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Cytogenetic Studies in the Genus *Helianthus* L. II. Karyological studies in twelve species

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The genus *Helianthus*, belonging to the tribe Heliantheae of the family Compositae, is a polymorphic genus and includes 100 species which are mostly North American (Bailey 1929–30). Different species have shown wide morphological diversity due to ecological adaptations. Consequently different species are distributed from tropical and subtropical plains to warm temperate climatic zones. They differ mainly in the pattern of plant height, leaf shape and other features of the inflorescence including its size, colour and diameter.

No extensive karyological work on the genus is available and only few species seem to have been studied (Tahara 1915, Georgieva 1967, Georgieva *et al.* 1972, Georgieva-Todorova and Ilieva 1976, Raicu *et al.* 1976, Ramakanth and Seetharam 1977). In the first paper of this series (Kulshreshtha and Gupta 1979), meiosis in 28 taxa belonging to 13 species and the results on some interspecific hybrids were described. The present paper communicates the results of a karyological study of 12 different species of *Helianthus*.

Material and methods

Material of 12 species of sunflowers used in the present study was collected through correspondence, from different Botanical Gardens and Seed Companies located in the different countries (details in Kulshreshtha 1976). The plants were raised at Meerut University Farm and their identifications were confirmed with the help of available literature.

For karyotypic analysis, root tips were pretreated with saturated solution of p-dichlorobenzene for 2–5 hours at 0–10°C and fixed in aceto-alcohol (1 : 3) at least overnight. The tips were squashed with 2.0% acetocarmine. The metaphase chromosomes were karyomorphologically analysed. Photomicrographs and camera lucida drawings were prepared and the idiograms were constructed on the basis of these measurements.

Results

In 10 out of 12 species examined. 17 pairs of chromosomes were observed. The only exceptions were *H. mollis* with 15 chromosome pairs and *H. tuberosus*

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Table 1. Karyomorphological data, including total length (TL), arm ratio (AR), relative length (RL), Tcl%, T.F.% and total chromatin values for twelve *Helianthus* species (values in parentheses are mean values)

Species		Chromosome type								
		Long			Medium			Short		
		M	SM	ST	M	SM	ST	M	SM	ST
1. *H. angustifolius* L.										
(2n=34)	TL (in μ)	3.9–3.6	—	—	2.6	2.9–2.6	2.9–2.6	1.9–1.6	1.9–1.4	2.3–1.5
TF%=42.45		(3.75)	—	—	(2.60)	(2.75)	(2.75)	(1.75)	(1.65)	(1.9)
	AR	1.00–1.16	—	—	1.00	1.25–1.36	2.22–4.20	1.00	1.50–1.33	2.00–1.66
		(1.08)	—	—	(1.00)	(1.30)	(3.21)	(1.00)	(1.41)	(1.83)
Total chromatin										
=41.1 μ	RL	100.0–92.3	—	—	66.6	74.3–66.6	74.3–66.6	48.7–41–0	48.7–35.8	58.9–38.4
		(96.15)	—	—	(66.60)	(70.45)	(70.45)	(44.85)	(42.25)	(48.65)
	Tcl%	9.4–8.7	—	—	6.3	7.0–6.3	7.0–6.3	4.6–3.8	4.6–3.4	5.5–3.6
		(9.05)	—	—	(6.30)	(6.65)	(6.65)	(4.2)	(4.0)	(4.55)
2. *H. annuus* L.										
(2n=34)	TL (in μ)	4.4–3.4	4.8–3.5	3.9	2.6	3.1–2.6	2.9	2.2–1.7	2.5–1.9	—
		(3.90)	(4.15)	(3.90)	(2.60)	(2.85)	(2.90)	(1.95)	(2.2)	—
	AR	1.09–1.12	1.18–1.33	1.78	1.16	1.21–1.36	1.63	1.00–1.12	1.20–1.38	—
TF%=44.70		(1.10)	(1.25)	(1.78)	(1.16)	(1.28)	(1.63)	(1.06)	(1.29)	—
Total chromatin										
=51.9 μ	RL	91.6–70.8	100.0–72.9	81.2	54.1	64.5–54.1	60.4	45.8–35.4	52.0–39.5	—
		(81.2)	(86.45)	(81.20)	(54.10)	(59.23)	(60.40)	(40.60)	(45.75)	—
	Tcl%	8.4–6.5	9.2–6.7	7.5	5.0	5.9–5.0	5.5	4.2–3.2	4.8–3.6	—
		(7.45)	(7.95)	7.5	5.0	(5.45)	5.5	(3.7)	(4.2)	
3. *H. argophyllus* T and G										
(2n=34)	TL (in μ)	4.5–3.2	4.1–3.8	3.5	3.1	—	2.6	2.2–1.7	2.5–1.8	1.8
		(3.85)	(3.95)	(3.50)	(3.10)	—	(2.60)	(1.95)	(2.15)	(1.80)
TF%=44.94										
	AR	1.04–1.00	1.3–1.2	2.88	1.06–1.00	—	1.88–1.60	1.12–1.00	1.27–1.25	1.57
		(1.02)	(1.25)	(2.88)	(1.03)	—	(1.74)	(1.06)	(1.26)	(1.57)
Total chromatin										
=49.5 μ	RL	100–71.1	91.1–84.4	77.7	68.8	—	57.7	48.8–37.7	55.5–40.0	40.0

		(85.55)	(87.75)	(77.7)	(68.80)	—	(57.70)	(43.25)	(47.75)	(40.00)
	Tcl%	9.0–6.4 (7.70)	8.2–7.6 (7.90)	7.0) (7.00)	6.2 (6.20)	— —	5.2 (5.20)	4.4–3.4 (3.90)	5.0–3.6 (4.30)	3.6 (3.60)
4. *H. californicus D. C.*										
(2n=34)	TL (in μ)	5.0–3.8 (4.40)	3.5 (3.50)	3.9–3.4 (3.65)	2.6 (2.60)	3.1–2.9 (3.0) —	— —	1.11–1.00 (1.05)	1.44 (1.44)	2.5–1.8 (2.15)
TF%=41.91	AR	1.08–1.00 (1.04)	1.33 (1.33)	3.25–2.54 (2.89)	1.16–1.00 (1.08)	1.41–1.21 (1.31)	— —	1.11–1.00 (1.05)	1.44 (1.44)	1.77–1.58 (1.67)
Total chromatin =49.5 μ	RL	100.0–76.0 (88.0)	70.0 (70.00)	78.0–68.0 (73.0)	52.0 (52.00)	62.0–58.0 (60.00)	— —	50.0–38.0 (44.00)	44.0 (44.00)	50.0–36.0 (43.00)
	Tcl%	10.1–7.6 (8.85)	7.0 (7.00)	7.8–6.8 (7.30)	5.2 (5.20)	6.2–5.8 (6.00)	— —	5.0–3.8 (4.40)	4.4 (4.40)	5.0–3.6 (4.30)
5. *H. debilis* Nutt.										
(2n=34)	TL (in μ)	5.2–3.5 (4.35)	3.8–3.5 (3.65)	3.5 (3.50)	3.0 (3.00)	2.9 (2.90)	2.9–2.6 (2.75)	2.5–2.0 (2.25)	2.5 (2.50)	2.2 (2.20)
TF%=448.3	AR	1.16–1.00 (1.08)	1.37–1.18 (1.27)	1.69 (1.69)	1.14 (1.14)	1.23 (1.23)	1.90–1.60 (1.75)	1.00 (1.00)	1.50 (1.50)	1.75 (1.75)
Total chromatin =55.2 μ	RL	100.0–67.3 (83.65)	73.0–67.3 (70.15)	67.3 (67.30)	57.6 (57.60)	55.7 (55.70)	55.7–50.0 (52.85)	48.0–38.4 (43.2)	48.0 (48.00)	42.3 (42.30)
	Tcl%	9.4–6.3 (7.85)	6.8–6.3 (6.55)	6.3 (6.30)	5.4 (5.40)	5.2 (5.20)	5.2–4.7 (4.95)	4.5–3.6 (4.05)	4.5 (4.50)	3.9 (3.90)
6. *H. divaricatus* L.										
(2n=34)	TL (in μ)	4.9–3.4 (4.15)	3.7 (3.70)	3.4 (3.40)	3.1–3.0 (3.05)	— —	3.1–2.6 (2.85)	2.2–1.6 (1.90)	2.5–2.2 (2.35)	— —
TF%=42.21	AR	1.13–1.04 (1.10)	1.17 (1.17)	3.25 (3.25)	1.14–1.00 (1.07)	— —	2.85–1.60 (2.22)	1.00 (1.00)	1.50–1.20 (1.35)	— —
Total chromatin =52.0 μ	RL	100.0–69.3 (84.65)	75.5 (75.5)	69.3 (69.30)	63.2–61.2 (62.2)	— —	63.2–53.0 (58.10)	44.8–32.6 (38.70)	51.0–44.8 (47.9)	— —
	Tcl%	9.4–6.5 (7.95)	7.1 (7.10)	6.5 (6.50)	5.9–5.7 (5.80)	— —	5.9–5.0 (5.45)	4.2–3.0 (3.60)	4.8–4.2 (4.50)	—

(cont.)

Table 1. Karyomorphological data, including total length (TL), arm ratio (AR), relative length (RL), Tcl%, T.F.% and total chromatin values for twelve *Helianthus* species (values in parentheses are mean values)

Species		Chromosome type								
		Long			Medium			Short		
		M	SM	ST	M	SM	ST	M	SM	ST
7. *H. lenticularis* CK11.										
(2n=34)	TL(in μ)	4.4–3.8 (4.10)	5.8–3.5 (4.65)	3.5–3.4 (3.45)	3.1–2.6 (2.85)	3.1–2.9 (3.0)	3.1–2.8 (2.95)	— —	2.4 (2.40)	— —
TF%=42.43	AR	1.09–1.00 (1.04)	1.33–1.20 (1.26)	2.77–1.91 (2.34)	1.16–1.00 (1.08)	1.41–1.38 (1.39)	2.50–2.10 (2.30)	— —	1.40 (1.40)	— —
Total chromatin =58.8μ	RL	75.8–65.5 (70.65)	100.0–60.3 (80.15)	60.3–58.6 (59.45)	53.4–44.8 (49.10)	53.4–50.0 (51.70)	53.4–48.2 (50.80)	— —	41.3 (41.30)	— —
	Tcl%	7.4–6.4 (6.90)	9.8–5.9 (7.85)	5.9–5.7 (5.80)	5.2–4.4 (4.80)	5.2–4.9 (5.05)	5.2–4.7 (4.95)	— —	4.0) (4.00)	— —
8. *H. maximilianii*										
(2n=34)	TL (in μ)	3.8 (3.80)	— —	— —	3.1 (3.10)	— —	3.1–2.6 (2.85)	2.5–1.4 (1.95)	2.5–1.5 (2.00)	2.2–1.1 (1.65)
TF%=41.91	RA	1.00 (1.00)	— —	— —	1.00 (1.00)	— —	3.33–1.58 (2.45)	1.08–1.00 (1.04)	1.50–1.20 (1.35)	2.16–1.75 (1.95)
Total chromatin =37.1μ	RL	100.0 (100.0)	— —	— —	81.5 (81.50)	— —	81.5–68.4 (74.95)	65.7–36.8 (51.25)	65.7–39.4 (52.55)	57.8–28.9 (43.35)
	Tcl%	10.2 (10.20)	— —	— —	8.3 (8.30)	— —	8.3–7.0 (7.65)	6.7–3.7 (5.20)	6.7–4.0 (5.35)	5.9–2.9 (4.40)
9. *H. mollius* Lam.										
(2n=30)	TL (in μ)	3.6 (3.6)	4.0–3.2 (3.6)	3.8 (3.80)	2.8–2.6 (2.7)	— —	2.6 (2.60)	— —	1.9 (1.90)	2.4–2.2 (2.3)
TF%=41.12	AR	1.00 (1.00)	1.35–1.22 (1.28)	1.71 (1.71)	1.16–1.00 (1.08)	— —	2.25–1.60 (1.92)	—	1.37 (1.37)	4.50–3.00 (3.75)
Total chromatin =42.8μ	RL	90.0 (90.00)	100–0–80.0 (90.0)	95.0 (95.00)	70.0–65.0 (67.50)	— —	65.0 (65.00)	— —	47.5 (47.50)	60.0–55.0 (57.50)

	Tcl%	(8.4) (86.4)	9.3–7.4 (8.35)	8.8 (8.80)	6.5–6.0 (6.25)	— —	6.0 (6.00)	— —	4.4 (4.40)	5.6–5.1 (5.35)
10. *H. pumilus* Nutt.										
(2n=34)	TL (in μ)	3.8–3.5 (3.65)	(4.4) (3.65)	— —	— —	— —	2.7–2.6 (2.65)	2.5–2.0 (2.25)	2.1–1.5 (1.80)	2.5–2.1 (2.30)
TF%=39.18	AR	1.11–1.00 (1.05)	1.20 (1.20)	— —	— —	— —	3.33–2.37 (2.85)	1.08–1.00 (1.04)	1.50–1.28 (1.39)	4.00–2.00 (3.00)
Total chromatin =43.0 μ	RL	86.3–79.5 (82.90)	100.00 (100.0)	— —	— —	— —	61.3–59.0 (60.15)	56.8–45.4 (51.10)	47.7–34.0 (40.85)	56.8–47.7 (52.25)
	Tcl%	8.8–8.1 (8.45)	10.2 (10.20)	— —	— —	— —	6.2–6.0 (6.10)	5.8–4.6 (5.20)	4.8–3.4 (4.10)	5.8–4.8 (5.34)
11. *H. trachaelifolius* Mill										
(2n=34)	TL (in μ)	4.9–3.4 (4.15)	3.4–3.3 (3.35)	— —	2.7–2.6 (2.65)	— —	3.1–2.7 (2.90)	— —	2.4 (2.40)	2.2–1.5 (1.85)
TF%=41.66	AR	1.04–1.00 (1.02)	1.35–1.26 (1.30)	— —	1.16–1.00 (1.08)	— —	2.37–2.10 (2.23)	— —	1.18 (1.18)	1.80–2.14 (2.47)
Total chromatin =51.0 μ	RL	100.0–69.3 (84.65)	69.3–67.3 (68.3)	— —	55.1–53.0 (54.05)	— —	63.2–55.1 (59.15)	— —	48.9 (48.90)	44.8–30.6 (37.70)
	Tcl%	9.6–6.6 (8.10)	6.6–6.4 (6.50)	— —	5.2–5.0 (5.1)	— —	6.0–5.2 (5.60)	— —	4.7 (4.70)	4.3–2.9 (3.60)
12. *H. tuberosus* L.										
(2n=102)	TL (in μ)	4.9–3.9 (4.40)	5.5–3.3 (4.40)	3.9–3.3 (3.60)	3.1–2.6 (2.94)	2.8 (2.80)	3.1–2.6 (2.81)	2.5–2.1 (2.30)	2.5–2.4 (2.45)	2.1–1.4 (1.75)
TF%=40.05	AR	1.15–1.05 (1.10)	1.44–1.20 (1.32)	3.50–1.53 (2.51)	1.16–1.00 (1.10)	1.33 (1.33)	3.33–1.58 (2.45)	1.10–1.00 (1.05)	1.50–1.40 (1.45)	3.00–1.62 (2.31)
Total chromatin =156.3 μ	RL	89.0–70.9 (79.95)	100.0–60.0 (80.0)	70.9–58.1 (64.50)	56.3–47.2 (53.85)	50.9 (50.90)	56.3–47.2– (51.75)	45.4–38.1 (41.75)	45.4–43.6 (44.50)	38.1–25.4 (31.75)
	Tcl%	3.1–2.4 (2.75)	3.5–2.1 (2.80)	2.4–2.0 (2.20)	1.9–1.6 (1.78)	1.7 (1.70)	1.9–1.6 (1.75)	1.5–1.3 (1.40)	1.5 (1.50)	1.3–0.8 (1.05)

Table 2. Karyotype formulae of twelve different species of *Helianthus*; (A, B and C represent long, medium and short chromosomes respectively; 'sc' used as superscript and subscript represent secondary constriction in short and long arm respectively; superscripts 'm', 'sm' and 'st' represent median, submedian and subterminal positions of centromere respectively)

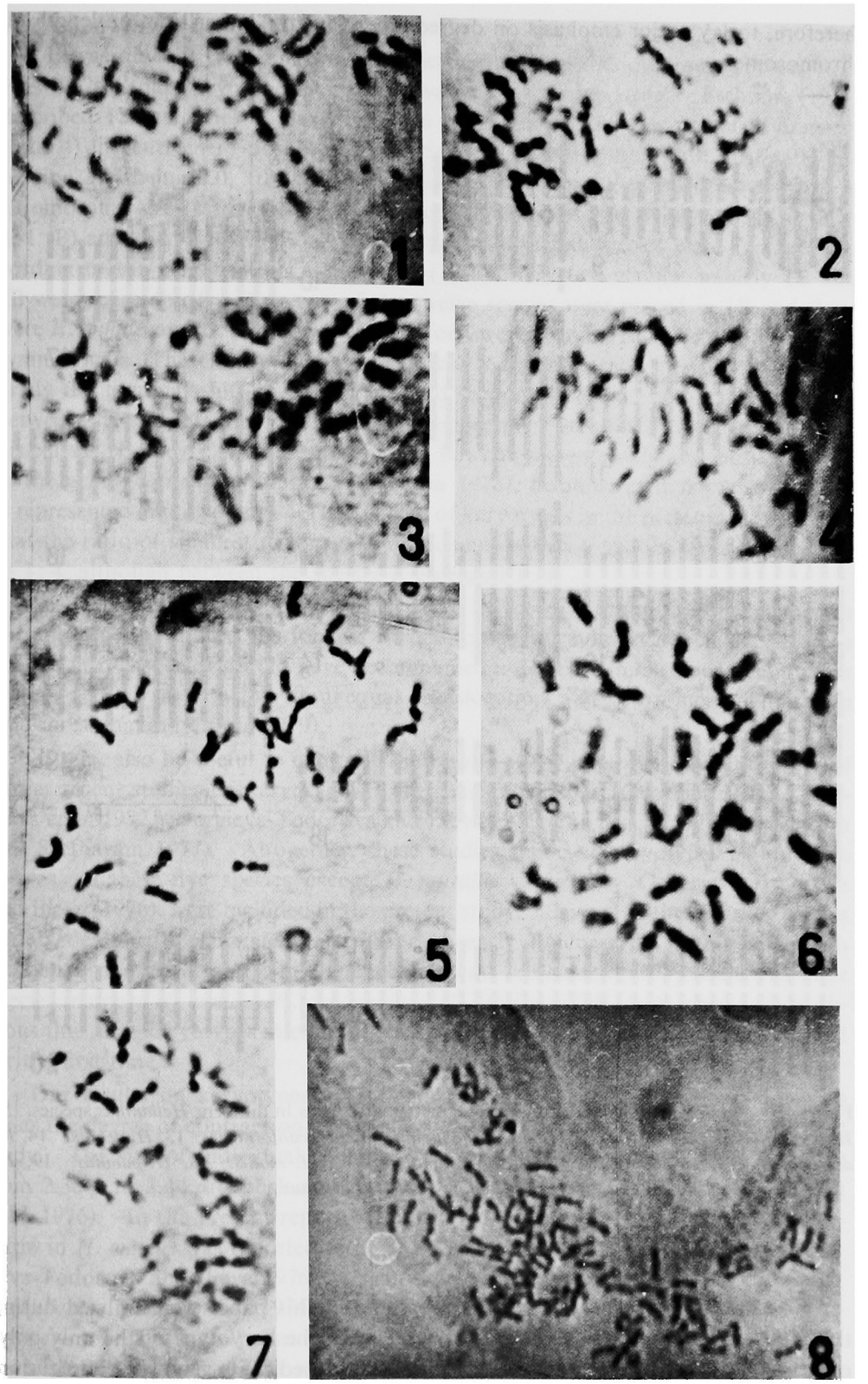
Species	Fig. no.	Karyotype formulae
1. *H. angustifolius*	9	$1^{sc}A^{m}+2A^{m}+1B^{m}+3B^{sm}+2B^{st}+2C^{m}+3C^{sm}+3C^{st}$
2. *H. annuus*	10	$2A^{m}+1_{sc}A^{sm}+3A^{sm}+1A^{st}+1B^{m}+3B^{sm}+1B^{st}+2C^{m}+3C^{sm}$
3. *H. argophyllus*	11	$1_{sc}A^{m}+2A^{m}+2A^{sm}+1A^{st}+3B^{m}+2B^{st}+3C^{m}+2C^{sm}+1C^{st}$
4. *H. californicus*	12	$1^{sc}A^{m}+1A^{m}+1A^{sm}+2A^{st}+2B^{m}+3B^{sm}+3C^{m}+1C^{sm}+3C^{st}$
5. *H. debilis*	13	$1_{sc}A^{m}++3A^{m}+4A^{sm}+1A^{st}+1B^{m}+1B^{sm}+2B^{st}+2C^{m}+1C^{sm}+1C^{st}$
6. *H. divaricatus*	14	$1^{sc}A^{m}+3A^{m}+1A^{sm}+1A^{st}+3B^{m}+4B^{st}+2C^{m}+2C^{sm}$
7. *H. lenticularis*	15	$3A^{m}+1^{sc}A^{sm}+3A^{sm}+2A^{st}+3B^{m}+2B^{sm}+2B^{st}+1C^{sm}$
8. *H. maximiliani*	16	$1^{sc}A^{m}+1B^{m}+3B^{st}+3C^{m}+6C^{sm}+3C^{st}$
9. *H. mollis*	17	$1A^{m}+1_{sc}A^{sm}+2A^{sm}+1A^{st}+4B^{m}+2B^{st}+1C^{sm}+3C^{st}$
10. *H. pumilus*	18	$2A^{m}+1_{sc}A^{sm}+4B^{st}+3C^{m}+4C^{sm}+3C^{st}$
11. *H. trachaelifolius*	19	$1^{sc}A^{m}+3A^{m}+3A^{sm}+2B^{m}+3B^{st}+1C^{sm}+4C^{st}$
12. *H. tuberosus*	20	$3A^{m}+2^{sc}A^{sm}+4A^{sm}+1_{sc}A^{st}+10A^{st}+9B^{m}+1B^{sm}+10B^{st}+3C^{m}+2C^{sm}+6C^{st}$.

with 51 chromosome pairs. The metaphase plates of some of these species are given in Figs. 1–8 and the idiograms for 12 species are presented in Figs. 9–20. Data on chromosome measurements are presented in Table 1. While presenting data in this table, the chromosome pairs are grouped into three size groups viz. long (A), medium (B) and short (C). Each class was further subdivided on the basis of centromere position, which included satellited (Sc), median (M), submedian (SM) and subterminal (ST). On the basis of this classification of chromosomes, chromosome formulae could be prepared, which are presented in Table 2 along with possible marker chromosomes. The morphological features of chromosomes utilized for the study included the following: a) absolute length of individual chromosomes measured in μ., b) relative length of each chromosome represented as per cent length of longest chromosome in a species, c) arm ratio for each chromosome (long arm/short arm), d) TCl% for each chromosome represented as per cent whole chromosome complement, e) TF% for each species representing the total length of all short arms as per cent total chromosome complement in the species, f) presence or absence of secondary constrictions.

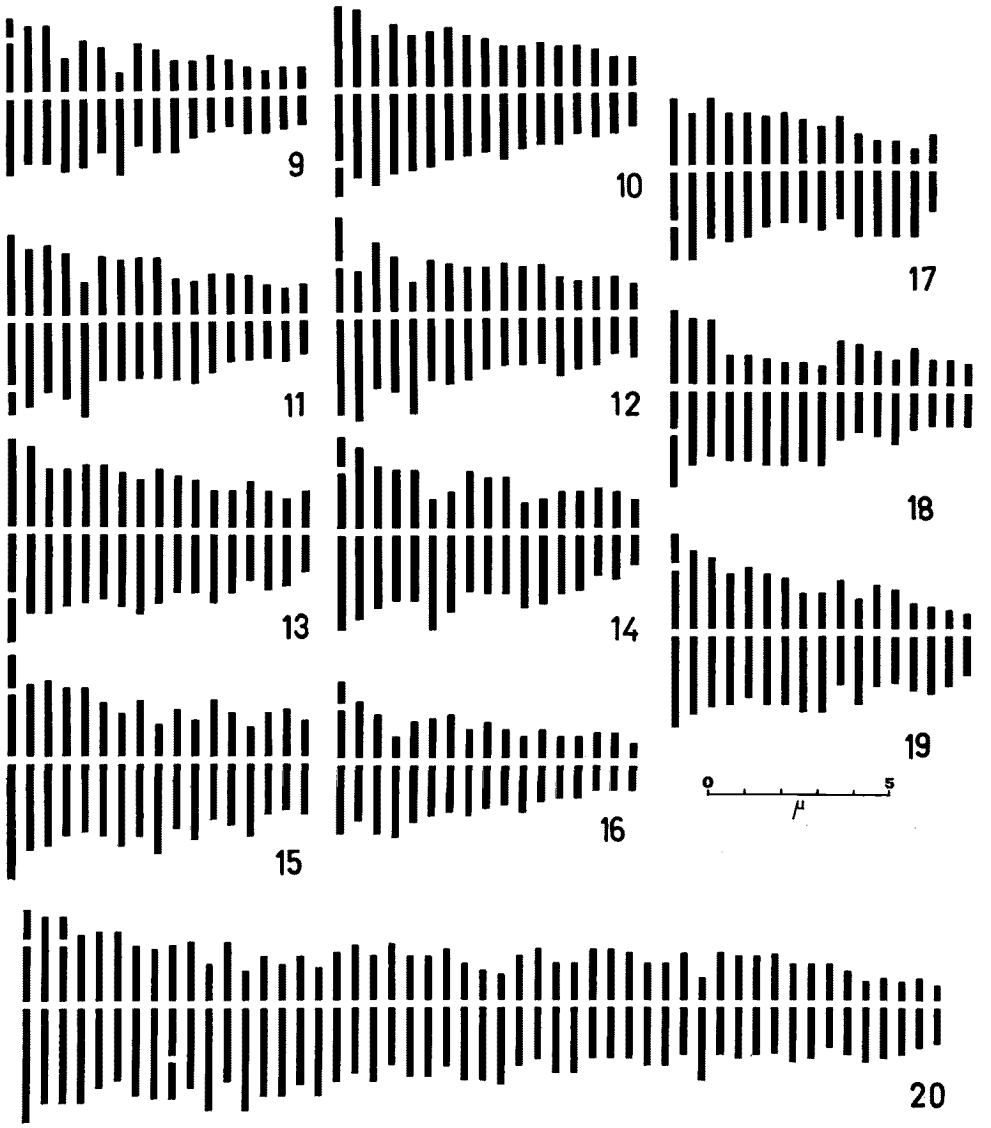
Table 1 will show that individual chromosomes in the different species ranged in length from 5.2 μ to 1.1 μ. The total chromatin length in diploid species with 17 pairs ranged from 58.8 μ in *H. lenticularis* to 37.1 μ in *H. maximilliani*. In the remaining two species, the total chromain was 42.8 μ in *H. mollis* (2n=30) and was 156.3 μ in *H. tuberosus* (2n=102).

It should be realized that the variability in chromosome size recorded in this study can be partly accounted for by differential condensation. It is necessary,

Figs. 1–8. Mitotic metaphase plates in some *Helianthus* species. 1, *H. argophyllus* (2n=34). 2, *H. californicus* (2n=34). 3, *H. debilis* (2n=34). 4, *H. divaricatus* (2n=34). 5, *H. mollis* (2n=30). 6, *H. pumilus* (2n=34). 7, *H. trachaelifolius* (2n=34). 8, *H. tuberosus* (2n=102).


1
2
3
4
5
6
7
8

therefore, to lay major emphasis on degree of asymmetry rather than on length of chromosomes.



Figs. 9–20. Idiograms prepared from mitotic metaphase plates in different *Helianthus* species. 9, *H. angustifolius*. 10, H. annuus. 11, *H. argophyllus*. 12, *H. californicus*. 13, *H. debilis*. 14, *H. divaricatus*. 15, *H. lenticularis*. 16, *H. maximiliani*. 17, *H. mollis*. 18, *H. pumilus*. 19, *H. trachaelifolius*. 20, *H. tuberosus*.

Discussion

The karyotypes of twelve species presented in this paper were utilized during this study to work out the degree of asymmetry. The karyotype of the only polyploid species (*H. tuberosus*) was also examined to predict its genomic constitution.

Karyotype symmetry

It was obvious from karyomorphometric data and the idiograms (Tables 1, 2; Figs. 9–20), that karyotype asymmetry was not of a high order. Stebbins (1971) described 12 categories of karyotypes on the basis of four degrees of asymmetry (1.2.3.4) in centromere position (proportions of chromosomes with arm ratio exceeding 2: 1 being 0.0, .01–0.50, .51–99 and 1.0) and three degrees of asymmetry in chromosome size (ratio of longest to shortest chromosome being <2: 1(A), 2:1–4: 1 (B) and >4: 1 (C)). When karyotypes of different species were arranged according to the classification of Stebbins (1971), only two classes, namely 1B and 2B were represented. Only two of the twelve species were placed in 1B and these were *H. annuus* and *H. debilis*, which therefore, were considered to be relatively more symmetrical. The change from symmetrical to asymmetrical karyotypes involves firstly the terminal shift of centromere and secondly the increase in the difference between the shortest and the longest chromosome. Stebbins (1971) thought that his classes 1B and 1C are absent in plants, but our present study and earlier reports in the genus *Crotalaria* (Gupta and Gupta 1978), demonstrated that the class 1B is represented among plants. The analysis of karyotypes in the present study showed that the ratio of smallest to longest chromosome within a species ranged from 1 : 2 to 1 : 4, although between the species it exceeded 1 : 4.

In *H. mollis*, the only species with n=15, an increase in the size of the smallest chromosome relative to the longest chromosome, was noticed (Table 1). Such a change in this species should have accompanied a decrease in chromosome number from n=17 to n=15 due to unequal translocation and centromere elimination (Kulshreshtha and Gupta 1979).

It may also be useful to compare the results of the present study with those of earlier recent studies on karyotypes in the genus *Helianthus* (Georgieva 1967, Georgieva *et al.* 1972, Georgieva-Todorova and Ilieva 1976, Raicu *et al.* 1976, Ramakanth and Seetharam 1977). Altogether, these studies reported karyotypes in only five species, all these five species except *H. nuttallii* studied by Georgieva-Todorova and Ilieva (1976), were included in the present study. Several of these earlier studies mainly dealt with *H. annuus*. However, recently Raicu *et al.* (1976) dealt with *H. annuus* and *H. debilis*, while Ramakanth and Seetharam (1977) dealt with four species, namely *H. annuus*, *H. argophyllus*, *H. debilis* and *H. lenticularis*. It is obvious thus that karyotypes in eight different species of *Helianthus* are being reported for the first time.

Our results on karyotypes differ from those of earlier workers mainly in so far as the degree of contraction of chromosomes was relatively higher in the present study. The size of individual chromosomes in *H. annuus* was reported to range from 2.38 μ to 3.44 μ (Babek and Kovacik 1974) or from 3.77 μ to 5.15 μ (Raicu *et al.* 1976). In the present report, it ranged from 1.7 μ to 4.8 μ. The total chromatin in *H. annuus* was reported to be 73.82 μ (Raicu *et al.* 1976) or 84.22 μ (Georgieva-Todorova and Ilieva 1976) as against 51.9 μ in the present study. Similarly, in *H. debilis*, Raicu *et al.* (1976) reported the length of individual chromosomes to range from 5.92 μ to 7.91 μ as against 2.2 μ to 5.2 μ in the present study. Ramakanth and Seetharam (1977) reported the chromosome length in four species to

range from 3.0 μ to 6.0 μ as against the range 1.1 μ to 5.2 μ in 12 species examined during the present study. These comparisons suggest that not only there was a higher degree of chromosome contraction in the present study, but in general also the ratio longest/smallest chromosome was relatively high.

Another important difference worth mentioning is that only a single sat-chromosome was observed in the haploid complement of each of the diploid species during the present study. In earlier studies two or three sat-chromosomes were always reported in each of the diploid species examined. Similar differences can also be pointed out with respect to the number of median, submedian and subterminal chromosomes. The differences can be accounted for partly due to higher degree of contraction.

When the details of the results of Ramakanth and Seetharam (1977) are compared with those of the present study, some conformity was observed, in so far as they reported that *H. annuus* had a relatively more symmetrical karyotype. In the present study, *H. annuus* as well as *H. debilis* were found to have relatively more symmetrical karyotypes.

From the above discussion, it is obvious that if the structural changes played any role in evolution in the genus *Helianthus*, these changes did not alter the karyotypes to any significant extent. That the chromosome repatterning in the genus *Helianthus* has not taken place to any appreciable degree, has been earlier demonstrated by us through the study of meiosis in interspecific hybrids (Kulshreshtha and Gupta 1979). However, in some cases interchange rings were observed in the hybrids showing structural changes in chromosomes.

Genome analysis

An effort has also been made during the present study to make a genome analysis on the basis of karyotypes available from diploid and polyploid taxa belonging to the genus *Helianthus*. An analysis of Fig. 20 will indicate that *H. tuberosus* may have three genomes from three diploid species. Two of these genomes might have come probably, one each from *H. annuus* (Fig. 10) and *H. lenticularis* (Fig. 15). The third genome did not match with any of the diploid species examined during the present study. It is possible that if more diploid taxa are used for karyotypic analysis, the progenitor of the third genome may also be tentatively identified. However, it should be emphasized that the progenitors of the three genomes will have to be confirmed through meiotic analysis of the interspecific hybrids. Such techniques were earlier utilized in the identification of diploid progenitors of hexaploid common wheat, tetraploid tobacco and tetraploid cotton.

Summary

Karyotypes were prepared in twelve species of *Helianthus* utilizing root tip metaphase mitoses. Ten species were diploid with 2n=34, *H. mollis* was diploid with 2n=30 and *H. tuberosus* was hexaploid with 2n=102. The mean chromosome length between species ranged from 2.2 μ to 3.5 μ, although within a species individual chromosomes could be as small as 1.1 μ and as long as 5.2 μ. The karyo-

types in eight species were presented for the first time and the results in the remaining four species are discussed in view of the earlier published results.

It is concluded that structural changes did not alter the karyotypes to any appreciable degree, since ten of the twelve species were placed in class 2B of Stebbins. Only *H. annuus* and *H. mollis* were placed in class 1B.

Karyotype of *H. tuberosus* was examined and two of the three genomes taking part in its constitution were tentatively assigned to *H. annuus* and *H. lenticularis*.

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