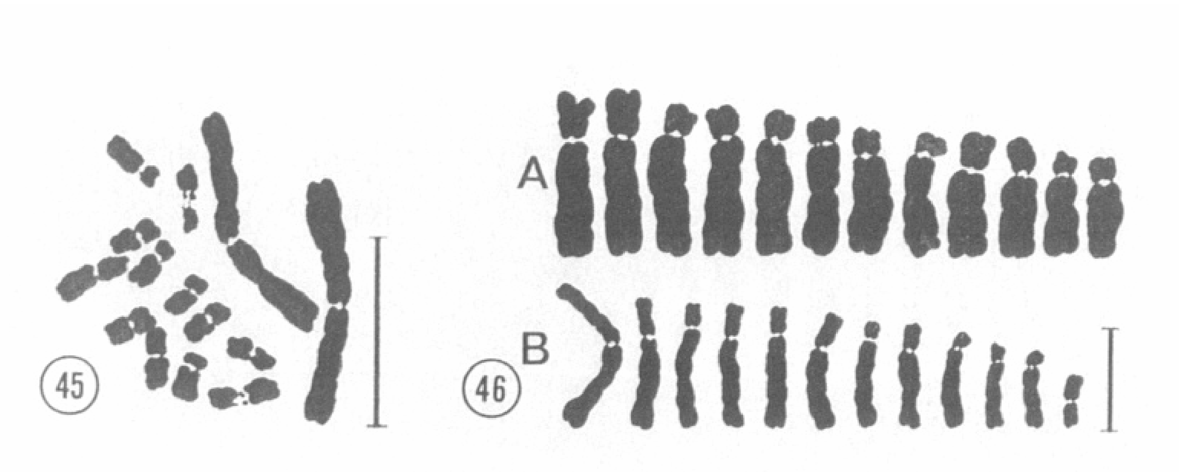
Evolutionary trends in chromosome number changes



Basic chromosome number (x)

- a relative concept [x has to be related to a certain taxonomic unit, e.g. genus or (sub)family]
- monobasic taxa (single x number), dibasic taxa (two x nos.) and polybasic taxa (>2 x nos.)
- are there any evolutionary trends in chromosome number changes?
- are the same chromosome number and similar karyotype structure indicative of close phylogenetic relationship?
- can polybasic taxa be regarded as monophyletic?
- is the most common basic chromosome number automatically the ancestral one?

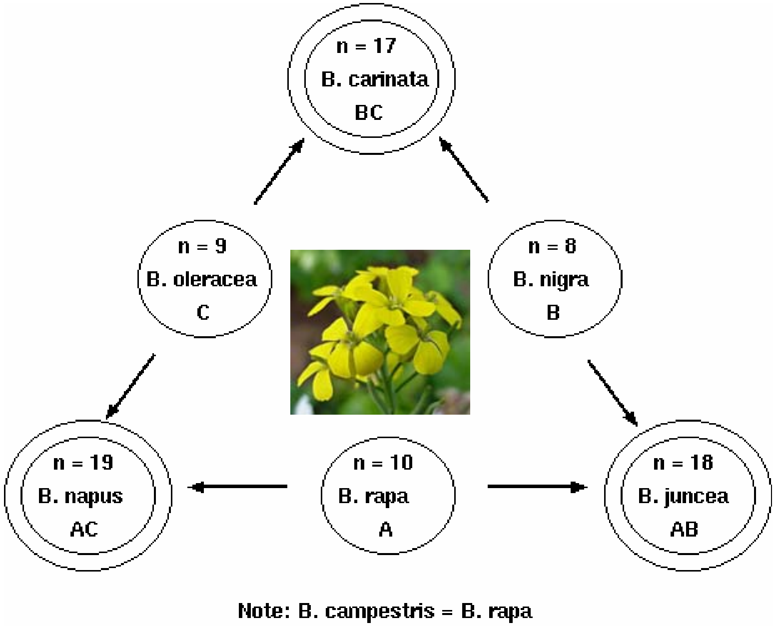
Asteraceae – example of a polybasic family

Table 4. Tri- and polybasic genera in the Astereae.

Genus	Region	"Basic" chromosome numbers
Amellus L.	(Africa)	x = 6, 8, 9 (diploid)
Aphanostephus DC.	(N. Am.–Mex.)	x = 3, 4, 5 (diploid)
Aster L.	(cosmopolitan)	x = (4–)5, 7, 8, 9, 13 (polyploid to 16x)
Astranthium Nutt.	(N. Am.–Mex.)	x = 3, 4, 5, 6, 8, 9, etc. (dysploid; polyploid to 6x?)
Brachyscome Cass.	(Austr., N.Z., N.G.)	x = 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, etc. (dysploid; polyploid to 18x?)
Calotis R. Br.	(New Zealand)	x = 4, 7, 8, 9, etc. (polyploid to 14x?)
Chrysopsis Nutt.	(N. Am.)	x = 4, 5, 9 (polyploid to 6x)
Felicia Cass.	(Africa)	x = 5, 6, 8, 9 (diploid and tetraploid)
Haplopappus Cass. sensu lato	(N. Am.–S. Am.)	x = 2, 3, 4, 5, 6, 7, 8, 9, etc. (dysploid; polyploid to 18x?)
Machaeranthera Nees	(N. Am.–Mex.)	x = 2, 4, 5, 8, 9? (dysploid; diploid and tetraploid)
Psilactis A. Gray	(N. Am.–S. Am.)	x = 4, 5, 9 (perhaps dibasic with dysploidy; diploid)

Evolutionary changes of basic chromosome number

I. allopolyploidy



II. aneuploidy

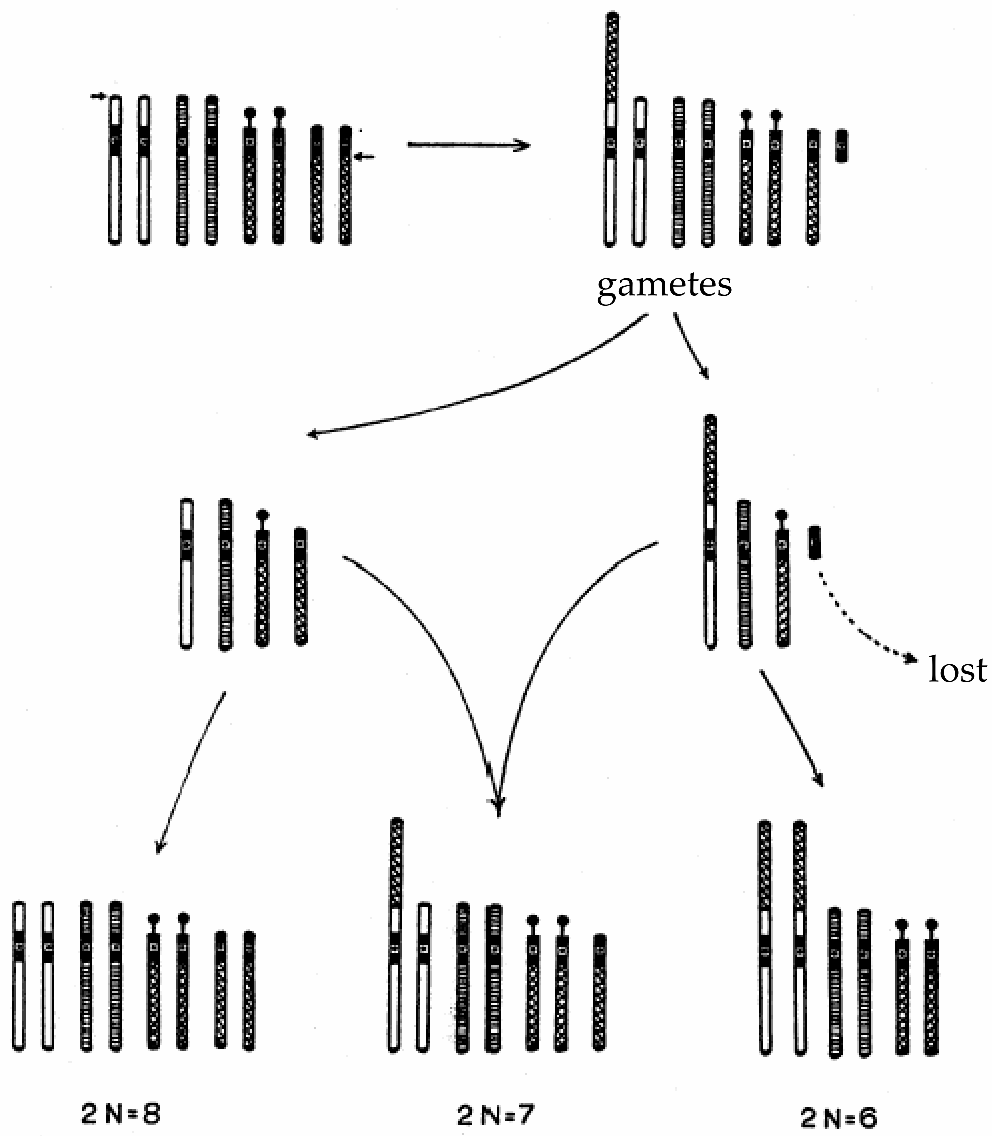
- descending aneuploidy
- ascending aneuploidy

Descending aneuploidy due to unequal reciprocal translocation (centric fusion)

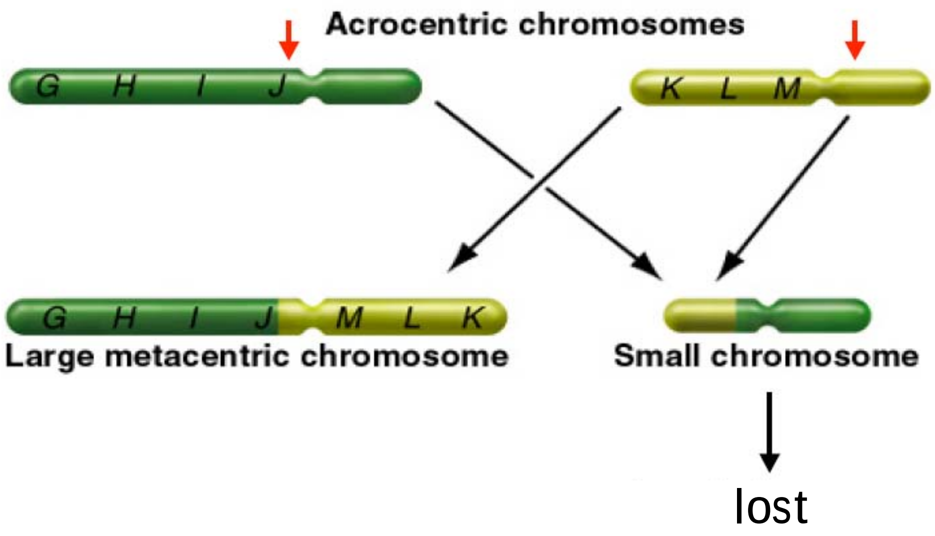
2n = 8

chromosome number reduction

2n = 8 or 7 or 6

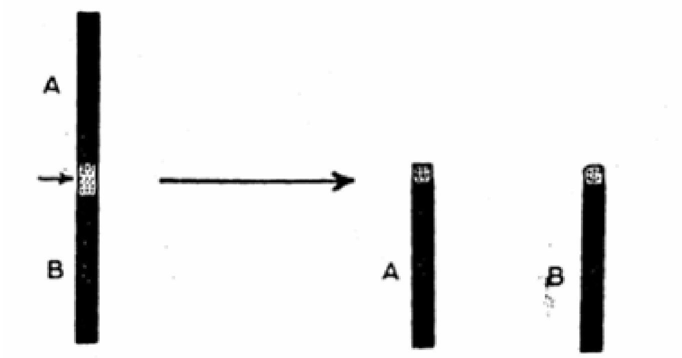


Descending aneuploidy due to Robertsonian translocation (centric fusion)



Ascending aneuploidy

1. Centric fission



2. Meiotic misdivision

- misdivision resulting in a tetrasomic plant (2n+2) (or first trisomy: 2n+1 followed by tetrasomy, 2n+2)

- the extra chromosome can diverge from their homologues through a translocation with non-homologous chromosomes

Chromosome number pattern congruent with phylogenetic relationships: *Ranunculaceae*

• Langlet (1927, 1932) recognized two subfamilies of *Ranunculaceae* (*Ranunculoideae* and *Thalictroideae*) on the basis of cytological characters, including chromosome size and basic number

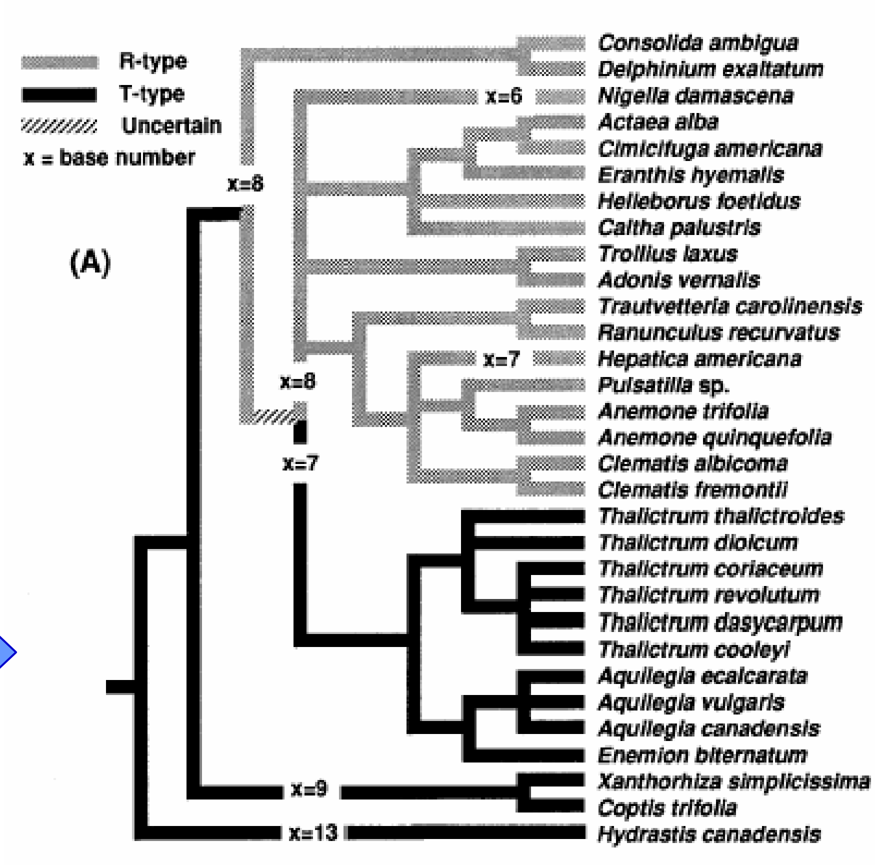
• the *Ranunculus* group of genera (R-chromosome group) has large and long chromosomes with a basic number of 8

• the *Thalictrum* group (T-chromosome group) has short and small chromosomes with a basic number of 7 or 9

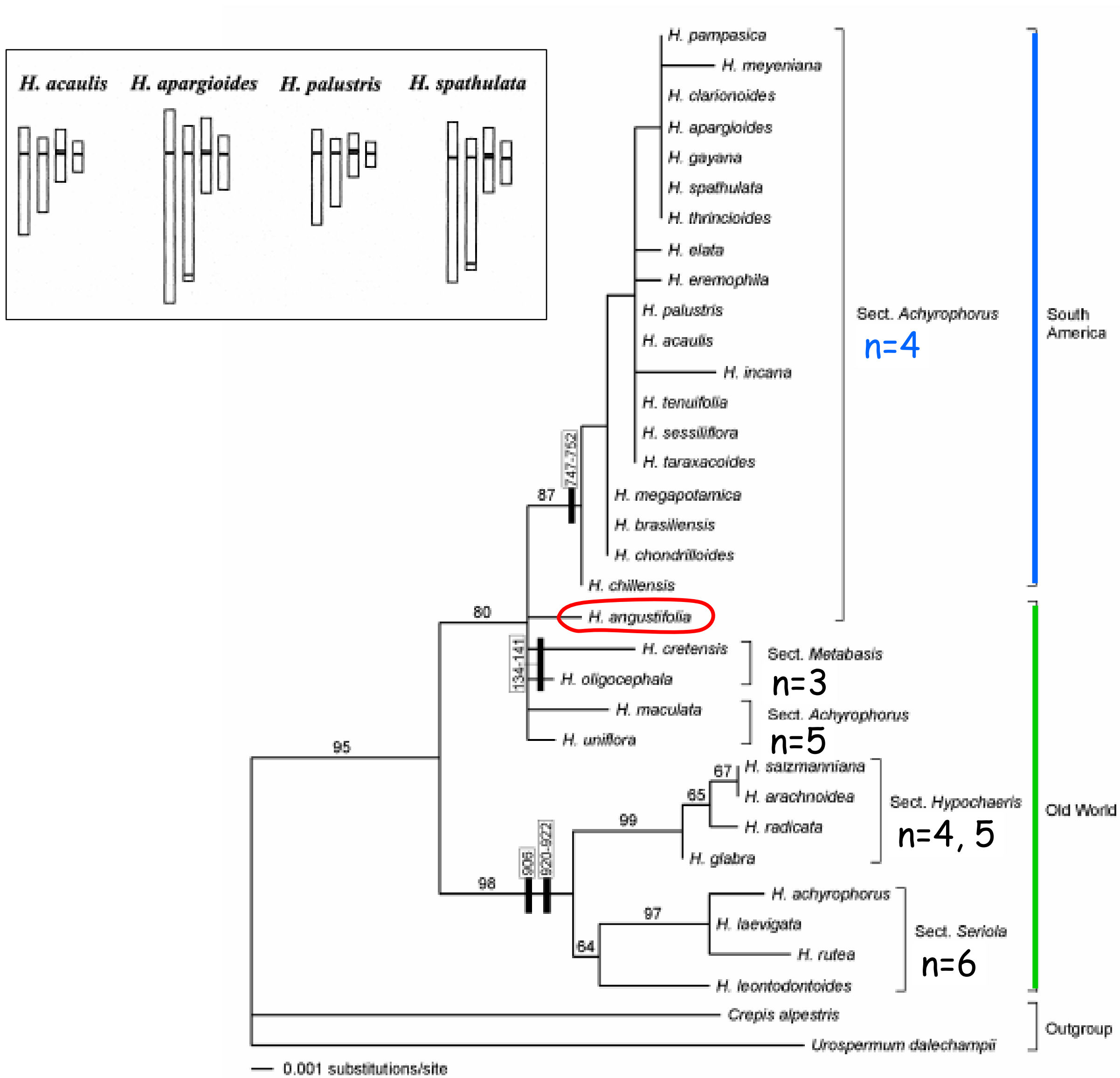



• Ro et al. (1997): chromosome type and base number are congruent with the inferred molecular (rDNA) phylogeny

• fruit type (often used for the higher classification) was not congruent with karyological data and phylogenetic patterns



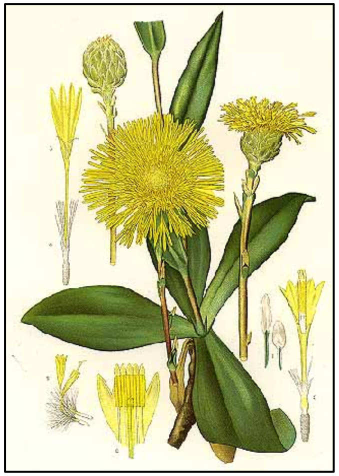
Descending aneuploidy in *Hypochaeris* (*Asteraceae*)



Descending aneuploidy in *Podolepis* (*Asteraceae*)

• the extraordinary series of chromosome numbers, n = 12, 11, 10, 9, 8, 7 and 3 (dysploidy)

• chromosome number of n = 10 is the most common in the genus, and thus, x = 10 was regarded as the ancestral chromosome base number for the genus



Descending aneuploidy in *Podolepis* (*Asteraceae*)

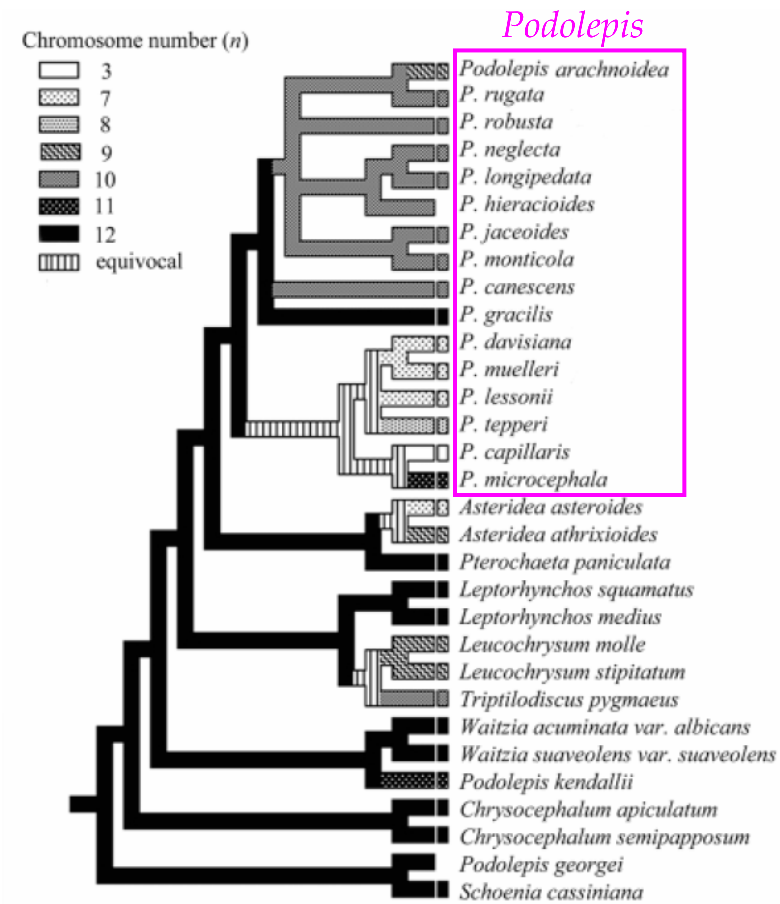
• the haploid chromosome number of n = 12 is the most common in the related genera (*Chrysocephalum*, *Waitzia*, *Leptorhynchos, Pterochaeta*)

• according to the phylogenetic analysis, the ancestral chromosome base number in the genus *Podolepis* may be x = 12

• chromosome number reduction has occurred in three lineages:
- from n = 12 to n = 10 and 9 in the subclade A
- from n = 12 to n = 8 and 7 in the subclade B1
- from n = 12 to n = 11 and 3 in the subclade B2

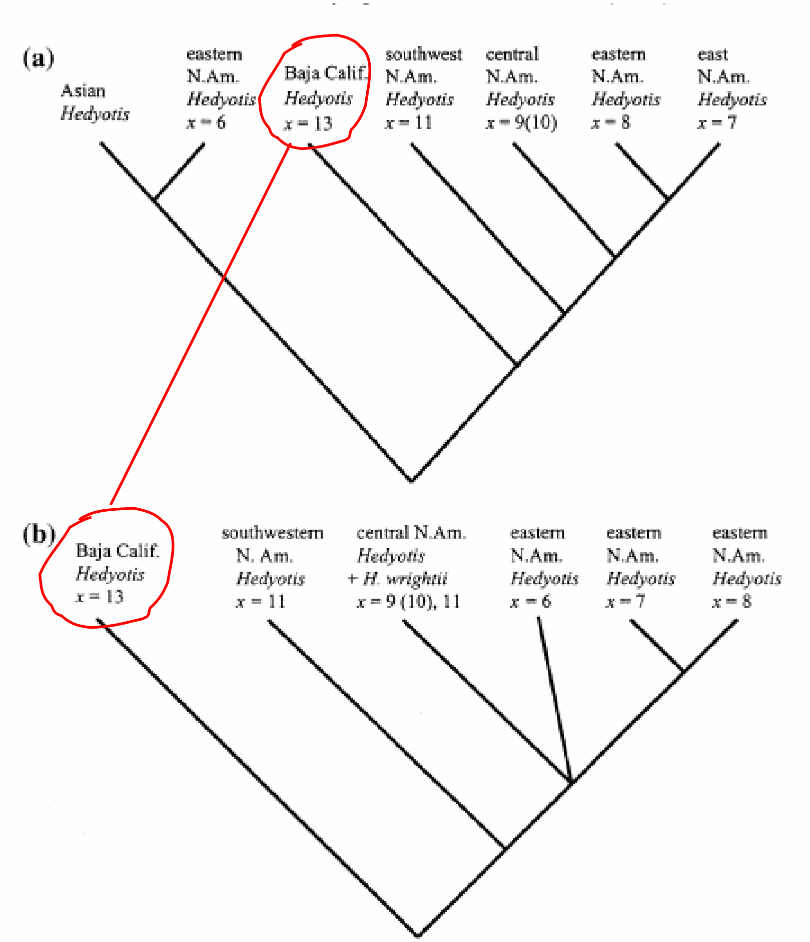
• the low chromosome numbers of n = 8, 7 and 3 were found only in annual species which were distributed in semi-arid regions

• comparing the karyotypes between the taxa with n = 12 (in *Waitzia* and *Chrysocephalum*) and n = 10 (perennial *Podolepis*), the increase in the number of large chromosomes accompanies the decrease in the number of medium-sized chromosomes in *Podolepis* → the reduction in chromosome number has been achieved by the unequal reciprocal translocations, followed by the loss of the short translocation product



Descending aneuploidy in *Houstonia* (*Rubiaceae*)

Proposed phylogenetic hypotheses for the *Hedyotis*/ *Houstonia* lineage in North America



(a) Phylogenetic hypothesis for North American *Hedyotis* based on chromosomes and morphologica characters (Lewis 1962)

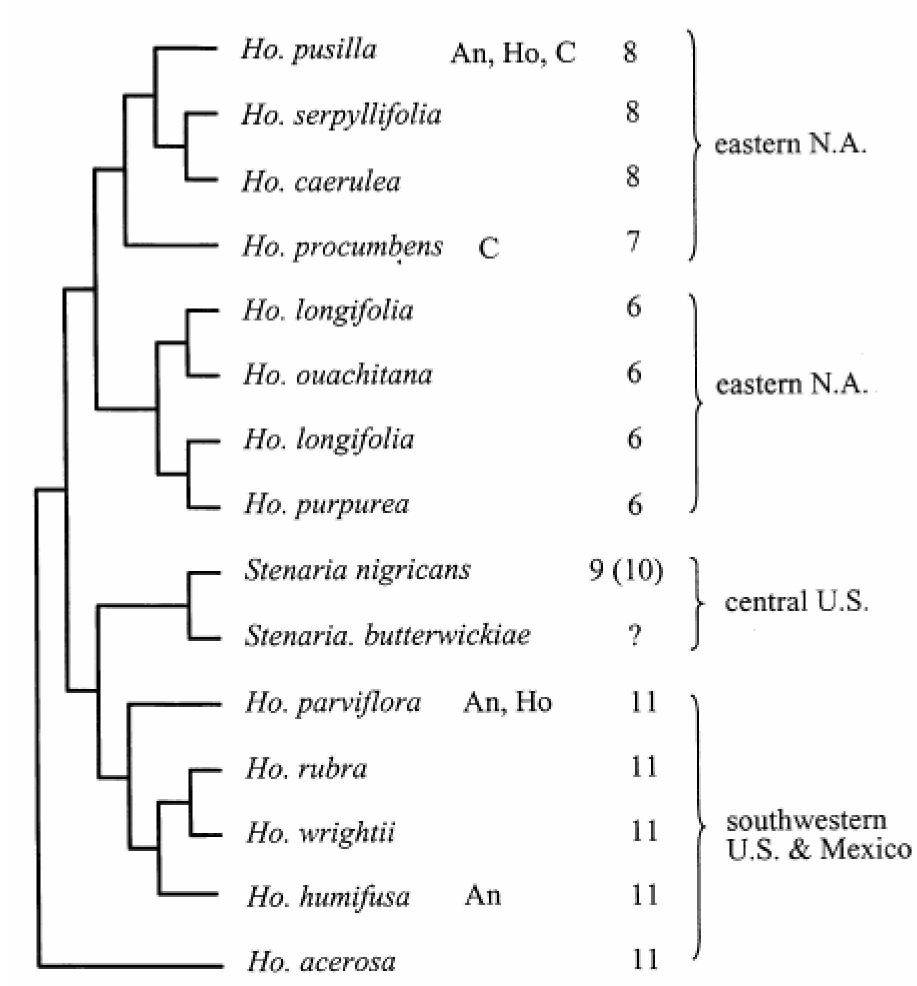
(b) Phylogeny of *Hedyotis* based on pollen morphology plus chromosomes and other morphology (Lewis 1965)

Descending aneuploidy in *Houstonia* (*Rubiaceae*)

Church (2003)

- molecular phylogeny is most concordant with the phylogenetic hypotheses of Lewis (1965) with minor modifications

- the radiation of the *Houstonia* lineage has been accompanied by changes in the basic chromosome number of the major clades through descending aneuploidy



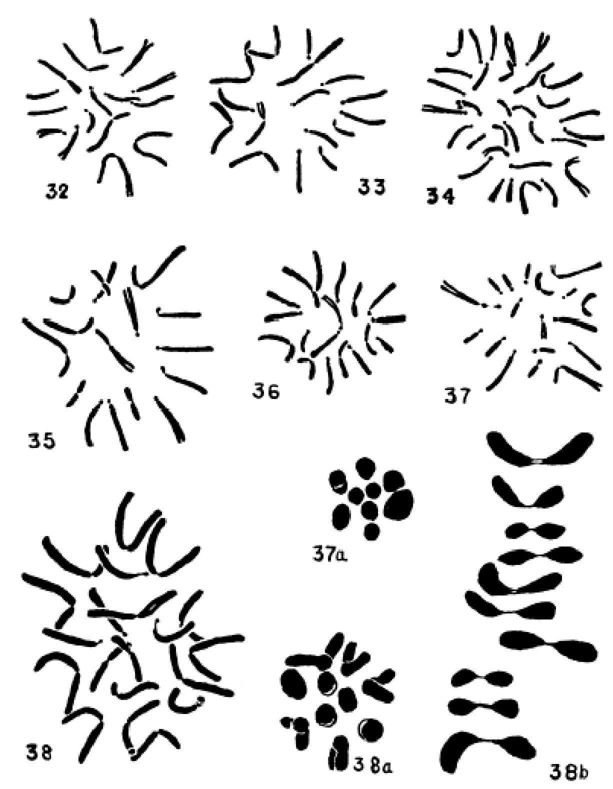
molecular phylogeny based on ITS (nrDNA) and trnL (cpDNA) sequences

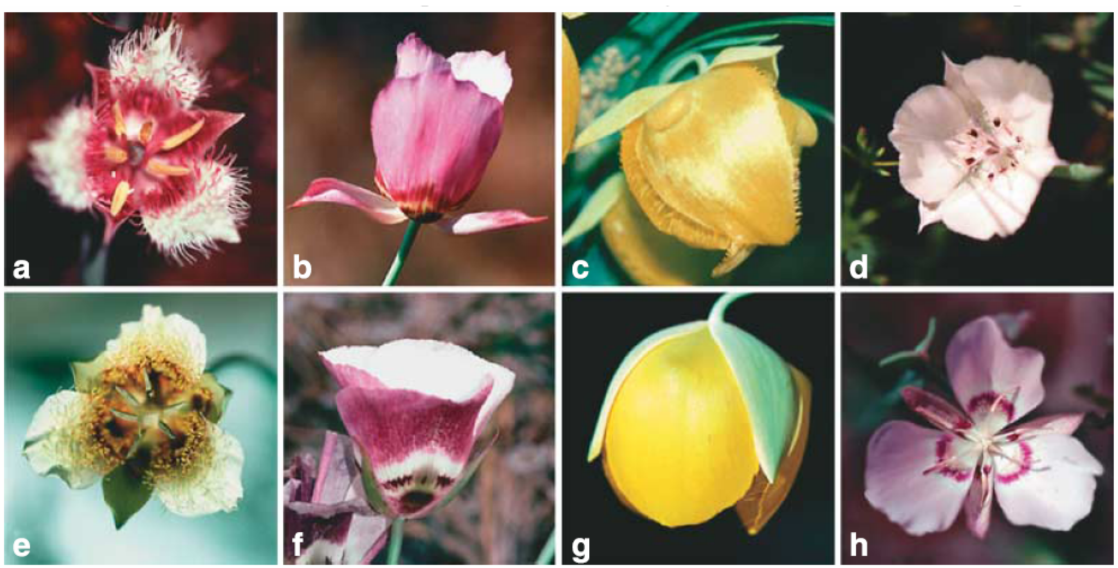
Descending and ascending aneuploidy in *Calochortus* (*Liliaceae*)

- c. 67 spp.

- chromosome numbers n = 6, 7, 8, 9, and 10

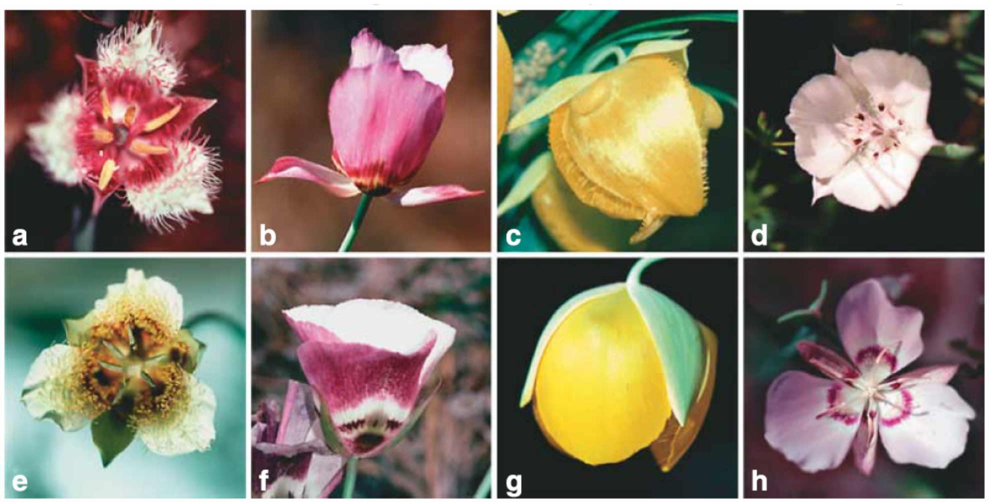
- molecular phylogenetic study carried out to test the monophyly of the three sections and 12 subsections erected by Ownbey (1940) based on morphology and chromosome number



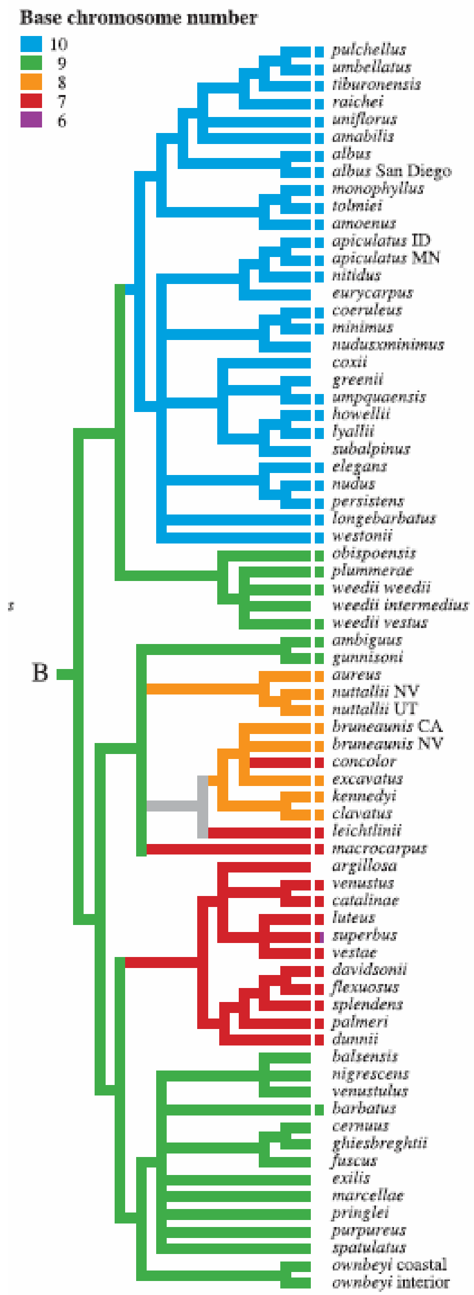


Descending and ascending aneuploidy in *Calochortus* (*Liliaceae*)

- the ancestral chromosome number of *Calochortus* is x = 9
- descending aneuploidy (9 $\rightarrow$ 8, 7, 6)
- ascending aneuploidy (9 $\rightarrow$ 10)

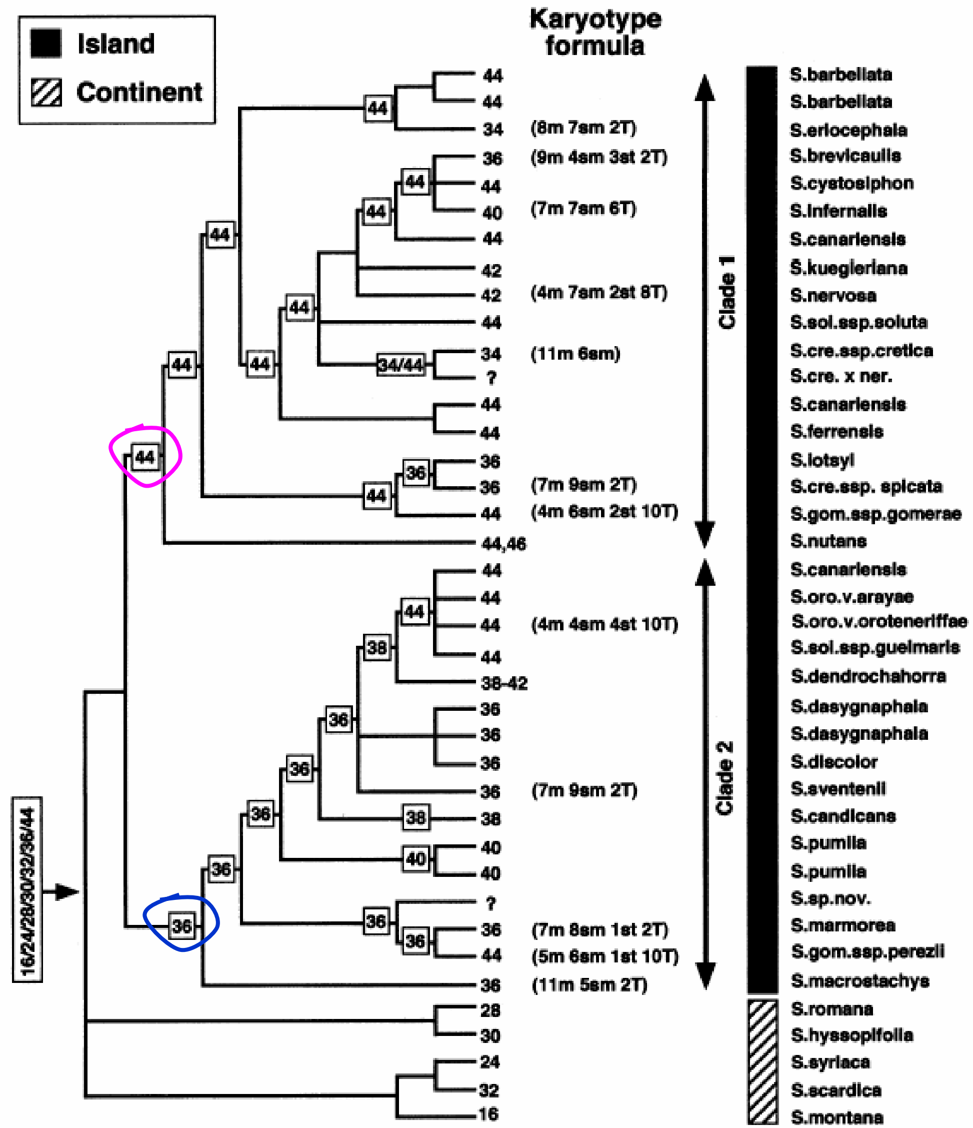


Patterson and Givnish (2003)



Descending and ascending aneuploidy *Sideritis* (*Lamiaceae*)

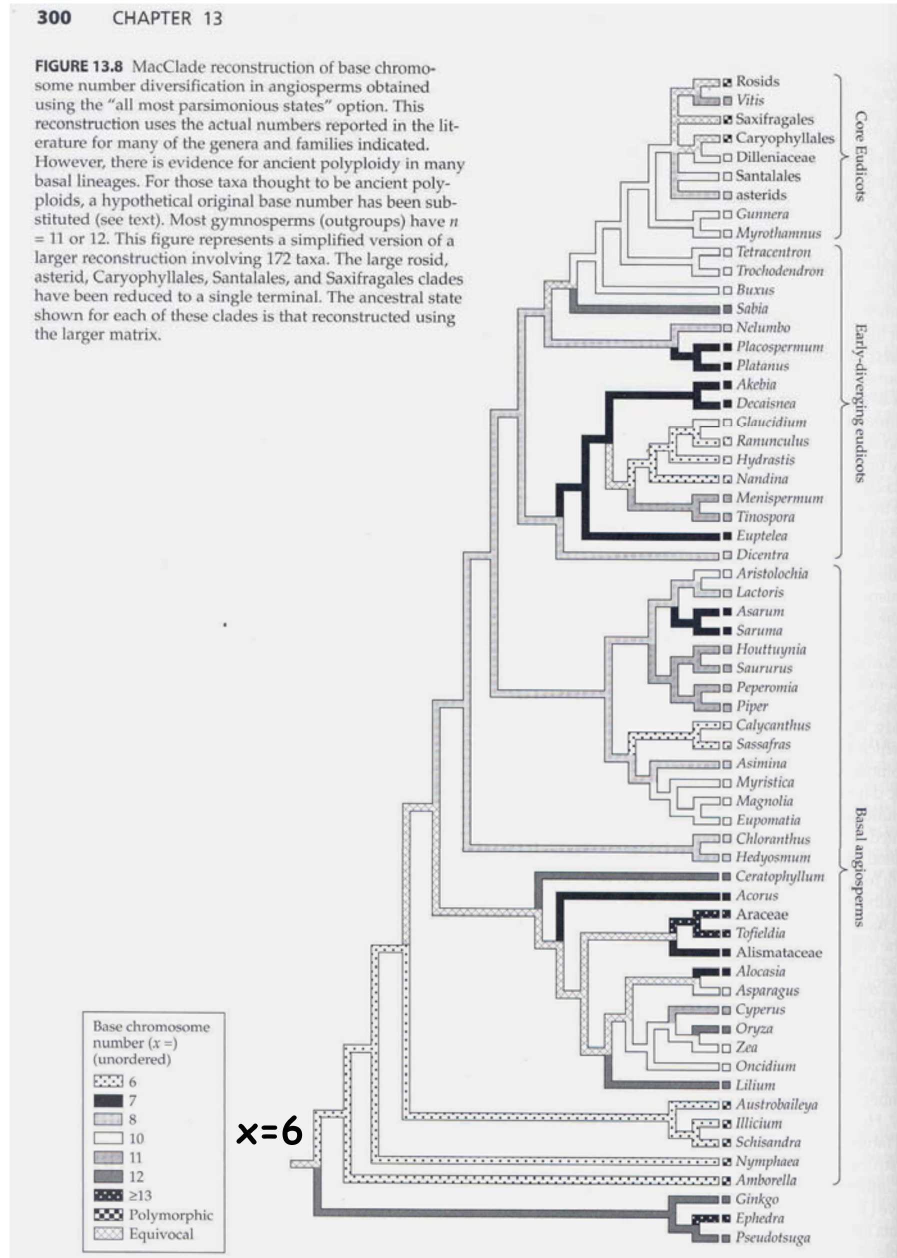
- bimodal pattern of chromosomal change
- Clade 1 shows decreasing aneuploid series, with 2n=44 being the ancestral number
- Clade 2 (with some ambiguity): 2n=36 is the ancestral number and ascending aneuploidy has occurred



Reconstructing the ancestral base number for angiosperms

- the reconstructed ancestral base chromosome number is x=6

- x=6 is a theoretical reconstructed base number, it can be said that the ancestral number was low - between x=6 nad 9



Soltis et al. 2005