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A new chromosome number for *Amaranthus blitum*

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ABSTRACT

The chromosome number of *Amarnathus blitum* has been found to be 2n=28 which gives a new chromosome number, previously characterized by 2n=34. The karyotype of *A. blitum* shows distinct features and is more symmetrical. In our laboratory a cytogenetic program in *Amaranthus* was devised in order to improve the karyological characterization of the wild and cultivated species, increase the knowledge of genetic resources and explore evolutionary trends. In the present contribution we report the karyotype formulae of *A. blitum* with the aim of increasing the knowledge of this important cereal like grain crop.

Key Words: *Amarnathus blitum*, chromosome number, karyotype, dysploidy.

INTRODUCTION

Amaranthus commonly called as "chaulai" belongs to the family Amaranthaceae. The genus *Amaranthus* includes a complex array of wild, weedy, leaf vegetables, cereals and ornamental species and consists of approximately 60 species. In India, the principal species grown for grain purpose are *Amarnathus hypochondriacus, A. cruentus, A. caudatus* and for vegetable purpose are *A. dubius, A. lividis* and *A. hybridus*. Weedy species are *A. viridis* and *A. spinosus* (National Academy of Sciences 1985). But there are some other species, *A. tricolor, A. blitum, A. spinosus* and *A. viridis*, which have great nutritional values (Srivastava 2011). Amaranth proteins proved to be one of the most promising food ingredients and capable of complementing cereal or legume proteins. The amaranth proteins have good digestibility and majority of proteins belongs to the group of water soluble albumin and salt soluble globulins (Srivastava and Roy 2011). The present paper deals with the kayotypic analysis of *A. blitum,* which reports a new chromosome number. *A. blitum*, a cultivated herb with broad leaves and small seeds, is distributed in the plains of East India. The present study is based on the material collected from Varanasi (U.P.), India.

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MATERIAL AND METHODS

For karyotypic studies actively growing roots (1.0-1.5 cm long) were excised from germinated seeds and pretreated with 1.5% freshly prepared aqueous solution of para-di-chlorobenzene for two hrs and kept at 15° C. After washing these were fixed in 1:3 acetic alcohol for 24 hr. The root tips were washed and hydrolysed in 1N HCl for 4-5 min at 58-60°C and stained in 2% aceto-orcein on cleaned glass slide. Degree of symmetry/asymmetry of karyotypes has been estimated following Stebbins (1958).

RESULTS AND DISCUSSION

Somatic chromosome number of 2n=28 has been observed in the present material (Fig 1), which is a new chromosome number for *A. blitum.* The chromosome number of this plant was not consistent and differed with the earlier reports (Behera and Patnaik 1974).

Fourteen pairs of chromosomes have been arranged in decreasing order of total lengths (Fig 2) and the mean karyotype measurements from three good spreads are presented in Table 1. Based on the location of centromere the karyotype formula of *A. blitum* is 7M+5SM+2ST and it belongs to 1b class (Stebbins 1958). The TF% is 38.46% which shows that the kayotype is moderately asymmetrical.

Fig. 1. Metaphase stage of mitotic division in the root tips of *A. blitum*. (Bar=5µm)

Table 1. Chromosome measurements of *A. blitum.*

S.No.	p(µm)	q(µm) CL (µm)	(p/q)	TF%	Karyotype formula
1.	0.80	0.75	1.55	1.1	
2.	1.00	0.90	1.90	1.1	
3.	0.70	0.50	1.20	1.4	
4.	0.55	0.50	1.05	1.1	
5.	1.05	1.00	2.05	1.1	
6.	0.50	0.50	1.00	1.0	
7.	1.05	1.00	2.05	1.1	
8.	0.80	0.40	1.20	2.0	38.46 7M+5SM+2ST
9.	1.00	0.50	1.50	2.0	
10.	0.95	0.45	1.40	2.1	
11.	1.50	0.70	2.20	2.1	
12.	1.40	0.50	1.90	2.8	
13.	0.90	0.20	1.10	4.5	
14.	1.10	0.35	1.35	3.1	

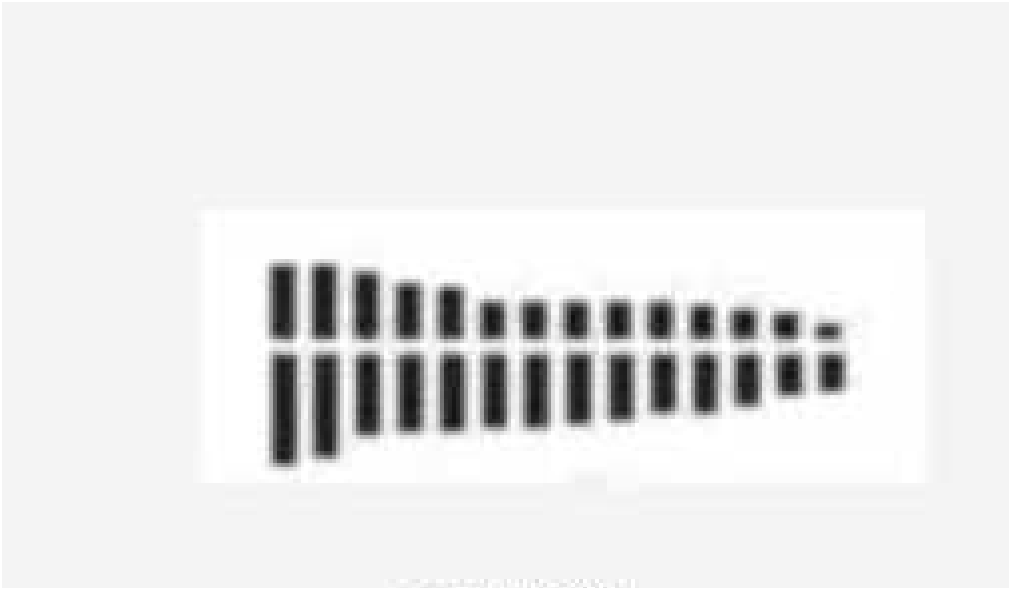

Fig. 2. Idiogram of *A. blitum*.

In the present study, findings of new chromosome number in *A. blitum* (2n=28) indicate that it must have derived from new basic number (x=14) and show similarity with the findings of Pal *et al*. (2000) as reported in *Amaranthus tenuifolius* (2n=28). This has added a new basic number (x=14) in the list of genus *Amaranthus*. The mechanism of derivation can be correlated with the species previously originated from basic number x=16 or 17 by the mechanism of ploidy and finally conclude that the genus could be tribasic x=14, 16 and 17 and thus here it is suggested the genus that *Amaranthus* could be categorized into three groups based on chromosome counts.The finding of new chromosome count of 2n=28 in *A. blitum* indicate that the chromosome numbers have been reduced secondarily with reference to the earlier chromosome number report in *A. blitum* (2n=34) (Grant 1959; Behera and Patnaik 1974).The basic number in *A. blitum* is x=14, this could be taken as secondary number which has been derived immediately from 16 or 17. For the first time ever in the family Amaranthaceae, the conjunction of cytological data with phylogenetic models permits a realistic appraisal of probable primitive chromosome number to some extent. The changes in basic chromosome number x=16 to x=14, which indicate the primitiveness and for the verification it requires to study atleast four generations. Further it could be aided that new number correlate with phylogenetic advancement in family Amaranthaceae. The decrease in basic number of chromosome may support the finding of Roser (1999) where it has been suggested the possibilities of major deficiency in the coverage of infra-familier taxa, where the numerical change has taken place due to dysploidy. In our finding, a pair-wise change in chromosome numbers pattern could be reason of the variation in 2n chromosome complement of *A. blitum*. This type of step-wise numerical change followed by the mechanism of dysploidy and is an indication of playing a major significant role in the evolution as reported in a number of other families of angiosperms (Roser 1999).

Several groups of angiosperm exist in which variable chromosome numbers have been raised as a result of dysploidy or aneuploidy (Stebbins 1971; Favager 1999 and Stace 2000), and this phenomenon is thought to have played an important role in the evolution of family *Boraginaceae,* genera such as *Pulmonaria* (Sauer 1987) *Omphalodes* Miller (Grau 1967), *Mertensia* Roth (Vasudevan 1975) and *Cynoglottis* (Bigazzi and Selvi 2001). The reduction in chromosome number from n=16 to n=14 suggested to be aneuploid or dysploid could be matter of discussion in my investigation. Although, they are two different phenomena, which have different consequences. A series of variation in number like n=14, 21 and 35 taken euploid variation but numbers n=6, 8, 9, 10 or 11 represents aneuploids (Lammers 1993). However, in our situation could not be

distinguished, so any noneuploid number of uncertain origins could be referred here as dysploid. The term "dysploidy" indicates the process whereby the euchromatin of a genome is rearranged by translocations onto a greater or lesser number of centromeres, which is evidenced in morphology of chromosome in our study. The term "aneuploidy" denotes the gain or loss of whole chromosomes. According to Lammers (1993), the races with n=6,8 and 10 were derived from the 12 paired race via a sequence of descending aneuploid mechanism followed by reciprocal translocations with the loss of a centric fragment. It is clearly evidenced in my finding that there is whole chromosome loss at diploid level in high number, so it is assumed that dysploid reduction from relatively high chromosome number (2n=34) has occurred in *Amaranthus*, due to repeated chromosome manipulation during hybridization in between the races. We can suggest that this type of change in chromosome number could be suggested as an example of dysploidy rather than aneuploidy.

Thus, reduction in chromosome number in *A. blitum* supports the earlier reports where dysploid mechanism has been taken in account. In our case, it may be suggested that extensive dysploid reduction from high primitive chromosome numbers, to the lower chromosome number species associated with derived morphological or ecological conditions. The evolutionary significance of these data has various interpretations, reflecting a contemporary paradigin that x=6, 7 always considered primitive in angiosperm. Indeed, dysploid reduction from diploid ancestors of high chromosome number may be the most common cyto-evolutionary pattern in angiosperm families.

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