

LOW BASE NUMBERS AND DYSPLOIDY IN ANNUAL HELICHRYSUM MILL. (ASTERACEAE: GNAPHALIEAE)

MERCÈ GALBANY-CASALS^{1*}, ALFONSO SUSANNA¹, AND JULIÁN MOLERO BRIONES²

¹Institut Botànic de Barcelona (CSIC-ICUB), Psg. Migdia s/n, E-08038 Barcelona, Spain ²Departament de Productes Naturals, Biologia Vegetal i Edafologia, Universitat de Barcelona, Avda. Joan XIII s/n, 08028 Barcelona, Spain

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We report one new base number for *Helichrysum*, x = 5, found in the South African species *H. indicum* (2n = 10), and additional evidence for the recently documented x = 4 found in several South African species: *H. litorale* (2n = 8), *H. spiralepis* (2n = 8) and *H. zwartbergense* (2n = 8). Dysploidy is shown as an additional evolutionary trend within the genus, apart from polyploidy which is most extensive and documented. The association of dysploidy processes with the acquisition of an annual life cycle and adaptation to aridity is discussed for these species and other plant groups.

Key words: Helichrysum evolution, karyology, karyotype symmetry, polyploidy.

INTRODUCTION

The genus *Helichrysum* Mill. (Asteraceae, Gnaphalieae) comprises \sim 500 (Hilliard, 1983) to \sim 600 (Anderberg, 1991; Bayer et al., 2007) species, distributed mainly on the African continent and Madagascar, but also with \sim 45 of them distributed in the Mediterranean basin, Macaronesia and Asia.

With regard to life cycle, the genus includes species ranging from annual plants to trees, although most are subshrubs or shrubs, or perennial herbs with basal leaf rosettes. Annual herbs are rare and only about 6% of the ~ 245 species from Southern Africa are annual (Hilliard, 1983). One example is Helichrysum indicum (L.) Grierson, an endemic to the SW Cape in South Africa, classified in group 15 in Hilliard's (1983) treatment of southern African species, and which occurs on sandy soils in open patches of shrubby communities. A group of species interesting in terms of life cycle are members of group 14 (Hilliard, 1983). Hilliard (1983) expressed her uncertainty about most of these species' life cycle: while some were considered to be exclusively annuals, others, for example Helichrysum litorale H. Bol., H. spiralepis Hilliard & B. L. Burtt. and H. zwartbergense H. Bol., are probably perennials because they have woody roots although their stems are annual. Annual and perennial cycles could appear in different individuals of the same species, depending on the particular micro-environmental and annual weather conditions.

The chromosome number most commonly found in *Helichrysum* is 2n = 28, mainly in Mediterranean, Macaronesian and Asiatic species, but in some African species as well. Some records of 2n = 14 for African species and 2n = 56 for some East Mediterranean and Asiatic species are also known (Galbany-Casals and Romo, 2008). We know of only two records of 2n = 42 in the literature (Febles, 1989; Galbany-Casals and Romo, 2008). These data indicate a predominant base number of x = 7, as Namur and Verlague (1976) first suggested. The existence of four different ploidy levels based on x = 7 shows polyploidy as the most significant evolutionary trend of chromosome number within the genus, as discussed in a previous paper (Galbany-Casals and Romo, 2008). However, a new base number was recently documented for the genus, x = 4, found in *H. litorale*, one of the species of group 14 (Hilliard, 1983) cited above (Galbany-Casals and Romo, 2008), which indicated the additional presence of dysploidy in the chromosome number evolution of the genus.

^{*}email: pallenis@yahoo.com

Taxon	Locality and voucher		Comments				
H. litorale H. Bol.	Republic of South Africa, Eastern Cape Province, Port Alfred, 5 Feb 2007, Arrabal, Galbany, Koekemoer & Romo 14500 (BC 867722)	8	Previous references: $2n = 8$ (Galbany-Casals and Romo, 2008)				
<i>H. spiralepis</i> Hilliard & B. L. Burtt.	Republic of South Africa, Eastern Cape Province, Katberg Pass, 4 Feb 2007, <i>Arrabal, Galbany,</i> Koekemoer & Romo 14479 (BC 867706)	8	First count				
H. zwartbergense H. Bol.	Republic of South Africa, Western Cape Province, Swartberg Pass, 6 Feb 2007, <i>Arrabal, Galbany,</i> Koekemoer & Romo 14520 (BC 867739)	8	First count				
<i>H. indicum</i> (L.) Grierson	Republic of South Africa, Western Cape Province, Worcester, Langeberg Mts., 10 Feb 2007, <i>Arrabal,</i> Galbany, Koekemoer & Romo 14547 (BC 867758)	10	First count				
<i>H. globosum</i> Schultz-Bip.	Kenya, Mount Kenya, between Minto's Hut and Meru Lodge, 13 Sep 2006, <i>Arrabal & Galbany s. n.</i> (BC 867838)	14	Previous references: 2 <i>n</i> = 14 (Thulin, 1970; Hedberg and Hedberg, 1977)				
<i>H. patulum</i> (L.) D. Don	Republic of South Africa, Western Cape Province, southern slopes of Swartberg Pass, 6 Feb 2007, Arrabal, Galbany, Koekemoer & Romo 14507 (BC 867729)	14	Previous references: 2n = 14 (Galbany-Casals and Romo, 2008)				
H. setosum Harv.	Tanzania, between Bulati and Empaakai crater, 5 Feb 2006, Arrabal & Galbany s. n. (BC 867824)	14	First count				
<i>H. pendulum</i> (C. Presl) C. Presl	Spain, Balearic Islands, Majorca, Cingles d'es Racó, 8 May 1997, <i>Sáez s. n.</i> (BCN 6118)	28	Previous references: $2n = 28$ (D'Amato, 1971, sub. <i>H. rupestre</i> var. <i>stramineum</i> and sub. <i>H. rupestre</i> var. <i>pendulum</i> ; Cardona, 1976, sub. <i>H. fontanesii</i> ; Galbany- Casals and Romo, 2008)				
H. serotinum (DC.) Boiss.	Spain, Tarragona, Ports de Beseit, road to Mt. Caro, 28 Jul 2001, <i>Blanco, Galbany & Lanau s. n.</i> (BCN 6120)	28	Previous references: <i>x</i> = 14 (Lorenzo-Andreu and García Sanz, 1950); 2n = 28 (Galbany-Casals and Romo, 2008).				
H. plicatum DC.	Turkey, Konya, between Çukuryurt pass and Gevne Valley, 25 km from Taşkent, 31 Jul 2002, <i>Susanna</i> 2276 et al. (BCN 25366)	56	Previous references: $2n = 56$ (Namur and Verlaque, 1976; Galbany-Casals and Romo, 2008)				

TABLE 1. Localities and vouchers of the studied species. 2n – somatic chromosome number

Previously, Turner (1970) provided chromosome counts for several Australian *Helichrysum* species that showed variation of base numbers comprising x = 8, 10, 11, 12 and 14. However, several phylogenetic works based on morphology (Anderberg, 1991) and on DNA sequences (Bayer et al., 2000; Galbany-Casals et al., 2004) lately suggested the need to exclude the Australian and New Zealand species from *Helichrysum*. Therefore, only x = 7 and x = 4 would remain as the known base numbers for the genus.

Nevertheless, chromosome number is known for only about 10–12% of the species of this large genus; the African species in particular are very poorly known in terms of karyology. To our knowledge, the karyotype of only one Western Mediterranean species, *H. crassifolium* (L.) D. Don, has been studied (Castro and Rosselló, 2007). In this paper we provide chromosome number and karyotypes for a group of annual South African species, and compare them with the chromosome number and karyotypes of several perennial species representing chromosome variability within the genus.

MATERIALS AND METHODS

We focused on four South African Helichrysum species, in view of their particular life cycle characteristics: *H. litorale*, *H. spiralepis*, *H. zwartbergense* and *H. indicum*. Some additional species have been included as well for comparison purposes, with the aim of representing the maximum chromosome variability of perennial species within the genus. Three are African species: *H. globosum* Schultz-Bip., which is found quite widespread in several tropical African countries; *H. setosum* Harv.,

TABLE 2. Karyological data of the studied species. N – number of mitotic metaphases measured; 2n – somatic chromosome number; SD – standard deviation; chromosomal formulae according to Levan et al. (1964): m – metacentric; sm – submetacentric; st – subtelocentric; L% and S%, according to Bazzichelli (1967); A₁ – intrachromosomal asymmetry index (Romero Zarco, 1986); A₂ – interchromosomal asymmetry index (Romero Zarco, 1986); Steb. – Stebbins symmetry category

Taxon	Ν	2n	Karyotype length (μm) ± SD	Length range (µm)	Chromosomal formula	L%	S%	A_1	A_2	Steb.
H. litorale	5	8	31.14 ± 4.12	5.98-9.16	2 sm + 6 st	77.73	22.27	0.69	0.50	4A
H. spiralepis	5	8	29.64 ± 2.74	5.64-9.8	2 m + 2 sm + 4 st	77.15	22.85	0.65	0.51	ЗA
H. zwarbergense	5	8	23.56 ± 2.32	5.12-6.65	2 sm + 6 st	75.34	24.66	0.66	0.49	4A
H. indicum	5	10	28.30 ± 5.69	4.32-7.29	2 sm + 8 st	78.47	21.53	0.73	0.18	ЗA
H. globosum	4	14	34.61 ± 7.04	3.95-6.29	6 m + 8 sm	64.60	35.40	0.45	0.14	2A
H. patulum	5	14	35.95 ± 2.82	3.76-7.23	12 m + 2 sm	60.39	39.61	0.33	0.21	2A
H. setosum	6	14	29.64 ± 3.95	3.47-5.40	10 m + 4 sm	60.66	39.34	0.35	0.14	2A
H. pendulum	8	28	21.10 ± 1.76	1.10-2.08	24 m + 4 sm	57.21	42.79	0.25	0.18	2A
H. serotinum	7	28	20.18 ± 2.10	1.09-2.22	24 m + 4 sm	58.43	41.57	0.28	0.22	2A

which grows in tropical Africa and Southern Africa and was classified in group 30 by Hilliard (1983); and *H. patulum* (L.) D. Don, which is endemic to the South and Southwest Cape in South Africa and belongs to Hilliard's group 18 (Hilliard 1983). Two more are Mediterranean species with 2n = 28, *H. pendulum* (C. Presl) C. Presl and *H. serotinum* (DC.) Boiss., and finally *H. plicatum* DC., which grows in the Eastern Mediterranean area and Western Asia and has 2n = 56 (Tab. 1).

Chromosome counts were made from somatic metaphases using squash technique. Seeds collected in the wild were used. Root tip meristems were obtained by germinating seeds on wet filter paper in Petri dishes at room temperature. Samples were pretreated with 0.05% colchicine for 2 h 15 min at room temperature. The material was fixed in 3:1 v/v absolute ethanol : glacial acetic acid for a minimum 24 h at 4°C. Meristems were hydrolyzed in 5N HCl for 50 min at room temperature. They were stained in 2% acetic orcein for a minimum 3 h at 4°C. Squashes were made in 45% acetic acid. Preparations were fixed by freezing with CO_2 , ethanol-dehydrating, and mounting in Canada Balsam. Photographs were taken through a Zeiss Standard microscope with an Olympus C3030 camera.

For each studied species, 4–8 metaphases were selected for measurements in order to characterize their karyotype, except for *H. plicatum*, which was excluded from this part of the study because of technical difficulties in obtaining a sufficient number of good metaphases. The nomenclature used for describing chromosome morphology follows Levan et al. (1964). Idiograms were drawn based on mean measurements and arranged in order of decreasing size. For numerical characterization of the karyotypes the following parameters were calculated: total karyotype length; chromosome length range; contribution of each arm of each chromosome to total length of karyotype according to Bazzichelli (1967) (L%, contribution of long arm; S%, contribution of short arm); asymmetry indices A_1 (intrachromosome) and A_2 (interchromosome) according to Romero Zarco (1986); and asymmetry categories according to Stebbins (1971).

RESULTS

Three base numbers are found within *Helichrysum*: x = 4, x = 5 and x = 7, the latter represented by diploids (2n = 14), tetraploids (2n = 28) and octoploids (2n = 56) (Fig. 1; Tab. 1). From Table 2, where chromosomal characteristics for each species are given, and Figure 2, where haploid idiograms are shown, two main groups can easily be distinguished by karyotype characteristics: one group is formed by *H.* litorale, *H.* spiralepis, *H.* zwartbergense (x = 4), and H. indicum (x = 5), which have rather asymmetrical karyotypes (Stebbins' categories 3A and 4A, the predominance of st chromosomes, and high A1 index) composed of large chromosomes; the second group comprises species with x = 7, which generally present more symmetrical karyotypes (Stebbins' category 2A, the predominance of m chromosomes, and much lower A_1 index). In Figure 3, where species are plotted for the relationship between A_1 and A₂ Romero Zarco asymmetry indices (Romero Zarco, 1986), four groups are seen: the first including the two Mediterranean species; the second including the African species with 2n = 14, which are very close to the Mediterranean species; the third including the South African species with 2n =8; and the fourth, containing only *H. indicum*, with 2n = 10.



Fig. 1. Mitotic metaphases. (a) *H.* litorale (2n = 8), (b) *H.* spiralepis (2n = 8), (c) *H.* zwartbergense (2n = 8), (d) *H.* indicum (2n = 10), (e) *H.* globosum (2n = 14), (f) *H.* patulum (2n = 14), (g) *H.* setosum (2n = 14), (h) *H.* pendulum (2n = 28), (i) *H.* serotinum (2n = 28), (j) *H.* plicatum (2n = 56). Bar = 10 µm.



Fig. 2. Haploid idiograms of the studied species. Chromosome number and chromosomal formula are indicated for each one: (a) *H. litorale* (2n = 8; 2 sm + 6 st), (b) *H. spiralepis* (2n = 8; 2 sm + 2 sm + 4 st), (c) *H. zwartbergense* (2n = 8; 2 sm + 6 st), (d) *H. indicum* (2n = 10; 2 sm + 8 st), (e) *H. globosum* (2n = 14; 6 m + 8 sm), (f) *H. patulum* (2n = 14; 12 m + 2 sm), (g) *H. setosum* (2n = 14; 10 m + 4 sm), (h) *H. pendulum* (2n = 28; 24 m + 4 sm), (l) *H. serotinum* (2n = 28; 24 m + 4 sm). Bars graduated in μm .



Fig. 3. Scatter plot of the Romero Zarco asymmetry indices. Values of A1 and A2 are summarized in Table 2. Species codes: 1. *Helichrysum* litorale; 2. *H. spiralepis*; 3. *H. zwartbergense*; 4. *H. indicum*; 5. *H. globosum*; 6. *H. patulum*; 7. *H. seto-sum*; 8. *H. pendulum*; 9. *H. serotinum*.

DISCUSSION

Our results provide evidence of a new base number in the genus *Helichrysum*, x = 5. Moreover, base number x = 4 is documented for two additional species, after the first record of this number for H. litorale in Galbany-Casals and Romo (2008). This finding slightly extends the small list of genera with such reduced base numbers within the whole tribe Gnaphalieae. Up to now it has seemed that the only documented cases are two species of the genus Leysera with 2n = 8 [L. gnaphalodes (Nordenstam, 1967) and L. tenella (Bremer, 1978)], one species of Nestlera, N. biennis with 2n = 10(Bremer, 1976), two species of Rhynchopsidium also with 2n = 10 [R. pumilum and R. sessiliflorum (Bremer, 1976)], Pogonolepis stricta with 2n = 8or 2n = 10 (Short, 1986; Watanabe et al., 1999), *Trichanthodium skirrophorum* with 2n = 8 (Short, 1990; Watanabe et al., 1999) and Epitriche demissus with 2n = 10 (Watanabe et al., 2007). Some species within the tribe have an even lower chromosome number, 2n = 6: Podolepis capillaris (Konishi et al., 2000), Trichanthodium baracchianum, T. exilis (Watanabe et al., 1999), T. scarletianum (Short, 1990; Watanabe et al., 1999) and Sondottia connata (Watanabe et al., 1999).

The finding of these two base numbers adds evidence for the importance of dysploidy as an evolutionary trend in the karyological evolution of the genus, apart from extensive and well documented polyploidy. Within the Gnaphalieae there are also several examples of infrageneric dysploidy series in Australian genera: Angianthus (n = 13, 12, 6), Asteridea (n = 9, 7), Millotia (n = 13, 11, 10, 8) and Pogonolepis (n = 6, 5, 4), among others (Watanabe et al., 1999). The differences in karyotype formulae (Tab. 2) and asymmetry indices (Fig. 3) suggest that dysploidy in Helichrysum is associated with deep structural changes in chromosomes. However, total genome size, interpreted from total karvotype length (Tab. 2), does not show notable differences between species with 2n = 14 and species with 2n = 8 and 10, although there is an evident decrease in chromosome length, correlated with an increase in chromosome number and ploidy level (Tab. 2). Insufficient sampling may account for the gap between 2n = 14 and 2n = 10 and 2n = 8; cytotypes or species of Helichrysum with intermediate numbers (2n = 12) belonging to the same or else to other African clades could exist.

It is generally believed that an annual life cycle can increase the overall evolutionary dynamics of a particular genome. It is also thought that more and faster evolutionary divergence enables annual plants to penetrate less favorable and more unstable habitats (Ehrendorfer, 1970). This evolutionary divergence can be represented by increased variability of chromosome number within a group of related plants (Nagl and Ehrendorfer, 1974). In particular, descending dysploidy is considered an active evolutionary mechanism in plants, especially in the Asteraceae (Garnatje et al., 2004, and references within). Garnatje et al. (2004) hypothesized adaptation to xeric habitats as a trigger of processes leading towards annuality and descending dysploidy in the Xeranthemum group (Cardueae), where perennial mountain species of Amphoricarpos have x = 14 while annual xerophytes of the genera Chardinia, Siebera and Xeranthemum show a complex dysploid series from x = 12 to x = 5. Subtribe Centaureinae (Cardueae) also shows a complex descending dysploid chromosome series ranging from x = 16 to x = 7 (Garcia-Jacas et al., 1996), in which species adapted to more extreme habitats show lower chromosome numbers, correlated with other secondary adaptations that suggest a similar course of evolution (Garcia-Jacas and Susanna, 2009). Watanabe et al. (1999) also found a relationship between low chromosome numbers, annual habits and dry habitats in the Australian Gnaphalieae genera Pogonolepis, Sondottia and Trichantodium. Finally, Selvi and Bigazzi (2002) also hypothesized descending dysploidy associated with a tendency to shorten the life cycle in Nonea (Boraginaceae) as an adaptation to arid habitats.

In our study, the annual life cycle or at least annuality of the aerial part of the plant in H. litorale, H. zwartbergense and H. spiralepis would agree with the observed low chromosome numbers. Moreover, with the exception of H. spiralepis and H. lineatum, the species of group 14 (Hilliard, 1983) are, in general, distributed in the Cape, some of them also in Namibia, and they are adapted to arid environments; the same is true of H. indicum, endemic to the SW Cape. However, until more chromosome number data are available and the molecular phylogeny of this huge genus is worked out comprehensively, we will not know whether the low chromosome numbers found in Helichrysum are due to descending, ascending or mixed (both ascending and descending starting from x = 5) dysploidy.

CONCLUDING REMARKS

Although polyploidy is known to play a very important role in *Helichrysum* evolution (Galbany-Casals and Romo, 2008), karyological evolution within the genus is shown here to be more complex than has been thought, since it becomes evident that dysploidy is also a significant force which seems to be correlated with an annual habit and adaptation to arid habitats. The extent of this phenomenon in *Helichrysum* is unknown because the chromosome data for this large and not satisfactorily delimited genus is sparse. We present our data as a starting point and a call for further karyological work focused on African *Helichrysum* species in the coming years.

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