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CYTOLOGICAL STUDY OF SOME SELECTED IRAQI BREAD WHEAT *(TRITICUM AESTIVUM* L.) GENOTYPES

Balqees Hadi Al- Musawi[1*], Nidhal Abdul Hussein Al–Bdairi[2] and Attyaf Jameel Thamir AL-Tamimi[3]

[1*]Department of Biology, College of Science, Kerbala University, Iraq.
[2] Department of Biology, College of Education for girls, Kufa University, Iraq.
[3]Department of Biology, College of Science, Kufa University, Iraq.

Abstract

Wheat *(Triticum aestivum* L.) is one of the major seed crops cultivated in most part of the world. Studies of cytogenetic has specific a major contribution to bread wheat genetic studies and breeding programs, due to viability of chromosomal various because of homoeology among genomes in this allohexaploid species like genus *Triticum*. In present study based on using cytological traits markers among of five Iraqi bread wheat (*Triticum aestivum* L., is an amphidiploid 2n=6x=42, AABBDD) with three genomes (ABD). The normal metapholic stages of chromosomes were typically observed in the root tip squash cytological studies. Aiming to study these genotypes of bread wheat to determine their genetic stability using cytological analysis which studied that included, chromosomes number in the somatic cells at the root tip of meristematic cells. This study confirmed the presence of 42 chromosomes in bread wheat (*T. aestivum* L.) at metaphase. These results which genotypes identification and cytological studies produce an efficient important tools for improvement of this crop species and will be helpful in future for genotypes selecting in wheat breeding programs.

Key words : Cytological study, Chromosome, Bread wheat, Metaphase.

Introduction

Wheat (*Triticum aestivum* L.) considered is the world's most important cultivated crop and the foremost food staple of mankind. At present prosperity of many countries largely depends upon wheat production because provides greater nourishment for people globally than any other food grain (Belderok *et al.,* 2000). Iraq is one of the Asian countries which has suitable agro climatic conditions for bread wheat cultivation, An estimated 300 million tons of wheat will be required for food needs (Mujeeb-Kazi *et al.,* 2017) and hence time bound swift impacts in wheat production are paramount.

Its belongs to the family Poaceae (Graminae), this family contains number of most important species (Pathak and Shrivastav, 2015). Genus of *Triticum* are grouped into diploids (2n=2x=14), tetraploids (2n=4x=28) and hexaploids (2n=6x=42), like *T. aestivum*.

Common bread wheat, contains 3 different but genetically related genomes (A, B and D) with a total genomic size of 1.7×1010 base pairs, illustrating the complex nature of wheat genome, agronomically and nutrionally, wheat consider very important among other cereal crops because of its large size genome and wide range of uses (Motawei *et al.,* 2007), thus its mainly for wheat improvement to determine local germplasm, germplasm diversity and genetic relationships among breeding lines (Abbas *et al.,* 2008).

Wheat feature accordingly one of the main cytological model organisms for studying mitotic division because of its well determined chromosomes, large, then ease in which mitotic stages can be identified cytologically, and its abundant genetics resources (Mirzaghaderi, 2010). Cytoglogical investigation is one of the best documented experimental proofing for the elucidation of the method of speciation on various groups of plants. Thus, the present work examined the possible chromosomal number of the genotypes studied to knowledge genetic stability, evolutionary relationships and to provide information about genetic similarity among the genotypes that would be useful to wheat breeders.

Author for correspondence : E-mail : balqees.hadi@uokerbala.edu.iq

Materials and Methods

Plant materials and karyotype studies

Five Iraqi bread wheat genotypes which proposed by institute of seed examination and certification /ministry of agriculture in Iraq which is : 1- Latifia 2- Abaa 99 3 - Rasheed 4- Baghdad 5-Abu- Ghraib was done according. Amongst plant tissues including actively dividing cells of root-tip meristematic cells were the ones most generally utilize to produce mitotic chromosome preparations (Sharma and Sharma, 2014). These bread wheat genotypes were chosen for somatic metaphase chromosome preparation in this study was synthetic amphiploid line (2n = 6x= 42; AABBDD).

Chromosome preparation

Classical cytological protocols of mitosis and meiosis (Mujeeb-Kazi *et al.,* 1994) were used with some modification. The seeds of five bread wheat (*Triticum aestivum* L.) genotypes put on moisten filter paper in petri dishes and were placed in a 26°C incubator until emergent roots reached 0.5 to 1 cm long from 1- to 2-week-old germinated seedlings were collected.

Wheat roots were cut and divided to 2 ports and each part was then separately pretreated with one of the later pretreatments in array to accumulate mitotic cells in metaphase: (1) 0.05% (w/v) colchicine solution for 3 h at 26°C, (2) Ice cold water (0°C) for 24 h. For ice water treatment the roots were cut and pretreated in tap water in 1.5 ml tubes on ice for 24 h. and root tips were fixed by solution fixative (Carnoy's fluid), a mixture of (3:1, v/v) via 3 parts of absolute ethanol and 1 part glacial acetic acid, which should be ready fresh daily for 1 hr. Then washing in distilled water, then fixed in the fixation solution. Then root tips were treated with 2-3 drops of 1 N HCl inside vials at 55-60ºC., placed in an oven for 10 min for softened roots were carefully and washed in distilled water. 1-2 cut from root tips were macerated in a drop of fixation solution utilize a fine-pointed forceps, after then the slide was soon "flamed-dried" above a small alcohol lamp and then transferred to another vial containing acetocarmin stain 2%, placed in an oven for 10 min.

Excess stain was removed carefully, then one drop of fresh stain was added on a dot-sized piece of the root tip before placing slide covers carefully, then root tips were squashed and for numerous well-diffusion metaphase chromosomes were stored at "20° until used.

The slides were examined using a compound light microscope Genex (40×) and the meristematic region of the root tip was allocated the slides were examined at 100× magnification and chromosomes at the various stages of mitosis were seen and photographed using digital camera.

Results and Discussion

Cytological characterization

Cytogenetics studies are being performed for a plant to determine the extent of its persistence and stability of genetically through knowledge of the numbers of chromosomes and chromosomal behavior so plant and its relation to the phenotypic stability, and its play an important role in field and improve plant breeding for the purpose of obtaining the highest degree of genetic variations at the level of numbers of chromosomes to knowledge to choose varieties stable and ensure genetic stability (Abella *et al.,* 1995; Al- Sudani, 2002; Al-Musawi, 2019). The somatic chromosomes complements of plants can be regarded as an important tool in the elucidation of evolutionary and biosystematic problems (Al-Bermani, 1991).

In the present cytological studies related the number of somatic chromosomes in the meristematic cells of root tips revealed that they somatic chromosomes were clearly seen in the metaphase stage. The somatic metaphase possessed 2n=42 chromosomes which is genetic stability on the level of chromosomal number and in a state of eupliod in all the investigated genotypes which have 42 chromosomes represent 2n (Fig. 1, 2).

These results agreed with the results of previous studies (Mujeeb-Kazi and Delgado, 2001; Ahmad, 2014) where confirmed the researchers that *W. aestivum* has 42 chromosomes and stable genetically condition and level numbers of chromosomes in the case of euploid and has a haploid set of 21 chromosomes and each member of the complement can be recognized by its architecture (Al-ansari and AL-saadon, 1999).

Chromosome numbers, karyotype and meiotic pairing behavior at metaphase-I in species and hybrid can supply beneficial information for the estimation of taxonomic relationships (Stace, 2000; Ghaffari and Tajik, 2007).

Conclusion

Karyotypes were prepared in five species of bread wheat employ root tip metaphase mitoses. Five species were diploid with 2n=6x=42. Level of evolution of cytogenetic techniques accomplished over the last 60 years has set wheat apart from other cereal crops in expression of potentially to inform genetic material from other species.

Cytogenetic accession have been inclusively used in chromosomal mapping and resistance gene transference from tribe *Triticeae*-regarding species.

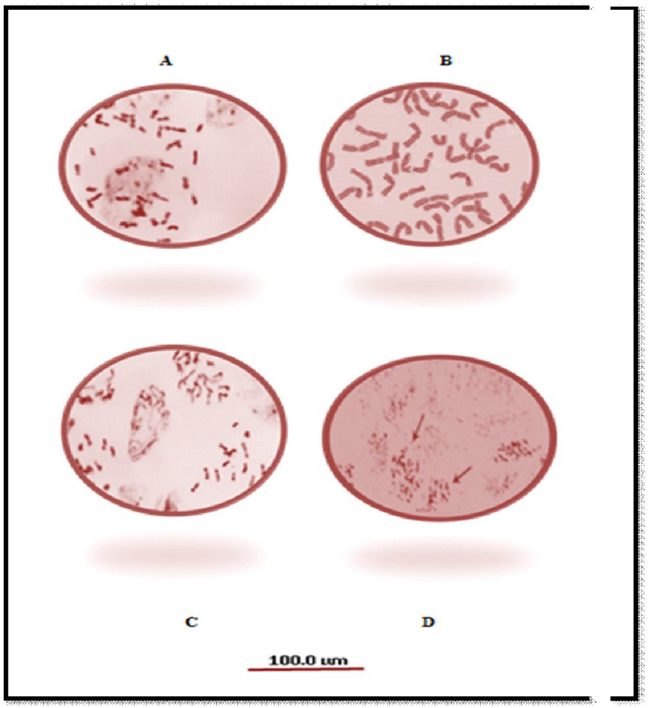

Fig. 1: Cytological studies in root tips of merstematic cells in bread wheat (*T. aestivum* L.) genotypes , A & B: Somatic wheat chromosomes, C & D: Mitotic devision, Scale bars represent= 10 µm (100X).

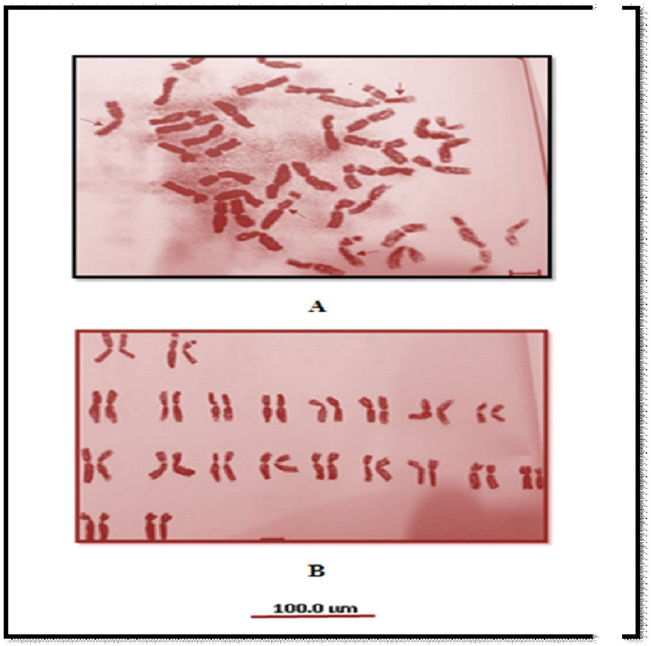

Fig. 2: Chromosomal number of bread wheat (*T. aestivum* L.) genotypes at metaphase , A: Mitotic metaphase root tip cells, B: Karyotype of chromosome, Scale bars represent= 10 µm (100X).

In present study was aimed to define the genetic stability among hexaploid bread wheat genotypes cultivated in Iraq using cytological analysis. This result confirmed that they stability of the chromosomal number of bread wheat genotypes.

Importance of cytological traits in clarifying the regularity of the process of division. It is particularly well suited for cytogenetic studies because of its extensive variation and many genetic tricks as well as sufficiently large chromosomes.

The ability to differentiate each of the chromosomes in an organism, namely, the karyotype, allows the investigator to recognize changes in chromosomal structure and to identify which chromosomes are involved.

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