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# Cytogenetic Studies of Six Species in Family Araceae from Thailand

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Abstract. The chromosome numbers and karvotypes of six species belonging to five genera of the family Araceae distributed in natural areas from Thailand were analyzed. These species are Aglaonema modestum Schott ex Engl., Ag. simplex (Blume) Blume, Amorphophallus serrulatus Hett. & A. Galloway, Arisaema maxwellii Hett. & Gusman, Hapaline benthamiana Schott and Homalonema griffithii (Schott) Hook.f. Three of them (Ag. simplex, Am. serrulatus and Ar. maxwellii) are not common and endemic species in Thailand. The chromosome number and karyotypes of all species were determined as Ag. modestum 2n = 40 with karyotype to be 20m + 14sm + 6st, Ag. simplex 2n = 42 with karyotype to be 6m + 26sm + 10st, Am. serulatus 2n = 26 with karyotype to be 12m + 6sm + 8st and two satellite chromosomes, Ar. maxwellii 2n = 24with karyotype to be 22m + 2sm and two satellite chromosomes, Ha. benthamiana 2n = 26 with karyotype to be 26m and one satellite chromosome and Ho. griffithii 2n = 40with karyotype to be 30m + 10sm and two satellite chromosomes. Karyotype analysis indicated that six species of family Araceae generally have metacentric, submetacentric and subtelocentric chromosomes. In addition, satellites were observed in Am. serrulatus, Ar. maxwellii, Ha. benthamiana and Ho. griffithii. The chromosome numbers from three species of them and karyotypes from five species of them in this study were determined for the first time in this study. These cytogenetic studies of this report can be used for classification of six species in the family Araceae.

Keywords: Araceae, Chromosome number, First report, Karyotype, Satellite, Thailand.

## INTRODUCTION

Family Araceae is the largest primitive monocot family and the most diverse (Grayum 1990; Boyce et al. 2012; Nauheimer et al. 2012). Currently, 120 genera and more than 3,800 species are recognized in worldwide. This family is distributed in tropical regions of North and South America, Asia and throughout tropical western pacific and eastern Australia, tropical Africa, temperate Eurasia, southern Africa, Madagascar and Seychelles (Mayo et al.1997; Boyce et al. 2012). In Thailand, 30 genera with about 210 species of family Araceae are reported by Boyce et al. (2012). The traditionally uses of this family are found to be local food, ornamental plants and medicinal plants (Boyce et al. 2012).

The status of cytogenetic data is vital for taxonomic decision-making and biosystematic investigations (Stace 2000). Classical cytological techniques and fundamentals are still an excellent starting point for basic plant cytogenetic studies. The chromosome numbers and chromosome characteristics can be used to identify the genetic diversity and phylogenetic information (Jahier 1996; Stace 2000; Guerra 2008; Figueroa and Bass 2010).

A few years ago, the authors collected specimens of the family Araceae in Thailand for study diversity and the chromosomes and found that the not common six species in this study - Ag. modestum Schott ex Engl., Ag. simplex (Blume) Blume, Am. serrulatus Hett. & A. Galloway, Ar. maxwellii Hett. & Gusman, Ar. maxwellii Hett. & Gusman, Ha. benthamiana Schott, and Ho. griffithii (Schott) Hook.f. were reported to use for daily life in the Thai communities. Ag. modestum Schott ex Engl. is used as an ornamental and medicinal plant (Boyce et al. 2012). Ag. simplex (Blume) Blume is reported conservation status from the IUCN Red List of Threatened Species to be a least concern (LC) species (Allen 2011). Am. serrulatus Hett. & A. Galloway is an endemic species in Thailand (Boyce et al. 2012). Ar. maxwellii Hett. & Gusman is reported conservation status in IUCN red list to be Vulnerable species (VU) and it is reported to be a rare species from Thailand which is presented in the book title threatened plants in Thailand (Chamchumroon et al. 2017). Ha. benthamiana Schott is used as traditional food in Thailand (Boyce et al. 2012). Ho. griffithii (Schott) Hook.f. is mainly distributed in the south of Thailand and used as an ornamental plant (Boyce et al. 2012). The chromosome numbers and karyotypes of few species from family Araceae was studied by few botanists - Larsen 1969; Okada 1982; Okada 2000; Chen et al. 2003; Eksomtramage et al. 2007; Liu et al. 2010; Senavongse et al. 2018; Saensouk et al. 2019 and Senavongse et al. 2020. This study is expected to find more new information of plant chromosome. Therefore, the aims of this study are to study the chromosome numbers and karyotypes of the six species of Araceae in Thailand.

# MATERIALS AND METHODS

Six species of Araceae in Thailand, namely Ag. modestum Schott ex Engl. (coll. no. R. Senavongse 001/2016), Ag. simplex (Blume) Blume (coll. no. R. Senavongse 006/2016), Am. serrulatus Hett. & A. Galloway (coll. no. R. Senavongse 031/2016), Ar. maxwellii Hett. & Gusman (coll. no. R. Senavongse 036/2016), Ha. benthamiana Schott (coll. no. R. Senavongse 056/2016) and Ho. griffithii (Schott) Hook.f. (coll. no. R. Senavongse 061/2016) were collected from the field in Thailand (Table 1) and voucher specimens were deposited in the Mahasarakham University Herbarium (MSU) All fresh specimens were grown in a nursery at the Walai Rukhavej Botanical Research Institute, Mahasarakham University, Maha Sarakham Province, Thailand. The chromosome numbers study follows Saensouk et al. (2019) and Senavongse et al. (2018, 2020). The nomenclature of the chromosome morphology follows the classification of Levan et al. (1964). The classification of the karyotype symmetry degree is proposed by following Stebbins (1971). The diploid chromosome numbers of each species in this study are counted from 20 cells. For the arrangement of the karyotypes the following parameters such as average length of the short arm (Ls), average length of the long arm (Ll), length of each chromosome (LT), average measurement of relative length (RL), chromosome index (CI), standard deviation (SD) of RL and CI from metaphase chromosomes were calculated by methods of Saensouk et al. (2019) and Senavongse et al. (2018, 2020).

#### RESULT AND DISCUSSION

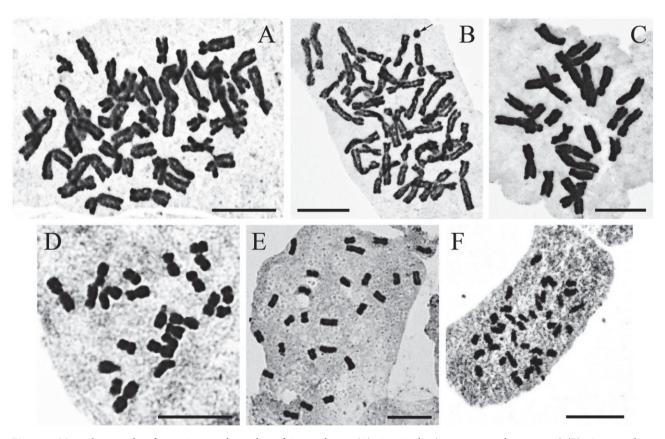
The chromosome number, chromosome length range, haploid chromosome length, arm ratio, relative length, and karyotype formula were determined from 20 metaphase cells in each species. The diploid chromosome numbers in this study are reported as 24–42 chromosomes (Table 1; Figure 1). The characteristics of karyotype of examined six species in family Araceae from Thailand is are given below (Table 1; Figure 2).

The somatic chromosome number of Ag. modestum was found to be 2n = 40 and Fundamental number (NF) = 80 (Figure 1(A)). The karyotype formula was 20m + 14sm + 6st including 10 pairs including metacentric chromosomes, seven pairs of submetacentric chromosomes and three pairs of subtelocentric chromosomes. It has an asymmetrical karyotype due to the karyotype formula ratio (symmetrical karyotype comprise of metacentric and submetacentric chromosome and asymmetrical karyotype comprise of metacentric, submetacentric, subtelocentric and telocentric chromosome). The short arm chromosome length ranged from  $1.01\pm0.01$  to  $4.72\pm0.02 \ \mu$ m, the long arm chromosome length ranged from  $2.13\pm0.01$  to  $5.07\pm0.03 \ \mu$ m, the

			Karyotype formulas	Previous recorded			
Species	Localities	2 <i>n</i>		2 <i>n</i>	Karyotype formulas	Author	
				60	-	Chen et al. (2003)	
Ag. modestum	Loei	40	20m+14s+ 6st	80	-	Eksomtramage et al. (2007)	
				40	22m+18sm	Liu et al. (2010)	
Ag. simplex	Kalasin	42**	6m+26sm+10st	42	-	Larsen (1969)	
Am. serrulatus	Ubon Ratchathani	26*,**	12m+6sm+8st	-	-	-	
Ar. maxwellii	Changmai	24*,**	22m+2sm	-	-	-	
Ha. benthamiana	Chaiyaphum	26**	26m	13	26	Larsen (1969)	
Ho. griffithii	Songkhla	40**	30m+10sm	40	-	Okada (1982) Okada (2000)	

Table 1. Summarizes of the cytogenetic reviews of studies in six species of the Araceae family in Thailand.

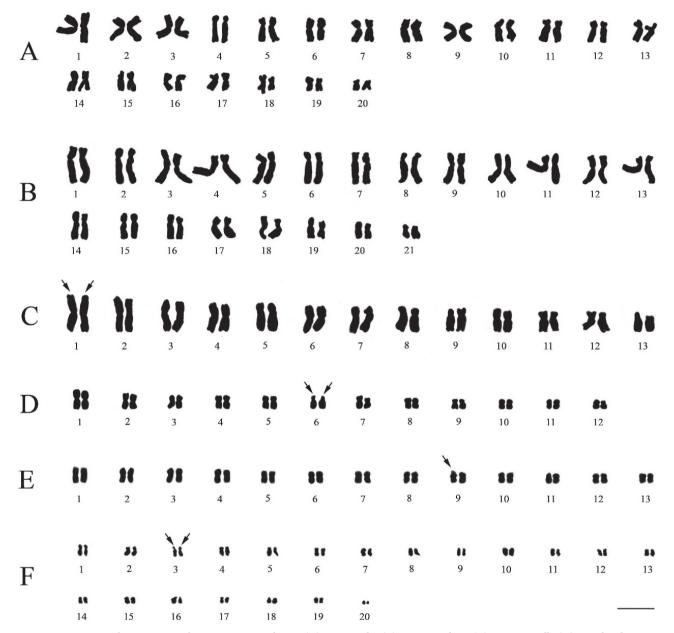
\* = new report chromosome numbers for the first time. \*\* = new report karyotype for the first time.



**Figure 1.** Microphotographs of somatic metaphase plate of *Ag. modestum* (A), *Ag. simplex* (arrow = non chromosome) (B), *Am. serrulatus* (C), *Ar. maxwellii* (D), *Ha. benthamiana* (E) and *Ho. griffithii* (F). Scale bars =  $10 \mu m$ .

total arm chromosome length ranged from  $3.14\pm0.02$  to  $9.79\pm0.05 \ \mu$ m. Relative lengths were 2.50-7.79 %. Centromeric indexes were 0.53-0.77 (Table 2; Figure 2(A)). The somatic chromosome number of *Ag. modestum* in this study differs from earlier reported (Chen et al. 2003)

2n = 60; Eksomtramage et al. 2007, 2n = 80). Whereas, the somatic chromosome number of this species in this study was corresponding to the previous reported by Liu et al. (2010) and they reported the karyotype to be 22m + 18sm, which differs from this study (Table 1).



**Figure 2.** Karyotypes by conventional staining. *Ag. modestum* (A), *Ag. simplex* (B), *Am. serrulatus* (C), *Ar. maxwellii* (D), *Ha. benthamiana* (E) and *Ho. griffithii* (F). Arrows in C-F indicate satellite. Scale bar =  $10\mu$ m.

The somatic chromosome number of Ag. simplex were 2n = 42 and NF = 84 (Figure 1(B)). The karyotype formula was 6m + 26sm + 10st including 21 pairs, which comprised three pairs of metacentric chromosomes, 13 pairs of submetacentric chromosomes and five pairs of subtelocentric chromosomes. It has an asymmetrical karyotype due to the karyotype formula ratio. The short arm chromosome length ranged from  $0.83\pm0.00$  to  $2.97\pm0.01 \ \mu$ m, the long arm chromosome length ranged from  $2.80\pm0.01$  to  $7.50\pm0.03 \ \mu$ m, the total arm chromosome length ranged from  $3.63\pm0.02$  to  $10.48\pm0.055 \ \mu$ m. Relative lengths were  $2.21-6.37 \ \%$ . Centromeric indexes were 0.51-0.75 (Table 3; Figure 2(B)). The somatic chromosome number of this species in this study was corresponding to the previous reported by Larsen (1969). The karyotype of *Ag.simplex* in this study is reported for the first time.

The somatic chromosome number of *Am. serrulatus* were found as 2n = 26 and NF = 52 (Figure 1(C)). The karyotype formula was asymmetrical karyotype due to

Chromosome pair	Ls±SD ( $\mu$ m)	Ll±SD ( $\mu$ m)	LT±SD (µm)	RL (%)	CI	Chromosome type
1	4.72±0.02	5.07±0.03	9.79±0.05	7.79	0.53	Metacentric
2	3.72±0.01	4.96±0.03	8.68±0.04	6.91	0.58	Metacentric
3	4.12±0.02	4.39±0.03	8.51±0.04	6.78	0.56	Metacentric
4	$1.70 {\pm} 0.01$	$5.92 \pm 0.03$	$7.62 \pm 0.04$	6.06	0.77	Subtelocentric
5	$1.96 \pm 0.01$	4.89±0.03	6.85±0.04	5.45	0.69	Submetacentric
6	$3.10 \pm 0.01$	$3.59 \pm 0.02$	$6.68 \pm 0.04$	5.32	0.54	Metacentric
7	$2.71 \pm 0.01$	3.84±0.02	$6.55 \pm 0.04$	5.22	0.58	Metacentric
8	$2.49 \pm 0.01$	3.89±0.03	6.38±0.03	5.08	0.56	Metacentric
9	$3.03 \pm 0.02$	$3.32 \pm 0.02$	6.35±0.03	5.06	0.59	Metacentric
10	$2.52 \pm 0.01$	3.64±0.02	6.16±0.03	4.90	0.57	Metacentric
11	$1.46 \pm 0.01$	$4.68 \pm 0.02$	6.14±0.03	4.89	0.72	Subtelocentric
12	$1.78 \pm 0.01$	$4.32 \pm 0.02$	6.11±0.03	4.86	0.74	Subtelocentric
13	$1.98 \pm 0.01$	$4.12 \pm 0.02$	6.10±0.03	4.86	0.59	Metacentric
14	$2.23 \pm 0.01$	$3.70 \pm 0.02$	$5.94 \pm 0.03$	4.73	0.62	Submetacentric
15	$2.29 \pm 0.01$	$3.46 \pm 0.02$	$5.75 \pm 0.03$	4.58	0.62	Submetacentric
16	$2.15 \pm 0.01$	$3.09 \pm 0.02$	$5.23 \pm 0.03$	4.17	0.63	Submetacentric
17	$2.13 \pm 0.01$	$3.00 \pm 0.02$	$5.13 \pm 0.03$	4.08	0.61	Submetacentric
18	$2.10 \pm 0.01$	$2.50 \pm 0.01$	$4.60 \pm 0.02$	3.66	0.60	Submetacentric
19	$1.33 \pm 0.01$	$2.59 \pm 0.01$	$3.92 \pm 0.02$	3.12	0.61	Submetacentric
20	$1.01 \pm 0.01$	2.13±0.01	3.14±0.02	2.50	0.59	Metacentric

**Table 2.** Mean length of short arm chromosome (Ls), long arm chromosome (Ll), total arm chromosome (LT), relative length (RL), centro-meric index (CI) and standard deviation (SD) of RL, CI from 20 metaphases of Ag. modestum (2n=40).

**Table 3.** Mean length of short arm chromosome (Ls), long arm chromosome (Ll), total arm chromosome (LT), relative length (RL), centromeric index (CI) and standard deviation (SD) of RL, CI from 20 metaphases of *Ag. simplex* (2*n*=42).

Chromosome pair	Ls±SD ( $\mu$ m)	Ll±SD ( $\mu$ m)	LT±SD (µm)	RL (%)	CI	Chromosome type
1	2.97±0.01	7.50±0.03	10.48±0.05	6.37	0.64	Submetacentric
2	$2.58 \pm 0.01$	7.41±0.03	$9.98 \pm 0.04$	6.07	0.66	Submetacentric
3	3.12±0.01	6.61±0.03	9.73±0.04	5.92	0.65	Submetacentric
4	$1.86 \pm 0.01$	7.83±0.03	$9.69 \pm 0.04$	5.89	0.75	Subtelocentric
5	$2.55 \pm 0.01$	$6.60 \pm 0.03$	9.16±0.04	5.57	0.69	Submetacentric
6	$2.52 \pm 0.01$	6.62±0.03	9.14±0.04	5.56	0.66	Submetacentric
7	2.37±0.01	6.56±0.03	8.93±0.04	5.43	0.75	Subtelocentric
8	$1.74 \pm 0.01$	7.07±0.03	8.81±0.04	5.36	0.60	Submetacentric
9	3.60±0.02	5.17±0.02	8.77±0.04	5.33	0.51	Metacentric
10	3.61±0.02	4.83±0.02	$8.44 {\pm} 0.04$	5.13	0.64	Submetacentric
11	2.58±0.01	5.66±0.03	8.23±0.04	5.01	0.55	Metacentric
12	3.10±0.01	$5.02 \pm 0.02$	8.12±0.04	4.94	0.70	Subtelocentric
13	$1.87 \pm 0.01$	5.76±0.03	7.63±0.03	4.64	0.68	Submetacentric
14	2.57±0.01	4.96±0.02	7.53±0.03	4.58	0.63	Submetacentric
15	2.46±0.01	4.68±0.02	7.14±0.03	4.34	0.73	Subtelocentric
16	1.91±0.01	4.92±0.02	6.83±0.03	4.16	0.75	Subtelocentric
17	$1.89 \pm 0.01$	4.29±0.02	6.18±0.03	3.76	0.70	Submetacentric
18	2.53±0.01	3.53±0.02	6.07±0.03	3.69	0.52	Metacentric
19	2.34±0.01	3.09±0.01	5.43±0.02	3.30	0.69	Submetacentric
20	$1.53 \pm 0.01$	3.01±0.01	4.53±0.02	2.76	0.69	Submetacentric
21	0.83±0.00	$2.80 \pm 0.01$	3.63±0.02	2.21	0.61	Submetacentric

Chromosome pair	Ls±SD (µm)	Ll±SD (µm)	LT±SD (µm)	RL (%)	CI	Chromosome type
*1	4.95±0.02	5.51±0.03	10.46±0.05	11.05	0.58	Metacentric
2	4.06±0.02	5.29±0.03	9.35±0.04	9.88	0.59	Metacentric
3	3.26±0.01	$5.55 \pm 0.03$	8.81±0.04	9.31	0.57	Metacentric
4	3.31±0.01	$4.65 \pm 0.03$	$7.96 \pm 0.04$	8.41	0.56	Metacentric
5	$2.02 \pm 0.01$	5.91±0.03	$7.94 \pm 0.04$	8.39	0.72	Subtelocentric
6	$3.19 \pm 0.01$	4.49±0.03	7.67±0.04	8.11	0.55	Metacentric
7	2.21±0.01	$5.03 \pm 0.03$	7.23±0.04	7.64	0.69	Submetacentric
8	$1.71 \pm 0.01$	$5.09 \pm 0.03$	$6.80 \pm 0.04$	7.18	0.74	Subtelocentric
9	$1.88 \pm 0.01$	4.38±0.02	6.26±0.03	6.61	0.71	Subtelocentric
10	$2.54{\pm}0.01$	$3.54 \pm 0.02$	6.09±0.03	6.43	0.59	Metacentric
11	$1.62 \pm 0.01$	$3.85 \pm 0.02$	$5.48 \pm 0.03$	5.79	0.68	Submetacentric
12	$1.54{\pm}0.01$	3.91±0.02	$5.45 \pm 0.03$	5.76	0.68	Submetacentric
13	$1.41 \pm 0.01$	3.75±0.02	$5.16 \pm 0.03$	5.45	0.72	Subtelocentric

**Table 4.** Mean length of short arm chromosome (Ls), long arm chromosome (Ll), total arm chromosome (LT), relative length (RL), centromeric index (CI) and standard deviation (SD) of RL, CI from 20 metaphases of *Am. serrulatus* (2n=26).

\*=satellite chromosome.

**Table 5.** Mean length of short arm chromosome (Ls), long arm chromosome (Ll), total arm chromosome (LT), relative length (RL), centromeric index (CI) and standard deviation (SD) of RL, CI from 20 metaphases of *Ar. maxwellii* (2*n*=24).

Chromosome pair	Ls±SD (µm)	Ll±SD (µm)	LT±SD ( $\mu$ m)	RL (%)	CI	Chromosome type
1	2.65±0.01	3.00±0.02	5.65±0.04	13.00	0.52	Metacentric
2	2.25±0.01	2.44±0.02	4.69±0.03	10.80	0.52	Metacentric
3	$1.91 \pm 0.01$	2.36±0.02	4.27±0.03	9.83	0.58	Metacentric
4	$1.87 \pm 0.01$	2.37±0.02	4.25±0.03	9.78	0.50	Metacentric
5	$1.75 \pm 0.01$	$2.05 \pm 0.02$	3.80±0.03	8.75	0.57	Metacentric
*6	$1.71 \pm 0.01$	2.03±0.02	3.74±0.03	8.61	0.51	Metacentric
7	$1.50 \pm 0.01$	$1.71 \pm 0.02$	3.21±0.03	7.39	0.59	Metacentric
8	$1.47 \pm 0.01$	$1.56 \pm 0.02$	$3.04 \pm 0.03$	6.99	0.51	Metacentric
9	$1.20 \pm 0.01$	$1.66 \pm 0.02$	2.86±0.03	6.58	0.63	Submetacentric
10	$1.23 \pm 0.01$	$1.46 \pm 0.01$	2.69±0.03	6.18	0.53	Metacentric
11	$1.33 \pm 0.01$	$1.34 \pm 0.02$	2.68±0.02	6.16	0.53	Metacentric
12	$1.28 \pm 0.01$	$1.30 \pm 0.01$	$2.58 \pm 0.02$	5.94	0.56	Metacentric

\*=satellite chromosome.

12m + 6sm + 8st with two visible satellite chromosomes including 13 pairs, which comprised six pairs of metacentric chromosome, three pairs of submetacentric chromosomes and four pairs of subtelocentric chromosomes with two visible satellite chromosomes. The short arm chromosome length ranged from 1.41±0.01 to 4.95±0.02  $\mu$ m, the long arm chromosome length ranged from 3.75±0.02 to 5.51±0.03  $\mu$ m, the total arm chromosome length ranged from 5.16±0.03 to 10.46±0.05  $\mu$ m. Relative lengths were 5.45–11.05 %. Centromeric indexes were 0.55 0.74 (Table 4; Figure 2(C)). This study of the chromosome number and karyotype of this endemic species to Thailand was never previously reported. The somatic chromosome number of *Ar. maxwellii*, Vulnerable species (VU) and a not common species from Thailand, is reported here to be 2n = 24 with NF = 48 (Figure 1(D)). The karyotype formula was asymmetrical karyotype due to 22m + 2sm with two visible satellite chromosomes including 12 pairs, which comprised 11 pairs of metacentric chromosomes and one pair of submetacentric chromosomes. The short arm chromosome length ranged from  $1.28\pm0.01$  to  $2.65\pm0.01 \ \mu$ m, the long arm chromosome length ranged from  $1.30\pm0.01$  to  $3.00\pm0.02 \ \mu$ m, the total arm chromosome length ranged from  $2.58\pm0.02$  to  $5.65\pm0.04 \ \mu$ m. Relative lengths were 5.94-13.00 %. Centromeric indexes were 0.50-0.63

Chromosome pair	Ls±SD (µm)	Ll±SD ( $\mu$ m)	LT±SD (µm)	RL (%)	CI	Chromosome type
1	2.20±0.01	2.32±0.02	4.52±0.03	9.74	0.51	Metacentric
2	2.11±0.01	$2.22 \pm 0.02$	4.33±0.03	9.34	0.53	Metacentric
3	$1.99 \pm 0.01$	2.21±0.02	4.20±0.03	9.06	0.54	Metacentric
4	$1.97 \pm 0.01$	$2.07 \pm 0.02$	4.03±0.03	8.70	0.58	Metacentric
5	$1.73 \pm 0.01$	$1.96 \pm 0.02$	3.69±0.03	7.96	0.58	Metacentric
6	$1.66 \pm 0.01$	$1.88 \pm 0.02$	$3.53 \pm 0.03$	7.62	0.54	Metacentric
7	$1.59 \pm 0.01$	$1.88 \pm 0.02$	3.47±0.03	7.48	0.54	Metacentric
8	$1.67 \pm 0.01$	$1.80 \pm 0.02$	3.47±0.03	7.48	0.55	Metacentric
*9	$1.52 \pm 0.01$	$1.71 \pm 0.02$	3.23±0.03	6.96	0.55	Metacentric
10	$1.46 \pm 0.01$	$1.75 \pm 0.02$	3.21±0.03	6.93	0.51	Metacentric
11	$1.48 \pm 0.01$	$1.71 \pm 0.02$	3.19±0.03	6.87	0.54	Metacentric
12	$1.28 \pm 0.01$	$1.48 \pm 0.02$	2.76±0.02	5.95	0.55	Metacentric
13	$1.24 \pm 0.01$	$1.49 \pm 0.02$	$2.73 \pm 0.02$	5.89	0.55	Metacentric

**Table 6.** Mean length of short arm chromosome (Ls), long arm chromosome (Ll), total arm chromosome (LT), relative length (RL), centromeric index (CI) and standard deviation (SD) of RL, CI from 20 metaphases of *Ha. benthamiana* (2n=26).

\*=satellite chromosome.

**Table 7.** Mean length of short arm chromosome (Ls), long arm chromosome (Ll), total arm chromosome (LT), relative length (RL), centromeric index (CI) and standard deviation (SD) of RL, CI from 20 metaphases of *Ho. griffithii* (2*n*=40).

Chromosome pair	Ls±SD ( $\mu$ m)	Ll±SD ( $\mu$ m)	LT±SD ( $\mu$ m)	RL (%)	CI	Chromosome type
1	$1.98 \pm 0.01$	2.01±0.02	3.99±0.03	9.05	0.55	Metacentric
2	$1.46 \pm 0.01$	$1.68 \pm 0.02$	3.14±0.03	7.13	0.58	Metacentric
*3	$1.26 \pm 0.01$	$1.68 \pm 0.02$	2.93±0.03	6.65	0.51	Metacentric
4	$0.60 \pm 0.01$	$1.96 \pm 0.02$	2.56±0.03	5.81	0.63	Submetacentric
5	$0.77 \pm 0.01$	$1.87 \pm 0.02$	2.64±0.03	5.98	0.62	Submetacentric
6	$0.92 \pm 0.01$	$1.46 \pm 0.02$	2.38±0.03	5.39	0.61	Submetacentric
7	$0.95 \pm 0.01$	$1.28 \pm 0.02$	2.23±0.03	5.06	0.59	Metacentric
8	$0.73 \pm 0.01$	$1.45 \pm 0.02$	2.18±0.03	4.94	0.62	Submetacentric
9	$0.77 \pm 0.01$	$1.39 \pm 0.02$	2.16±0.02	4.91	0.59	Metacentric
10	$0.93 \pm 0.01$	$1.20 \pm 0.01$	2.13±0.02	4.82	0.59	Metacentric
11	$0.81 {\pm} 0.01$	$1.25 \pm 0.02$	2.06±0.02	4.66	0.55	Metacentric
12	$0.82 \pm 0.01$	$1.23 \pm 0.01$	2.05±0.02	4.65	0.56	Metacentric
13	$0.73 \pm 0.01$	1.33±0.02	$2.05 \pm 0.02$	4.65	0.68	Submetacentric
14	0.91±0.01	$1.11 \pm 0.01$	$2.02 \pm 0.02$	4.58	0.53	Metacentric
15	$0.88 \pm 0.01$	$1.02 \pm 0.01$	$1.89 \pm 0.02$	4.29	0.58	Metacentric
16	$0.90 \pm 0.01$	$1.00 \pm 0.01$	$1.89 \pm 0.02$	4.29	0.53	Metacentric
17	$0.77 \pm 0.01$	$1.03 \pm 0.01$	$1.80 \pm 0.02$	4.08	0.55	Metacentric
18	$0.73 \pm 0.01$	$1.03 \pm 0.01$	$1.76 \pm 0.02$	3.99	0.55	Metacentric
19	$0.69 \pm 0.01$	$0.93 \pm 0.01$	$1.62 \pm 0.02$	3.67	0.58	Metacentric
20	0.21±0.00	$0.41 \pm 0.01$	$0.62 \pm 0.01$	1.40	0.59	Metacentric

\*=satellite chromosome.

(Table 5; Figure 2(D)). The chromosome number and karyotype including the cytological characteristics of this species in this study is reported for the first time.

The somatic chromosome number of *Ha. bentha*miana was recognized to be 2n = 26 and NF = 52 (Figure 1(E)). The karyotype formula was asymmetrical karyotype due to 26m with one visible satellite chromosomes including 13 pairs, which comprised 13 pairs of metacentric chromosomes. The short arm chromosome length ranged from  $1.24\pm0.01$  to  $2.20\pm0.01 \ \mu$ m, the

long arm chromosome length ranged from  $1.48\pm0.02$  to  $2.32\pm0.02 \ \mu$ m, the total arm chromosome length ranged from  $2.73\pm0.02$  to  $4.52\pm0.03 \ \mu$ m. Relative lengths were 5.89-9.74 %. Centromeric indexes were 0.51-0.58 (Table 6; Figure 2(E)). The somatic chromosome number of *Ha. benthamiana* in this study is consistent with Larsen (1969) reported 2n = 26. The karyotype studies of this species were reported for the first time.

The somatic chromosome number of *Ho. griffithii* was found to be 2n (diploid) = 40 with NF = 80 (Figure 1(F)). The karyotype formula was asymmetrical karyotype due to 30m + 10sm with two satellite chromosomes including 20 pairs, which comprised 15 pairs of metacentric chromosomes and five pairs of submetacentric chromosomes (Table 7; Figure 2(F)).

The short arm chromosome length ranged from 0.21±0.00 to 1.98±0.01  $\mu$ m, the long arm chromosome length ranged from 0.41±0.01 to 2.01±0.02  $\mu$ m, the total arm chromosome length ranged from 0.62±0.01 to 3.99±0.03  $\mu$ m. Relative lengths were 1.40–9.05 %. Centromeric indexes were 0.51–0.68 (Table 7; Figure 2(F)). The somatic chromosome number of *Ho. griffithii* is consistent with Okada (1982) and Okada (2000). In addition, the karyotype of this study was investigated for the first time.

While, Darlington and Wylie (1955) reported the chromosome numbers of plants in the family Araceae between 2n = 24–140 because it is able to cross-pollinate, and when there are hybrids, the doubling of the chromosome number and resulting plant species have allopolyploidy, and it was found that the polyploidy was related to the evolution of this family (Larsen 1969) or environmental factors, such as weather, humidity, light, soil or altitude above sea level in each of the areas.

From the literature, it was found that this family has a wide range of chromosome numbers between 2n = 24-140. However, this study found that all five genera with six species had chromosome numbers 2n = 24-42, including three species with symmetry and three species with asymmetry.

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