
6A	6.15	1.1	9.8	1.1
7A	7.87	1.1	11.3	1.0
1B	8.48	1.7	11.8	1.7
2B	9.43	1.2	12.9	1.2
3B	9.92	1.2	13.8	1.3
4B	8.56	1.1	11.4*	1.1*
5B	8.81	2.0	12.1	2.0
6B	9.18	1.2	12.7	1.2
7B	9.02	1.5	12.5	1.5
1D	5.82	1.7	8.4	1.7
2D	6.92	1.3	10.1	1.3
3D	7.29	1.4	10.7	1.4
4D	5.98	1.8	9.0	1.8
5D	7.17	1.9	10.4	1.9
6D	6.39	1.2	9.9	1.2
7D	6.56	1.1	10.1	1.1

* Values of 4A and 4B are interchanged for meaningful comparison. Please see text for further explantation.

genome are shortest. Chromosome 5B is most heterobrachial. The rest of the chromosomes are not substantially different from each other and thus are classified on the basis of total length and the arm rations. These values are given in the Table 1 for all homoeologous groups of three genomes. For the sake of a comparison corresponding values obtained by Gill (2) on cv. 'Chinese Spring' a standard variety used in many cytological investigations are given as well. Now that the homoeologous groups 4A and 4B have been reclassified by interchanging them at the seventh international wheat Genetic symposium held at Cambridge in 1988 (10), the chromosomes have been arranged in both, Figure 2 and Table 1 according to new classification. The cytological technique employed in the present study seems to be not only reliable and reproducible but gives excellent spread of chromosomes, that is of prime importance in karyotype analysis.

REFERENCES

1. Gerlach WL : N banded karyotypes of wheat species. Chromosoma 62:49-56, 1977.

2. Gill BS : Chromosome banding methods, standard band nomeclature, and applications in cytogenetic analysis. IN Wheat and Wheat Improvement. Agronomy Monograph. 2nd Ed 13:243-254, 1987.

3. Gill BS, Kimber G : Recognition of translocations and alien chromosome transfers in wheat by the Giemsa C-banding technique. Crop Sci, 17:264-266, 1977.

4. Khan SI : Karyotype analysis of Holdfast a cultivar of Triticum aestivum L. Cellule 63:291-305, 1963.

5. Kimber G : The rationale of measuring chromosomes. Seiken Ziho 22:5-8, 1971.

6. Kimber G, Feldman M : Wild Wheat, and introduction. Sepical Report 353. College of Agriculture, University of Missouri, Columbia, 1987.

7. Miller TE : Systematics and evolution. IN Wheat Breeding by F.G.H. Lupton. Chapman and Hall 1-30, 1987.

8. Mujeeb-Kazi A, Miranda JL : Enhanced resolution of somatic chromosome constrictions as an aid to identifying intergenetic hybrids among some triticeae. Cytologia 50:701-709, 1985.

9. Schulz-Schaeffer J, Haun CR : The chromosomes of hexaploid common wheat, Tritucum aestivum L.Z. Pflanzenzuchtg. *46:112-124, 1961.*

10. Sears ER: Personal communication, 1988.

Correspondence:
Qamar Jahan
Dept. of Genetics,
University of Karachi
Karachi 75270, PAKISTAN.