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Cytogenetic Analysis of Four *Hosta* Species Native to Korea

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ABSTRACT : The chromosome numbers and karyotypes were investigated in four Korean native species of the genus *Hosta*. The chromosome complements were diploid of 2n=60 in *H. japonica* var. *lancifolia* Nakai and *H. capitata* Nakai, aneuploid of 2n=59 in *H. minor* (Bak.) Nakai, and modified triploid of 2n=92 in *H. longipes* (Fr. et Sav.) Matsumura. All the species carried four sets of distinctly large chromosomes of which the chromosome types were telocentrics or subtelocentrics with 4.4~7.2 ㎛ in length. The other chromosomes were meta-, submeta, subtelo-, or telocentric types and showed gradual length degradation in the range of 1.0~3.0 ㎛. The satellites appeared vestigially in a pair or a triplet set of chromosomes which depends on the species. New chromosome number and karyotype in *H. longipes* were the first report in this species. The structural rearrangement was suggested to explain the modified triploid composition of 2n=92.

Key words : genus *Hosta*, chromosome number, karyotype, triploid, aneuploid

INTRODUCTION

More than 40 species of *Hosta* plants belonged to the family Liliaceae are widely distributed throughout the East Asia. Ten species of *Hosta* plants have been reported in Korean natural populations (Lee, 1996). *Hosta* plants are widely used for decorative material, and the rhizomes and leaves of these plants are also used for medicinal purposes such as the sources of steroidal glycosides and saponins (Budzianowski, 1990; Mimaki *et al.*, 1997; Mimaki *et al.*, 1998).

The chromosome complements of these plants were known to be species- specific. Their karyotypes could be a useful tool for the identification of the species accurately. Almost all of the *Hosta* species have the basic chromosome numbers of 2n=2x=60 (Darlington & Wylie, 1955; Bolkhovskikh *et al.*, 1969; Takahashi, 1994). Diverse chromosome compositons depending on the species were also reported in the natural populations (Kaneko & Maekawa, 1968; Kaneko, 1970). The chromosome investigations of the wild species of *Hosta* plants have been carried out in the very limited species in Korea (Lee, 1967, 1972; Seo & Song, 1983).

In the present study, karyotypes were examined in four species of *Hosta* plants distributed in Korea; *Hosta japonica* var. *lancifolia, H. minor, H. capitata*, and *H. longipes*.

MATERIALS AND METHODS

The plant materials were collected from the mountainside near Inje-gun, Kangwon Province, Korea and were provided after being propagated vegetatively at Chuncheon Experimental Station in Kangwon Provincial Agricultural Research and Extension Services. For plant materials, each species was planted in pot of well mixed peat moss, perlite, and vermiculite. These, then, were kept in a green house, where temperature, humidity and water supply

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were carefully watched for one to two weeks. After cutting off the fresh root tips, they were processed to make the preparations for microscopic observation.

The root tips were pretreated in 2 mM 8-hydroxyquinoline solution for 6~7 hours and then placed in the refrigerator for over-night in aceto-ethanol fixative. It was then washed, hydrolysed at 60℃ for 15~30 seconds, and stained in 1% aceto-orcein for 1~2 minutes to make squash preparation. Metaphase chromosomes were photomicrographed with a Fuji HR-20 microfilm negative (ASA 25) with a magnitude of 500X in oil immersion state. The chromosome types were classified according to the methods of Levan *et al.* (1964).

RESULTS AND DISCUSSION

Metaphase chromosome complements and their karyotypic idiograms of *Hosta* species are shown in Fig. 1 and Fig. 2. The chromosome compositions of each species were very similar, but showed species-specific pattern, enabling these results to be used as a basic data to identify the species.

Chromosome compositions of *H. japonica*, *H. minor* and *H. capitata* had diploid patterns of 2n=60 (Seo & Song, 1983), while those of *H. minor* and *H. longipes* showed aneuploid (2n=59) and triploid (2n=92) patterns, respectively.

The chromosomes of *H. japonica* consisted of 4 pairs of relatively big chromosomes (chromosomes 1 to 4), ranged 4.4~5.0 ㎛ and the rest ones ranged 1~3.1 ㎛ showing gradual length degradation. Of 4 pairs of relatively big chromosomes, 2 pairs (chromosomes 1 and 4) were telocentrics, and the other two pairs (chromosomes 2 and 3) were identified as subtelocentrics. Among the other chromosomes, 5 pairs (chromosomes 5, 7, 10, 20, and 21) were confirmed as submetacentrics, and the remaining 21 pairs as metacentrics (chromosomes 6, 8, 9, and 11 to 19). However, the small chromosomes of 1~2 ㎛ were hard to identify the type under a Light Microscope. Satellites were observed tracely in one pair of chromosomes (chromosome 2), thus judged it difficult to grasp by general staining method. The results of this study were similar to the report of Lee (1967).

The *H. minor* chromosomes were similar to *H. japonica* in length (1.0~5.0 ㎛) but showed minor differences in chromosome type. Among four pairs (chromosomes 1 to 4) with distinguished size, only one pair (chromosome 1) was subtelocentrics and the other three pairs (chromosomes 5, 6 and 7) telocentrics. The rest of the chromosomes were mostly metacentrics but small chromosomes around 1 m in length were hard to identify the exact types.

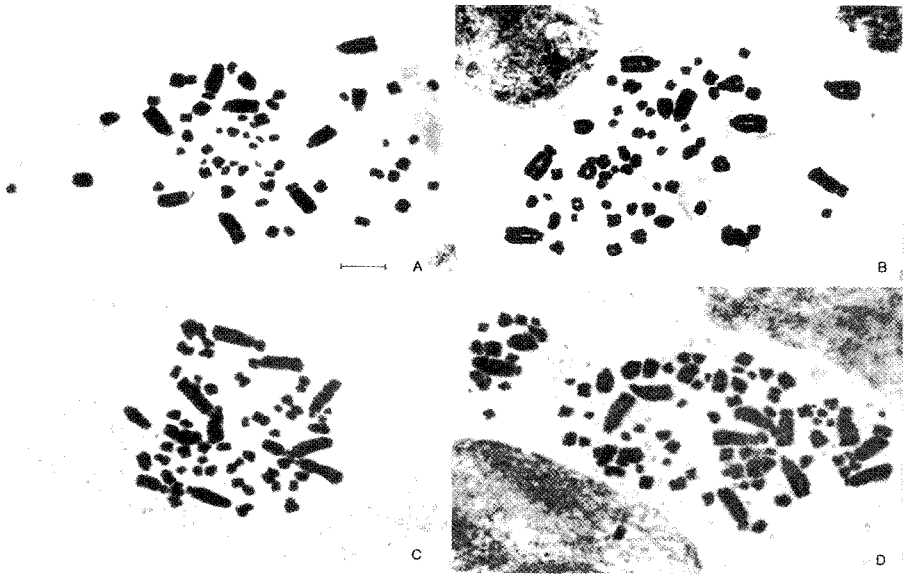

Fig. 1. Metaphase plates of *Hosta* species. A; *H. japonica* var. *lancifolia* (2n=60), B; *H. minor* (2n=59), C; *H. capitata* (2n=60), D; *H. longipes* (2n=92). Scale bar, 5 ㎛.

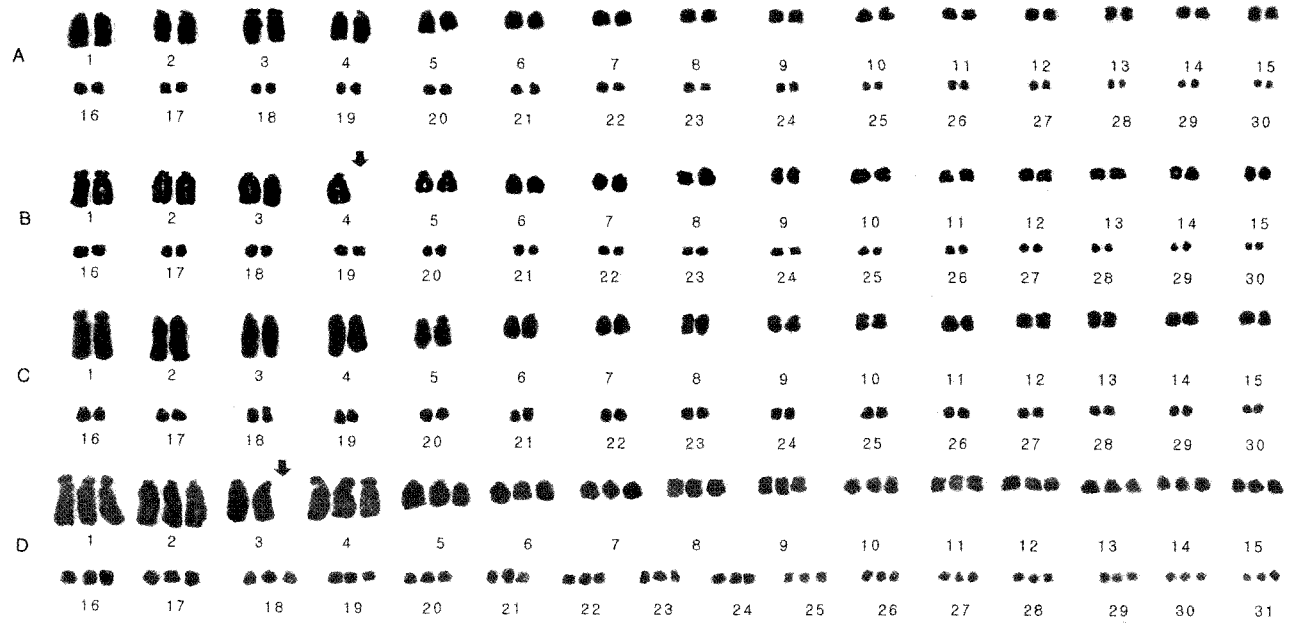

Fig. 2. Karyotype idiograms of *Hosta species*. A; *H. japonica* var. *lancifolia*. B; *H. minor* C; *H. capitata*, D; *H. longipes*. Arrows indicate unpaired chromosome sites in homologoues (B) and triplet set (D).

Satellites were observed as a faded trace in the fifth chromosome as the result of Seo & Song (1983).

The chromosome number of *H. capitata* was reported as 2n=58 (Bang, 2004), while our study found this species as a diploid of 2n=60. The chromosome complement consisted of distinguished big chromosomes (chromosomes 1to 4) of 6.2~7.2 ㎛ and relatively small ones (chromosomes 5 to 30) that showed gradual decrease of length within 1.2~4.2 ㎛. The big four pairs of chromosomes were either subtelocentrics (chromosomes 1 and 4) or telocentrics (chromosomes 2 and 3) and the rest of the chromosomes were confirmed as metacentrics (chromosomes 8 to 10, 12 to 15, 18 and 20), submetacentrics (5 chromosomes), subtelocentrics (chromosomes 11, 17 and 19) and telocentrics (chromosomes 6, 7 and 16). However, the remaining small chromosomes were extremely tiny in size of 1㎛ and unclear in chromosome type. Satellite chromosome was traced in one pair (chromosome 5) but not verified in other chromosomes. This result was similar to the result of Kaneko & Maekawa (1968), which examined and analyzed the chromosome composition of *H. capitata* collected in Korean populations.

The chromosome number of the *H. longipes* was reported as a diploid of 2n=60 (Bang, 2004). In the present study, the chromosome number was a modified triploid of 2n=92. Four pairs of chromosomes (chromosomes 1 to 4) were much bigger than others. Chromosomes 1, 2 and 4 showed triplet sets, while chromosomes 3 was composed of only two. The length and the type of these chromosomes were either subtelocentrics (chromosome 1 and 4) or telocentrics (chromosomes 2 and 3) of 6.1~7.0 ㎛ in length. The rest of the chromosomes showed similar pattern of *H. capitata* in length and type except they were triplet sets of chromosomes. Satellites were observed in the chromosome 2 as the faint trace only. The chromosome number of *H. longipes* was reported as a diploid of 2n=60 and the triploid plants should have 2n=90. However, the *H. longipes* in our study had 2n=92. Instead of the one missing large chromosome, two new small chromosomes were added. Thus the triploid chromosome composition is assumed to be numerically changed by the structural rearrangement.

To clarify the interspecific relationships among native *Hosta* plants in Korea, other approaches, such as the banding technique and molecular cytogenetic method using a specific DNA probe should be applied (Zonneveid & Van Iren, 2001; Lee & Chang, 2002).

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