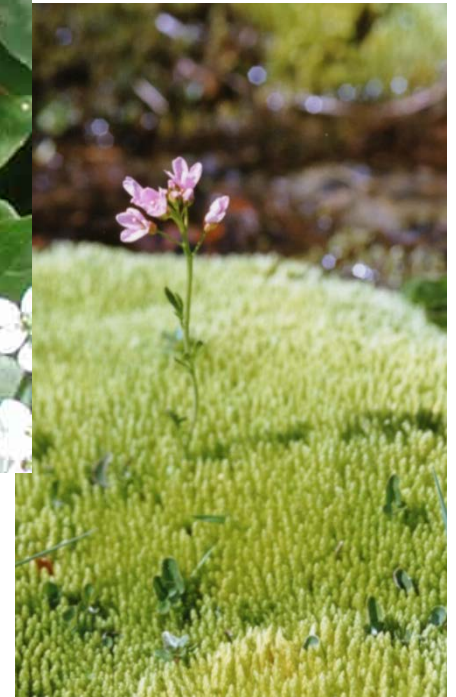


Genus *Cardamine* (Brassicaceae/Cruciferae)

at least **280 spp. worldwide**, mostly N Hemisphere, **54 spp. in Europe**, ca. 50 spp. in N and C America, centre of diversity in Far East and Himalayas (about 70 spp.)



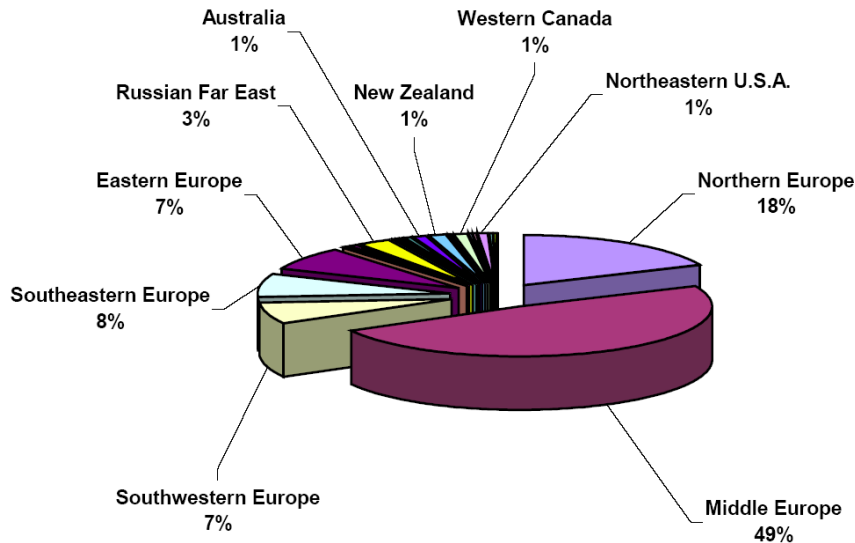
Chromosome numbers and polyploidy

Large karyological diversity

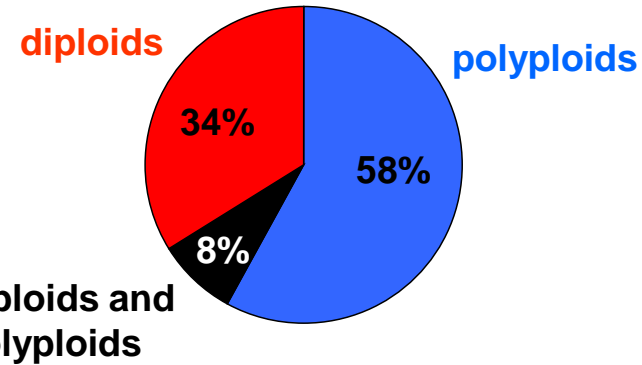
diploids with 16 chromosomes to 32-ploid with 256 chromosomes - N American *C. concatenata*, *C. diphylla*

Several taxonomically critical **polyploid complexes** with unresolved evolutionary history

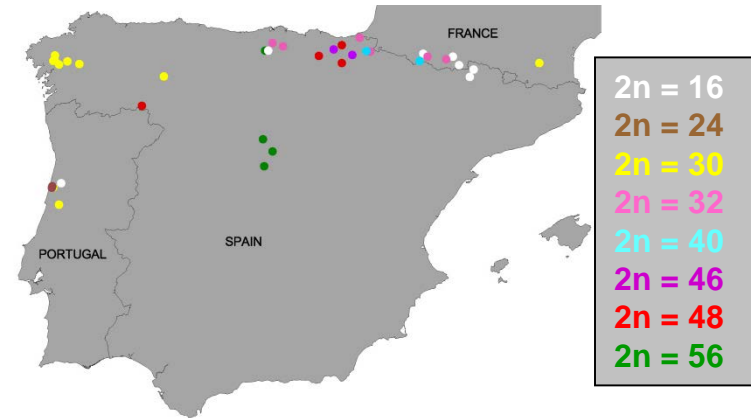
Species with several cytotypes



Kučera et al. 2005, *Biologia (Bratislava)* 60: 473-476.



Iberian populations of *Cardamine pratensis* s. str.



Lihová et al., 2003, *Taxon* 52: 783-802

Unequal geographical distribution of chromosome number records

- chromosome number records for 48% of species (3020 records)

- Europe gathers 1/4 of species, but 89% of chromosome number records

Japan (Hokkaido), Russia (Sakhalin)
Cardamine fauriei or *C. yezoensis*?
C. valida as a synonym?



Japan (Hokkaido,
Honshu, Shikoku,
Kyushu)

Cardamine
yezoensis, *C.*
kiushiana,
or *C. torrentis*?



Korean Peninsula

Cardamine
amariformis?



Japan (Hokkaido)
Cardamine schinziana?

Published chromosome numbers from Japan and Russian Far East

Taxon	$2n$	Locality	Author	Original determination	Note
<i>C. torrentis</i> s.l. (<i>C. valida</i>)	32	Japan, Hokkaido	Kurosawa, 1981	<i>C. yezoensis</i>	Only <i>C. valida</i> was found at this locality in 2004.
<i>C. torrentis</i> s.l. (<i>C. valida</i>)	32	Japan, Hokkaido	Kurosawa, 1981	<i>C. yezoensis</i>	Only <i>C. valida</i> was found at this locality in 2004.
<i>C. torrentis</i> s.l.	56	Japan, Honshu	Kurosawa, 1981	<i>C. torrentis</i>	
<i>C. torrentis</i> s.l. (<i>C. valida</i>)	32	Russia, Sakhalin	Rudyka, 1984	<i>C. yezoensis</i>	Specimen deposited in VLA was revised (incomplete plants only).
<i>C. torrentis</i> s.l. (<i>C. valida</i>)	16 => 32	Russia, Sakhalin	Sokolovskaya, 1960	<i>C. yezoensis</i>	Most likely referring to the same locality and the same chromosome count as the next record.
<i>C. torrentis</i> s.l. (<i>C. valida</i>)	16 => 32	Russia, Sakhalin	Probatova and Sokolovskaya, 1988	<i>C. yezoensis</i>	Specimens deposited in LEU and VLA were revised.
<i>C. yezoensis</i>	72	Japan, [Hokkaido	Nishikawa, 1986	<i>C. yezoensis</i>	
<i>C. yezoensis</i> ?	46-48	plants from Botanical Garden Edinburgh	Manton, 1932	<i>C. leucantha</i> prol. <i>yezoensis</i>	•No voucher specimen was found in herbaria CGE, LDS and MANCH.

Sampling

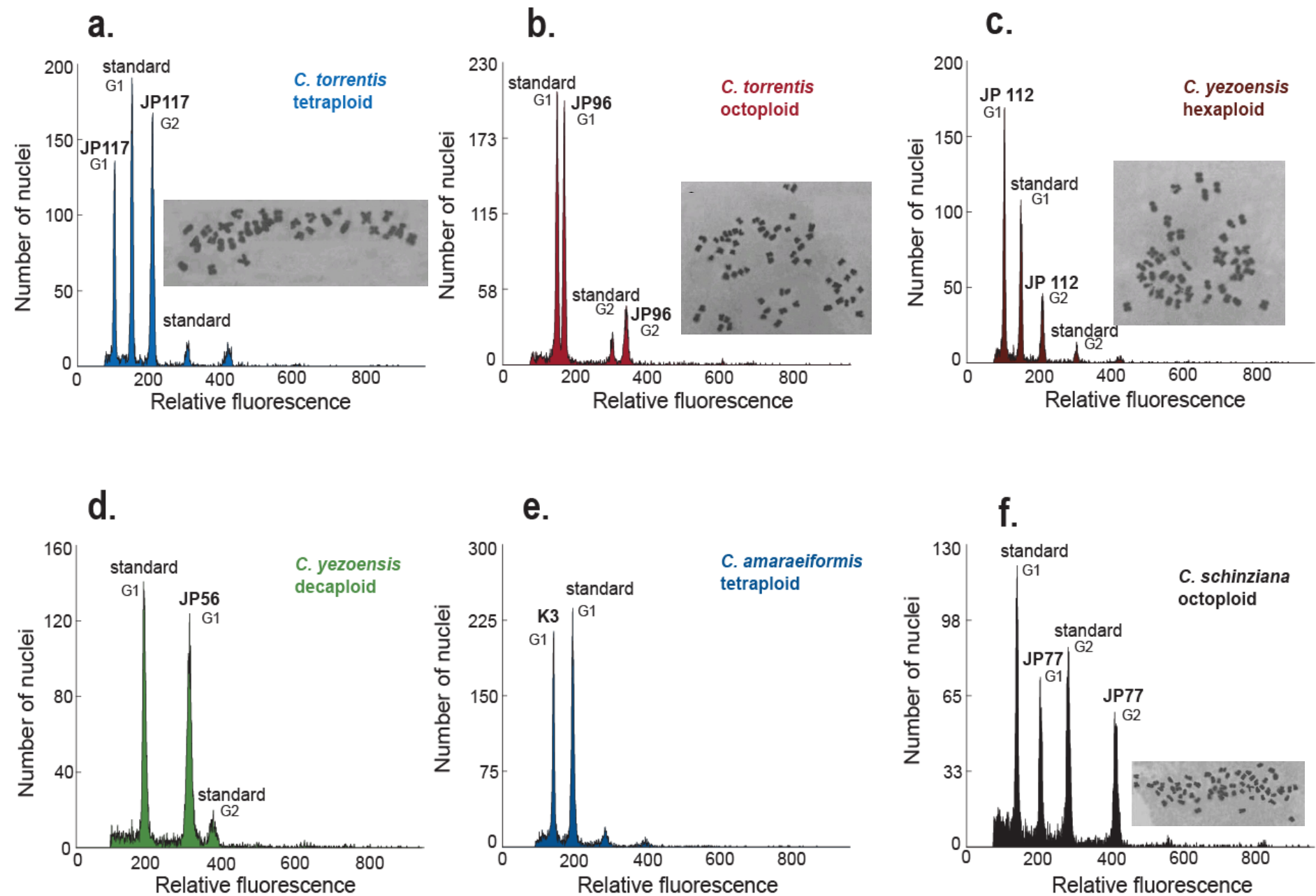
We sampled 55 populations throughout Japan, including material from original localities of *Cardamine akitensis*, *C. fauriei*, *C. geifolia*, *C. kiusiana*, *C. nasturtiiformis*, *C. schinziana*, *C. torrentis*, and *C. yezoensis*.

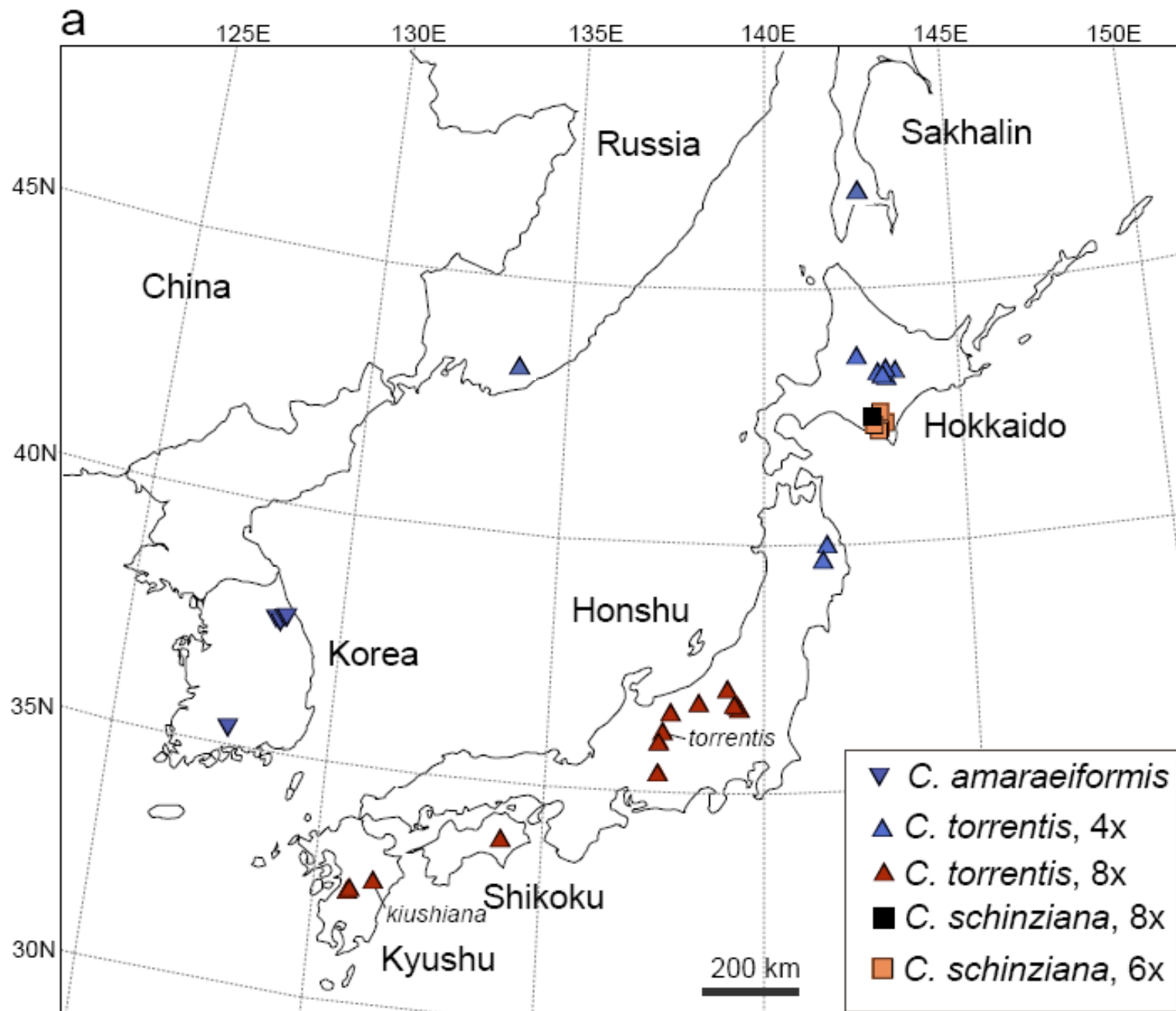
Four populations of *C. amariformis* were sampled in South Korea.

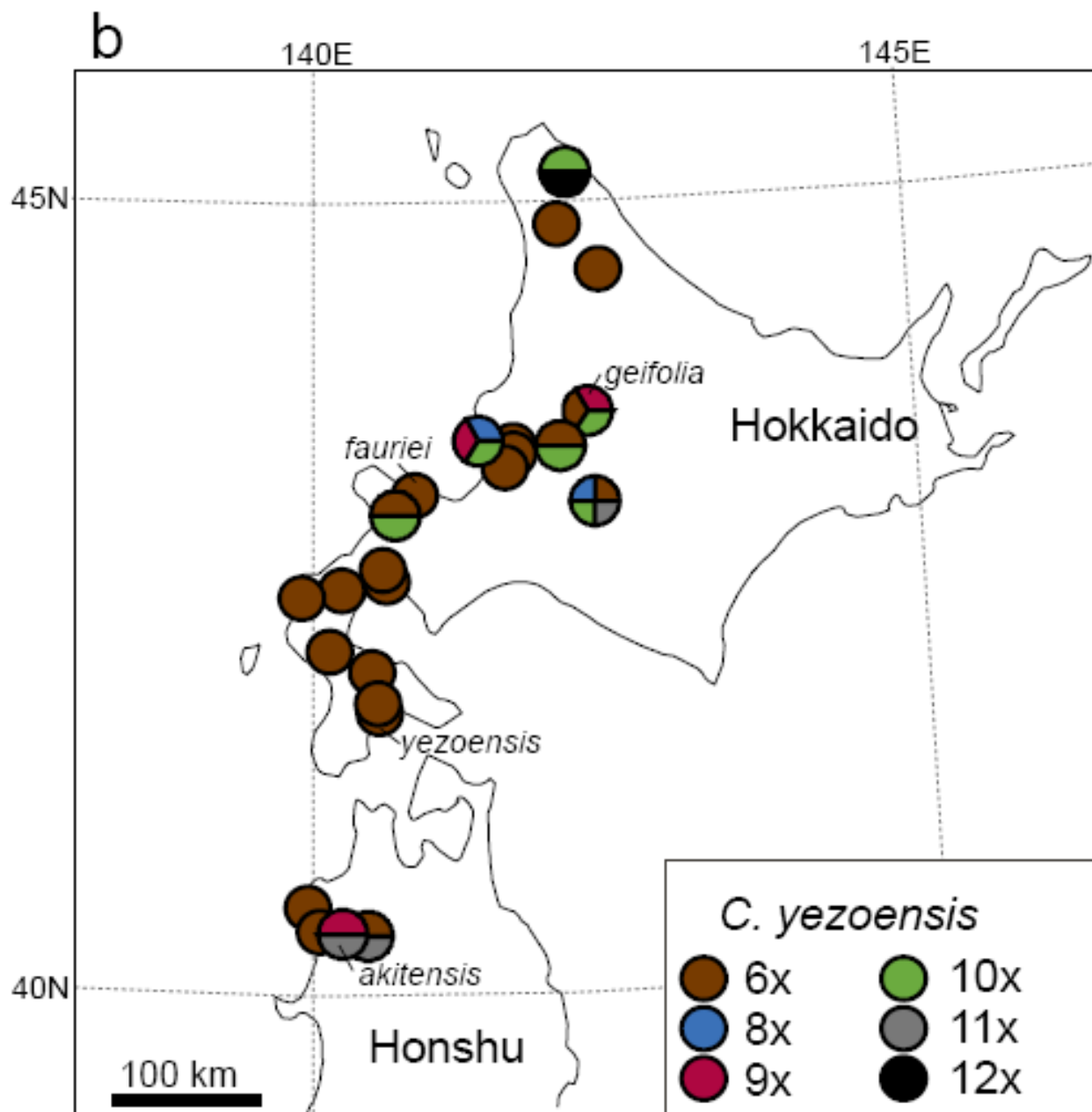
One to 14 living plants were collected from each population, transferred to pots in experimental gardens, and materials from these plants were used for flow cytometric measurements and chromosome counting.

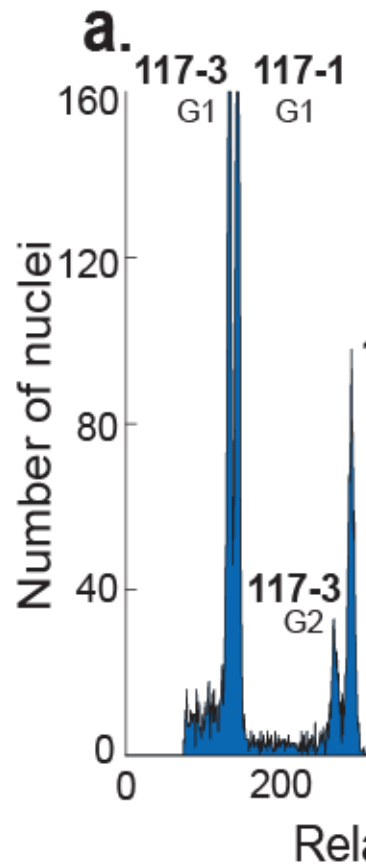
For morphometric evaluation 40 populations (9–32 plants per population, 1018 plants altogether) throughout the Japanese Archipelago and one population sample of *C. amariformis* (28 plants) was collected in South Korea.

In 2010-2012 additional material was collected in Far East Russia.

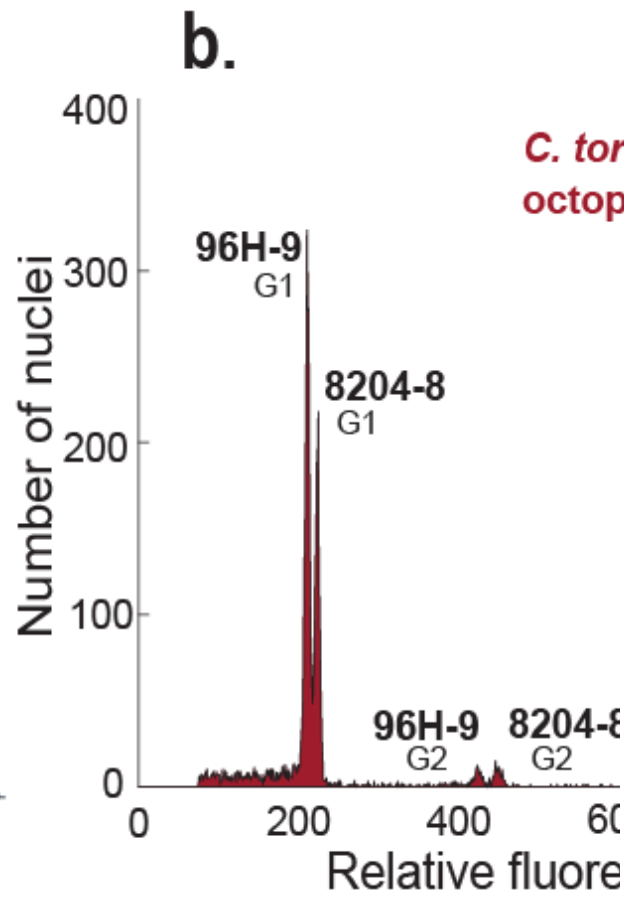




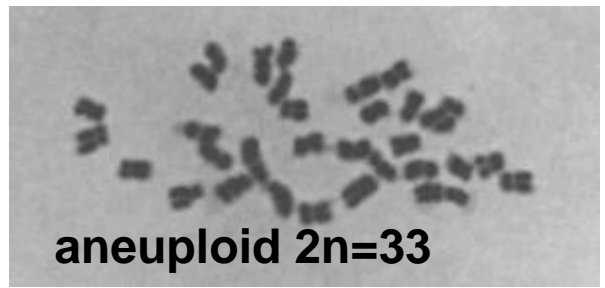




C. torrentis
tetraploids

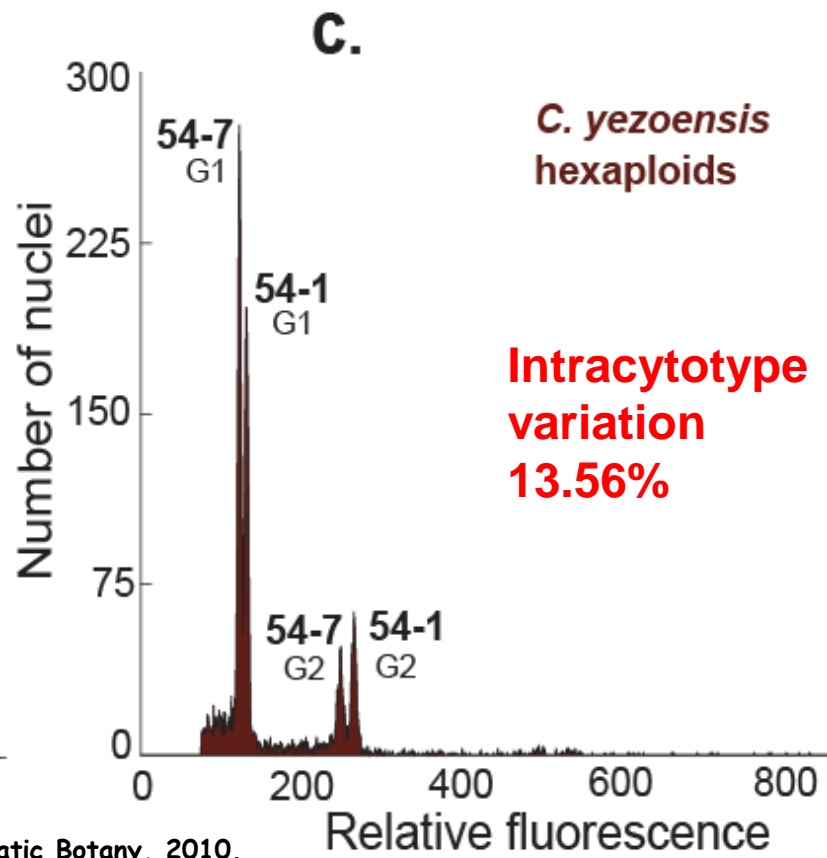


C. torrentis
octoploids



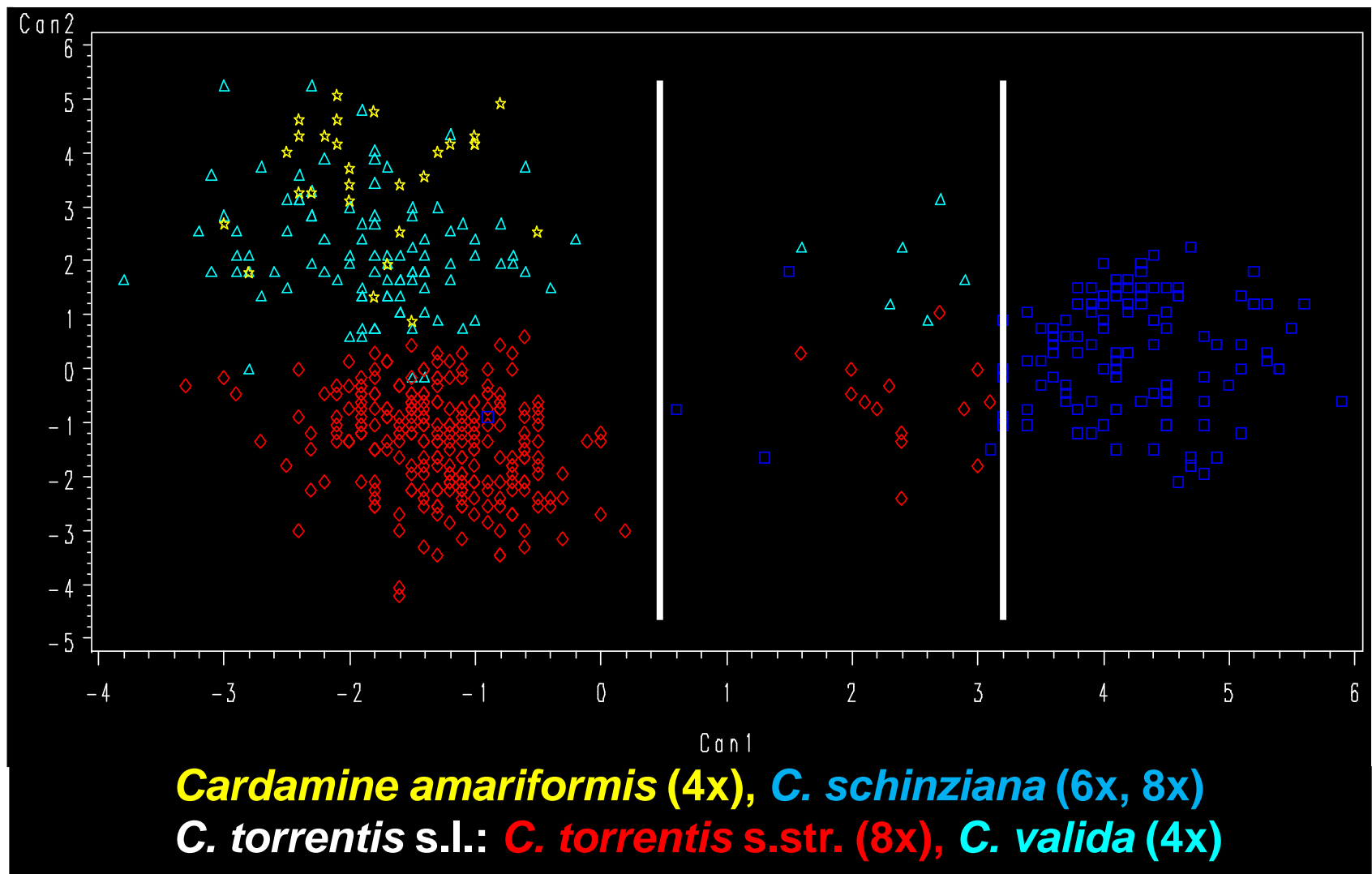
Intracytotype
variation
11.84%

Intracytotype
variation
9.25%

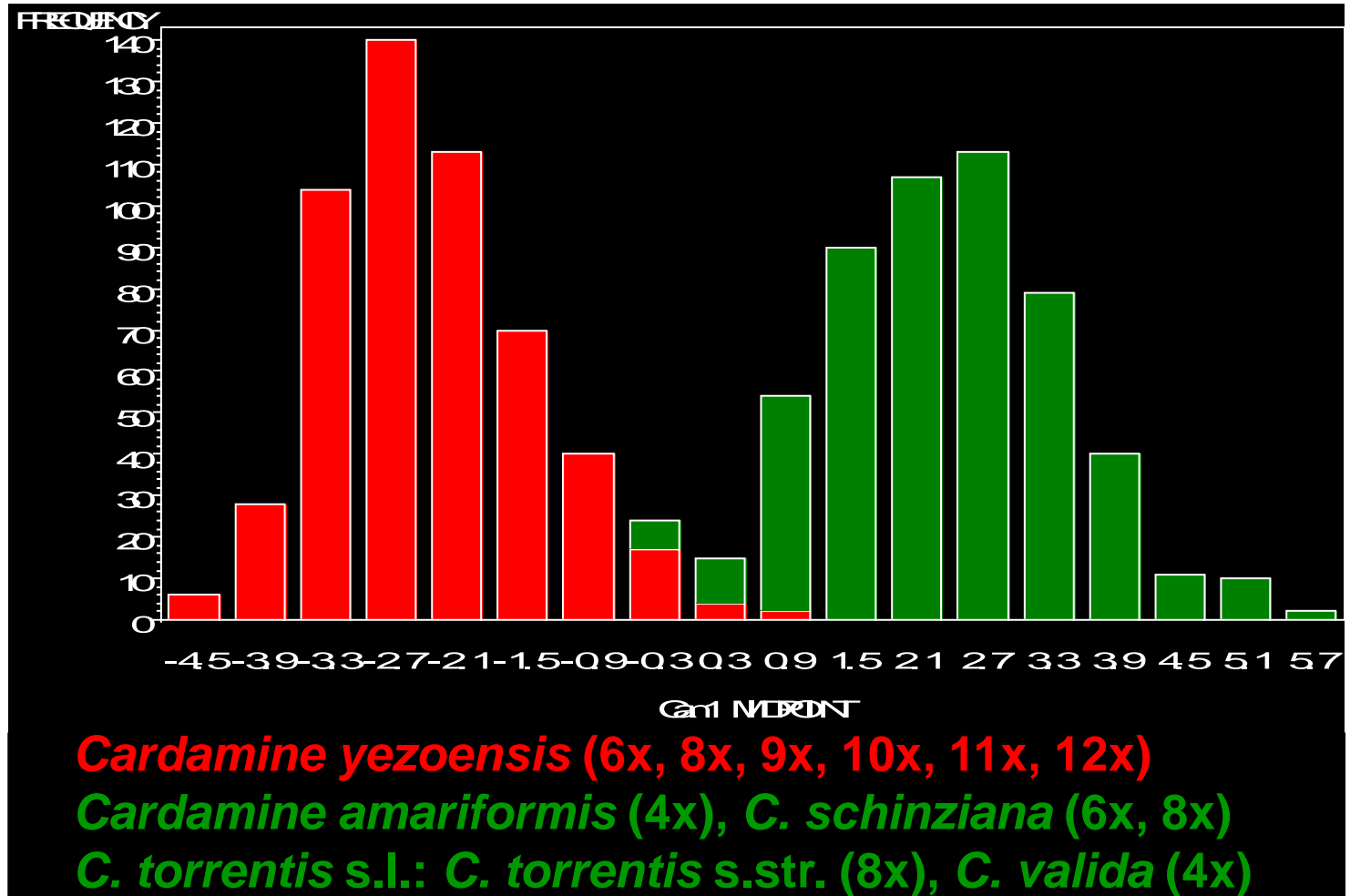


C. yezoensis
hexaploids

Intracytotype
variation
13.56%



Discriminant analysis based on morphological characters



Discriminant analysis based on morphological characters



Cardamine yezoensis
= *C. fauriei*
= *C. geifolia*
= *C. akitensis*

**Japan (Hokkaido, N Honshu),
Russia (S Sakhalin)**



Cardamine schinziana

Japan (Hokkaido)



Cardamine torrentis
= *C. kiusiana*
 $2n=8x=64$

**Japan (Kyushu, Shikoku, S
Honshu)**



Cardamine valida

$2n=2x=32$

**Japan (N Honshu,
Hokkaido, Russian Far
East, incl. Sakhalin)**



Cardamine amariformis
 $2n=4x=32$

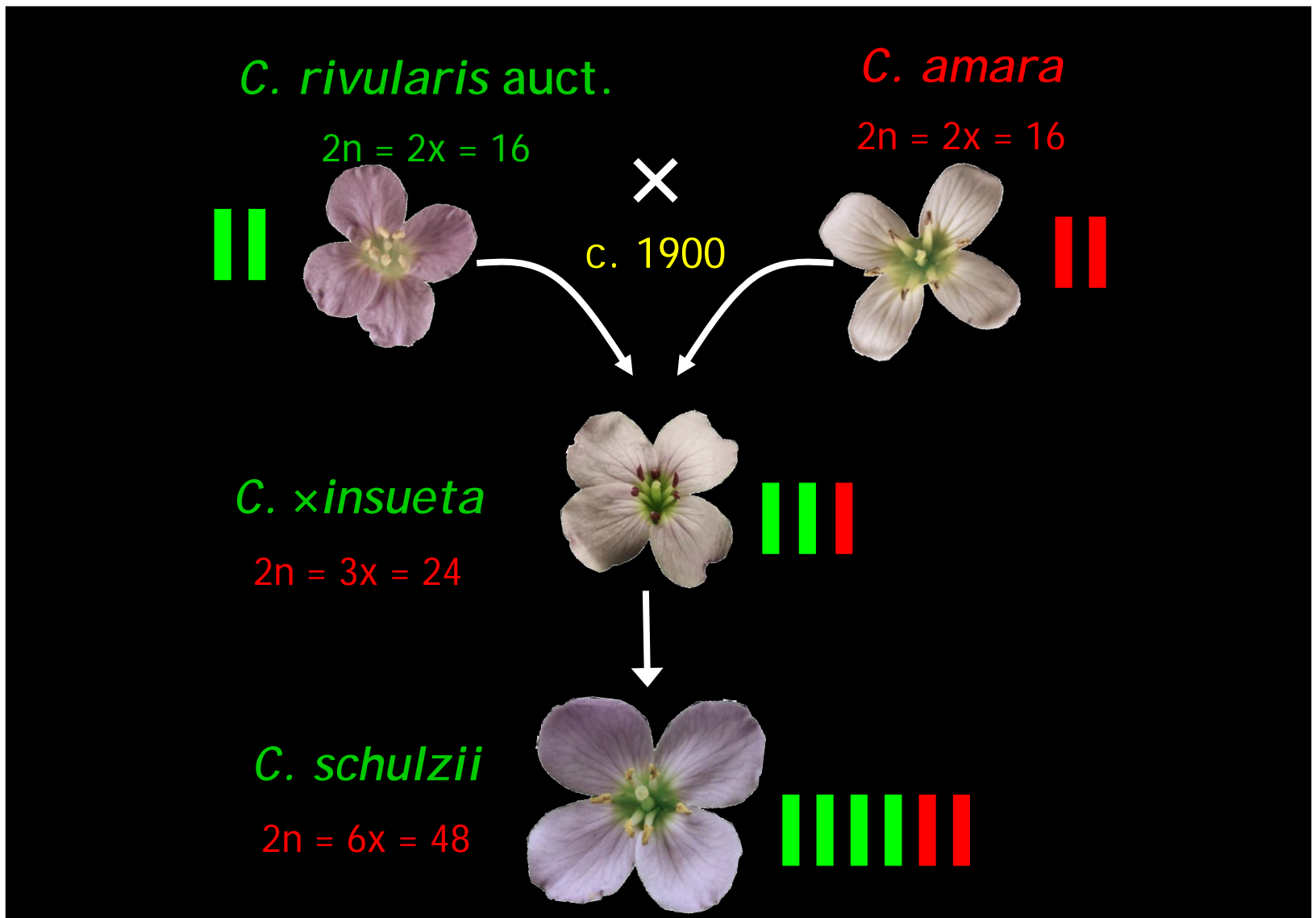
Korea

conspecific with *C. valida*?

Textbook example of the origin of hybrid and polyploid specie

Urnerboden, Switzerland

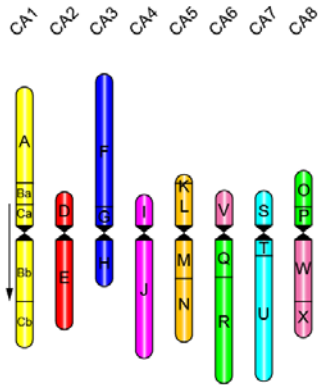




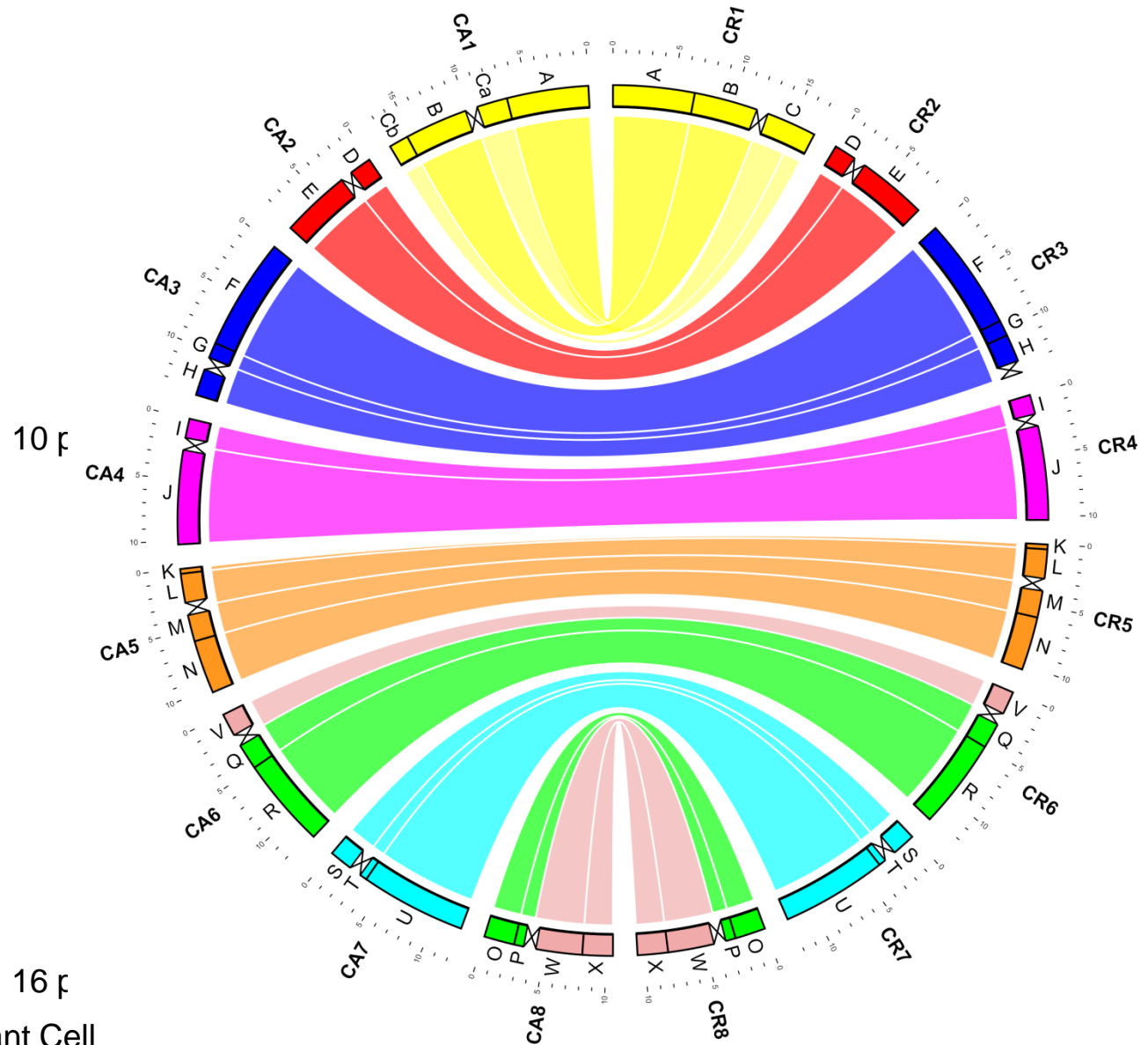
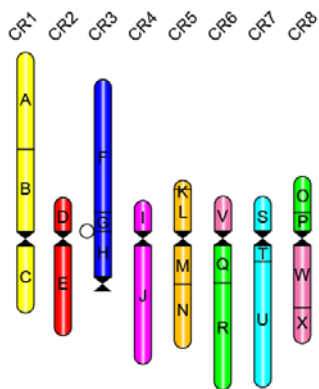
Urbanska, 1977, Ber. Geobot. Inst. ETH Stiftung Rübel 44: 2-85, 44:86-103;
 Urbanska & Landolt, 1972, 1978, Ber. Geobot. Inst. ETH Stiftung Rübel 41: 88-101,
 45: 30-53; Urbanska et al., 1997, Pl. Syst. Evol. 204:233-256;

Karyotype structure of parental diploid species

C. amara
(n=8; **A**)

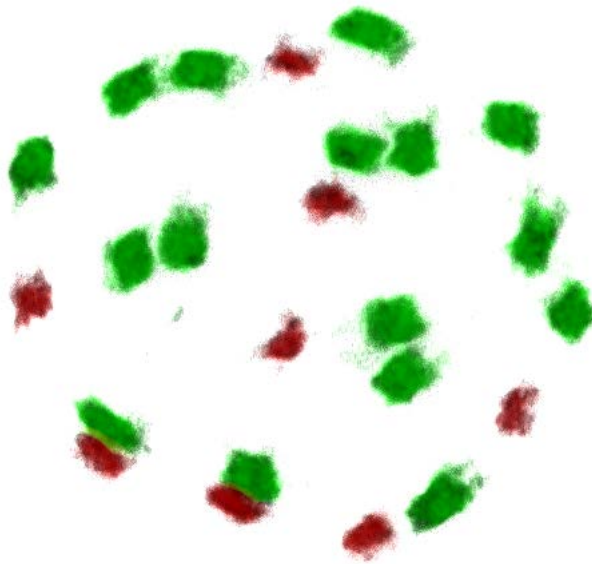


C. rivularis
(n=8; **R**)

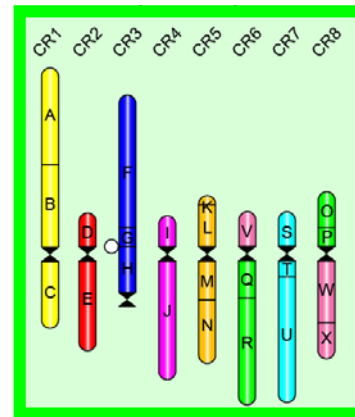


Genome structure of *C. × insueta*

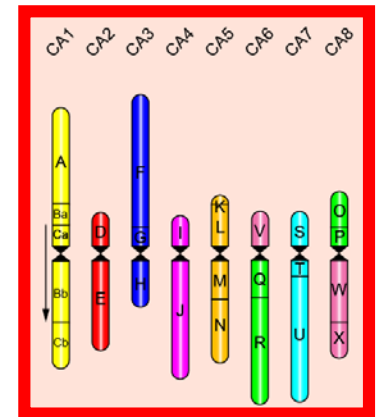
C. × insueta ($2n = 24$)
RRA (16+8)



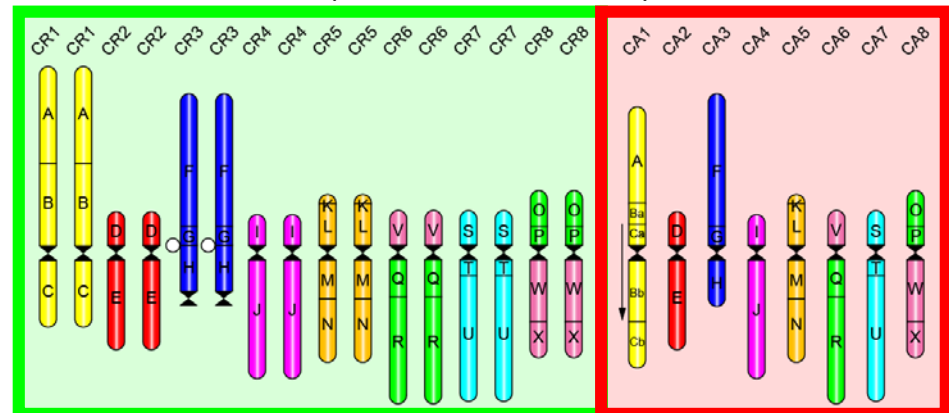
C. rivularis
 ($n=8$; **R**)



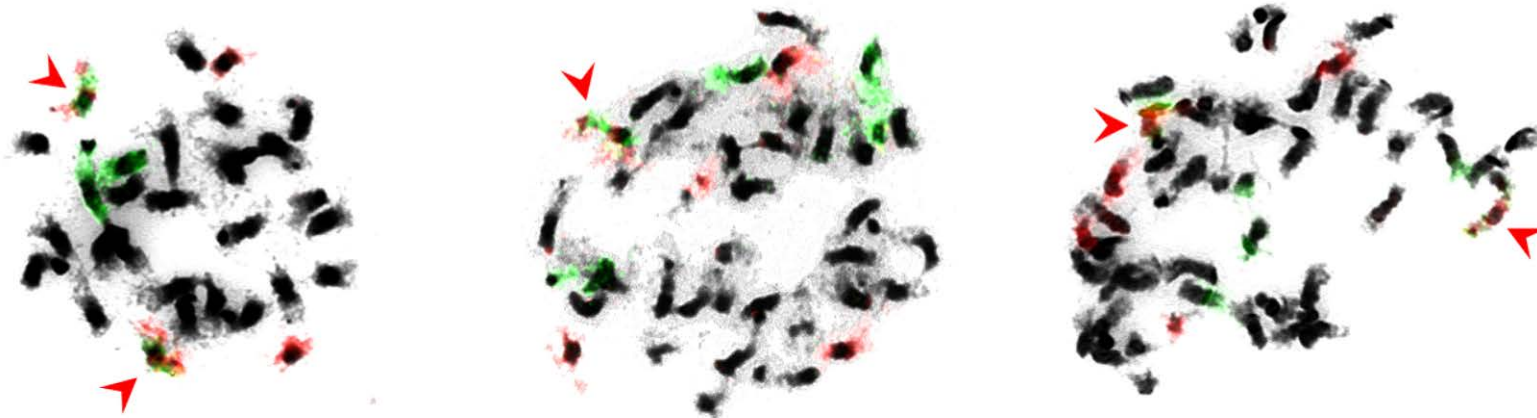
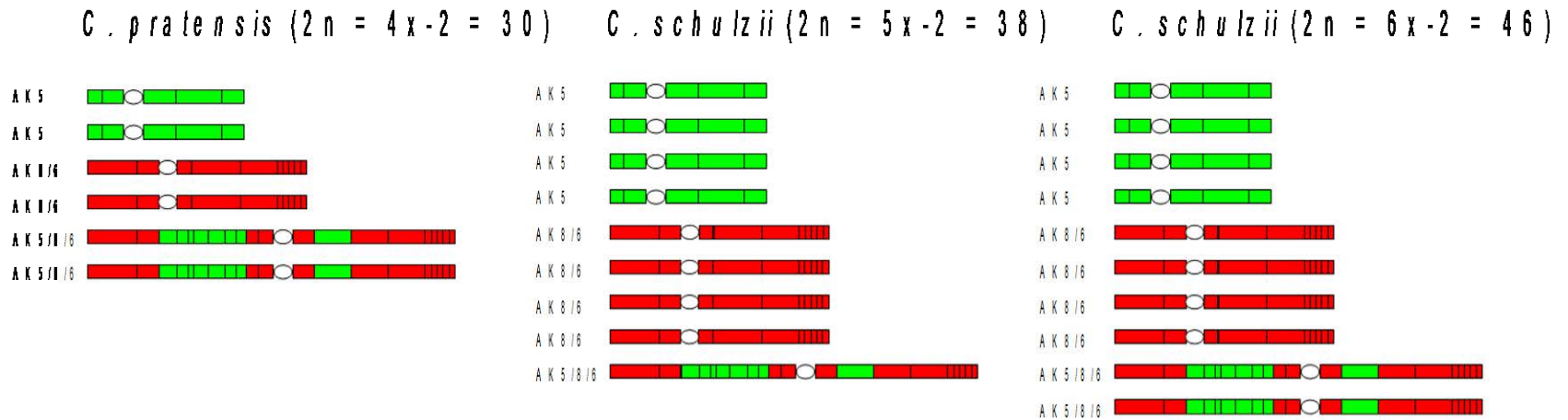
C. amara
 ($n=8$; **A**)



C. × insueta
 ($2n=3x=24$; **RRA**)



Descending dysploidy of *C. pratensis* and both cytotypes of *C. schulzii*



$$2n = 6x = 48, \text{ ~~RRRRAA (32+16)~~}$$

Hexaploid RRRRAA plants not found at Urnerboden

instead

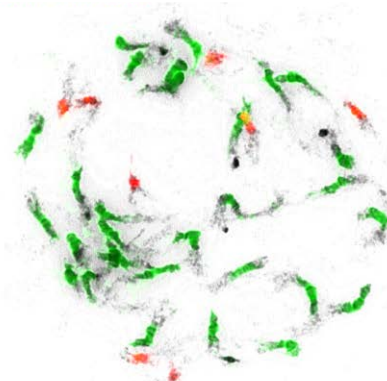
non-*insueta* hybrid individuals with 38 or 46 chromosomes were found

Both comprise eight smaller A chromosomes plus 30 or 38 chromosomes labeled by gDNA of *C. rivularis*

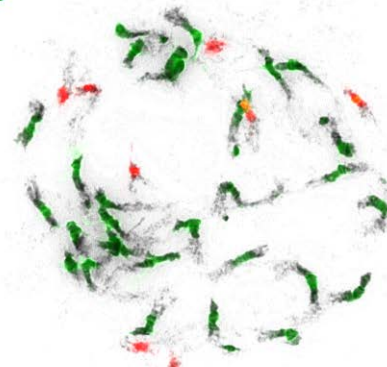
Out of 30 or 38 chromosomes six ones were bearing terminal heterochromatic knobs not labeled by *C. rivularis* gDNA, but typical for hypotetraploid *C. pratensis* ($2n=30$)

Cardamine schulzii
($2n = 5x-2 = 38$)
PPRRA (30+8)

gDNA *C. amara*
gDNA *C. rivularis*

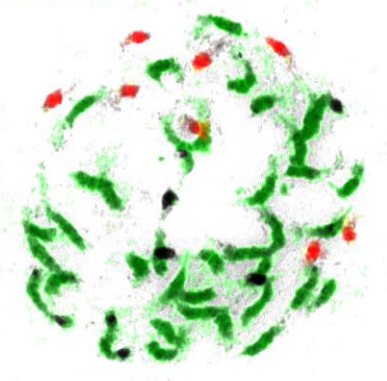


gDNA *C. amara*
gDNA *C. rivularis*

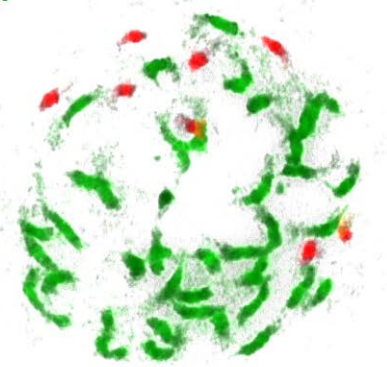


Cardamine schulzii
($2n = 6x-2 = 46$)
PPPPRA (38+8)

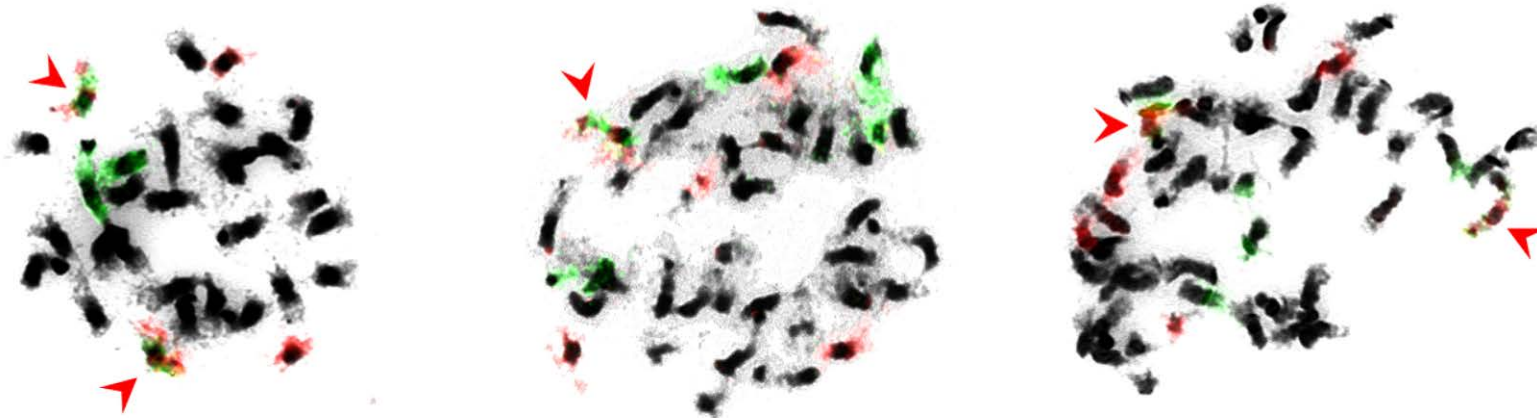
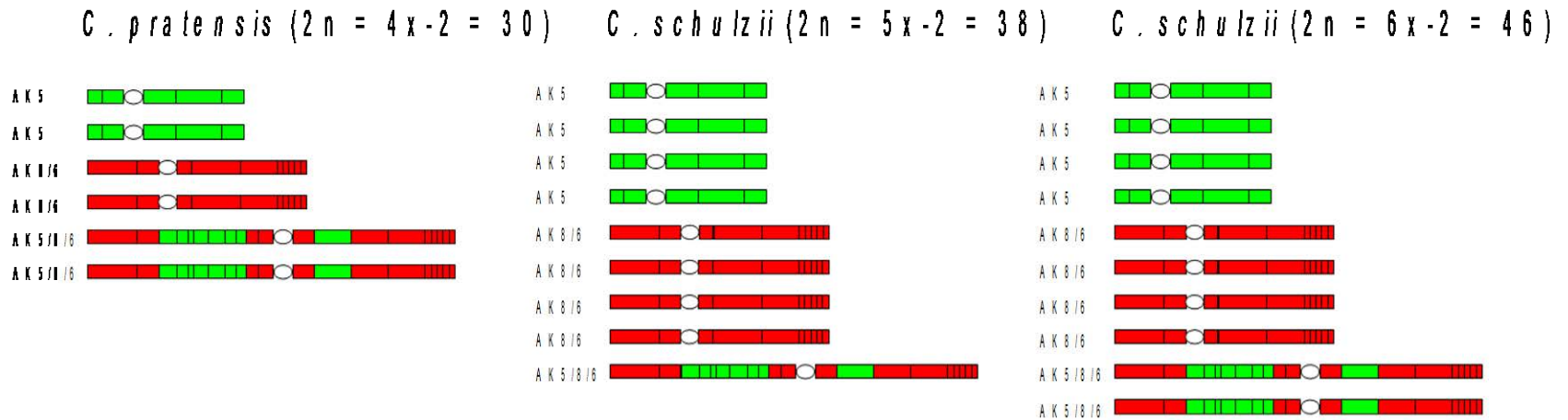
gDNA *C. amara*
gDNA *C. rivularis*



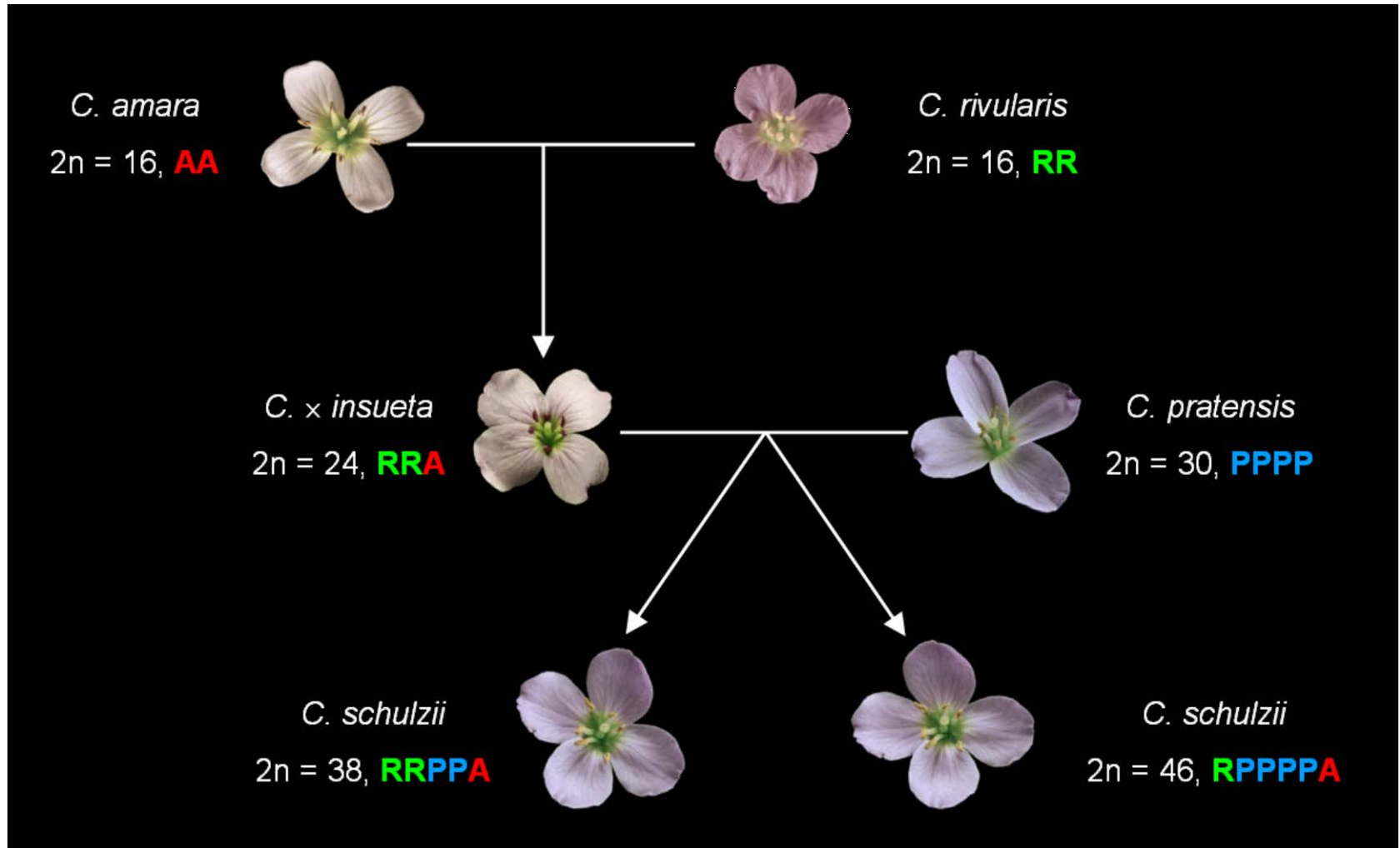
gDNA *C. amara*
gDNA *C. rivularis*



Descending dysploidy of *C. pratensis* and both cytotypes of *C. schulzii*



True story after all ???



***Cardamine pratensis* complex**

Complex study of Central European and Balkan populations of the currently and previously recognised taxa:

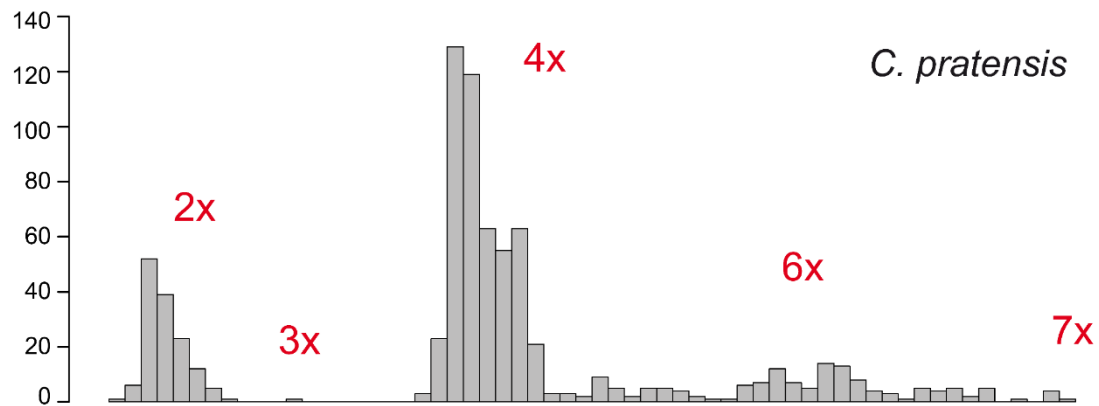
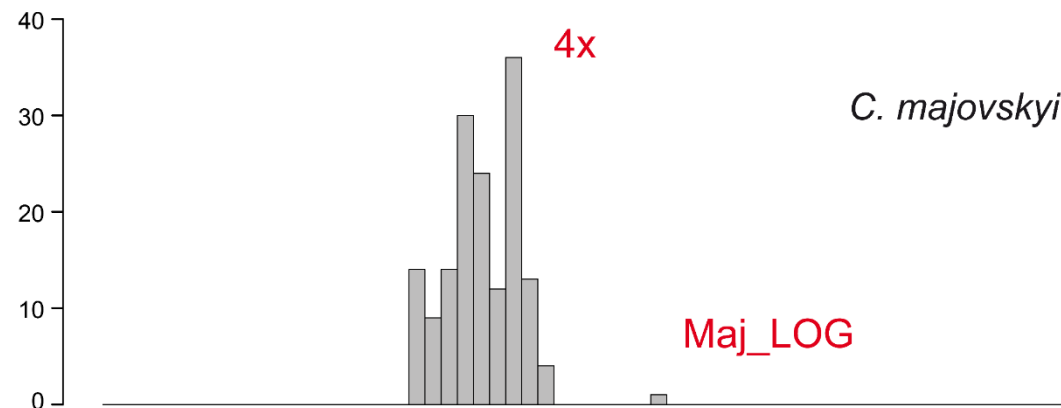
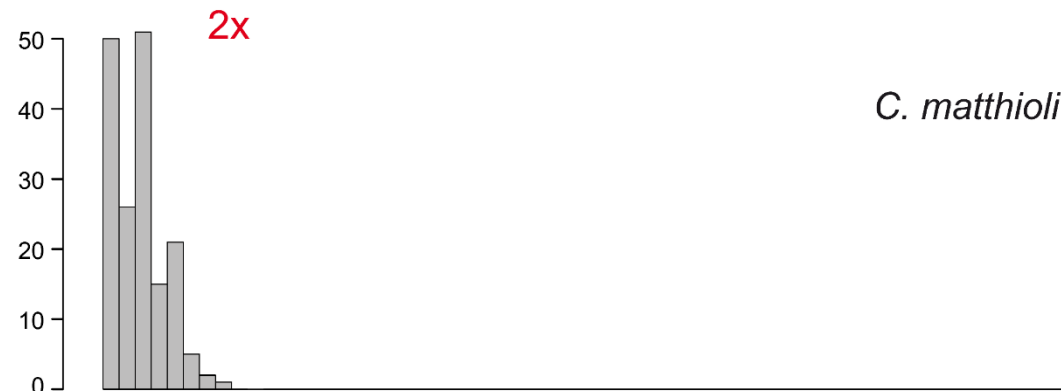
C. pratensis* s.str., *C. nemorosa*, *C. udicola*, “*C. ucranica*”, *C. rivularis*, *C. rivularis* auct., *C. matthioli*, *C. majovskyi

All plants were checked for chromosome numbers (219 plants from 58 populations) and/or ploidy level by **chromosome counting** or **FCM**

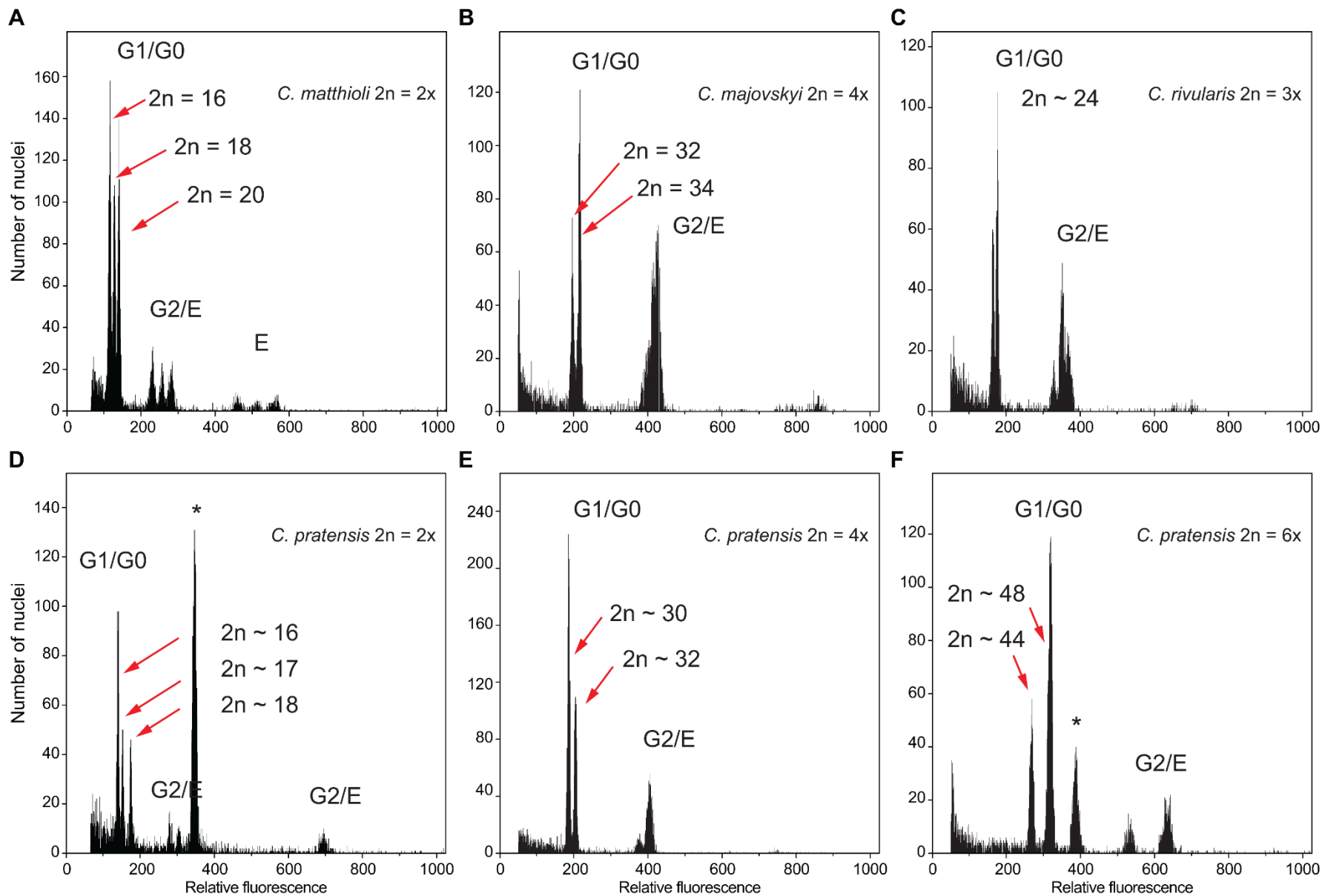
Microsatellite study on 145 populations (1104 plants), 18 microsatellite loci used yielded 394 alleles

HybSeq study based on the reduced set of plants from 47 populations (one plant per population)

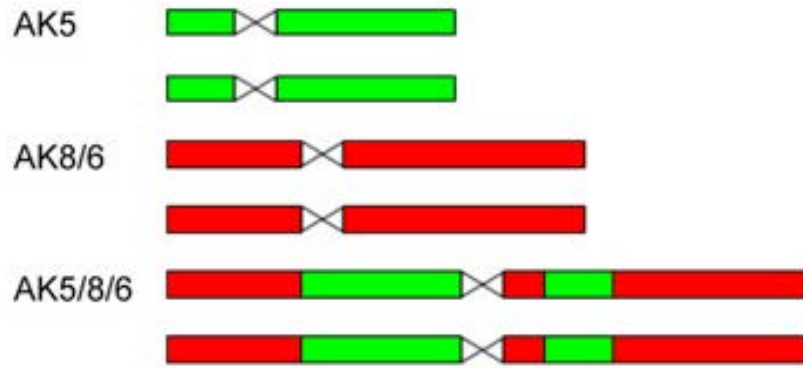
Number of samples



Relative genome size

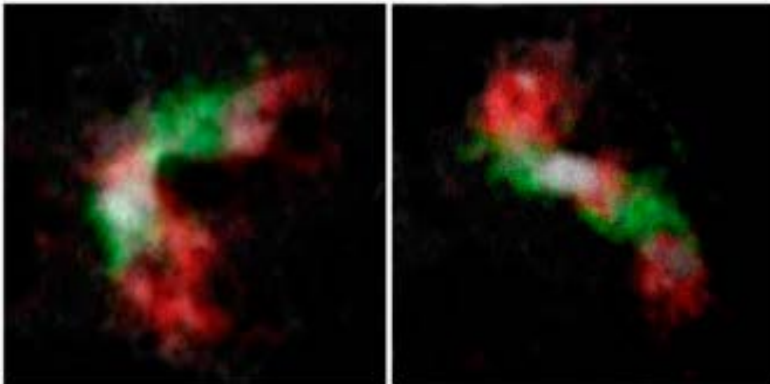
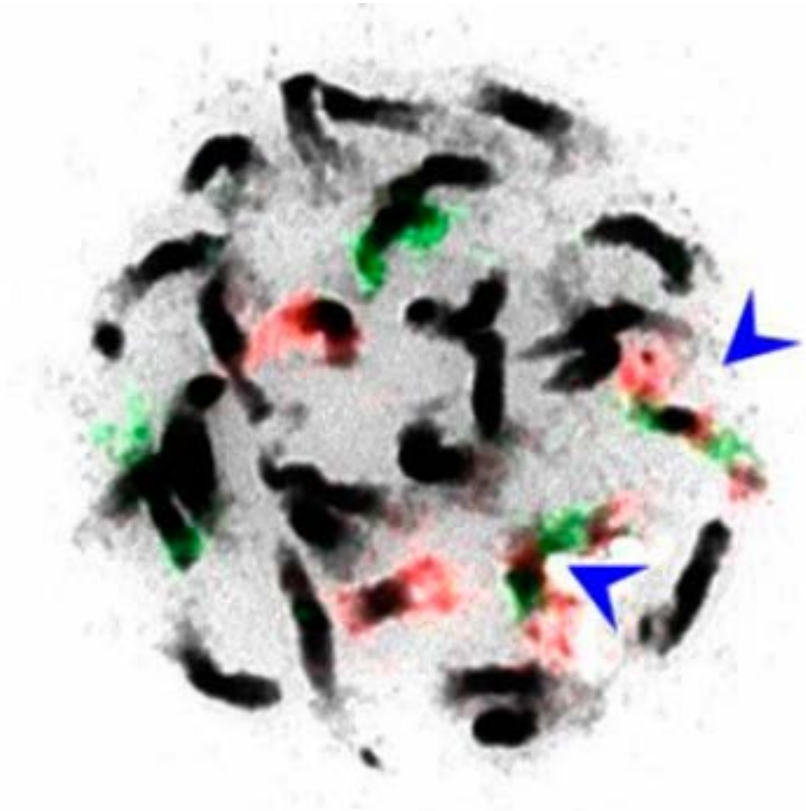


$$2n = 4x - 2 = 30$$

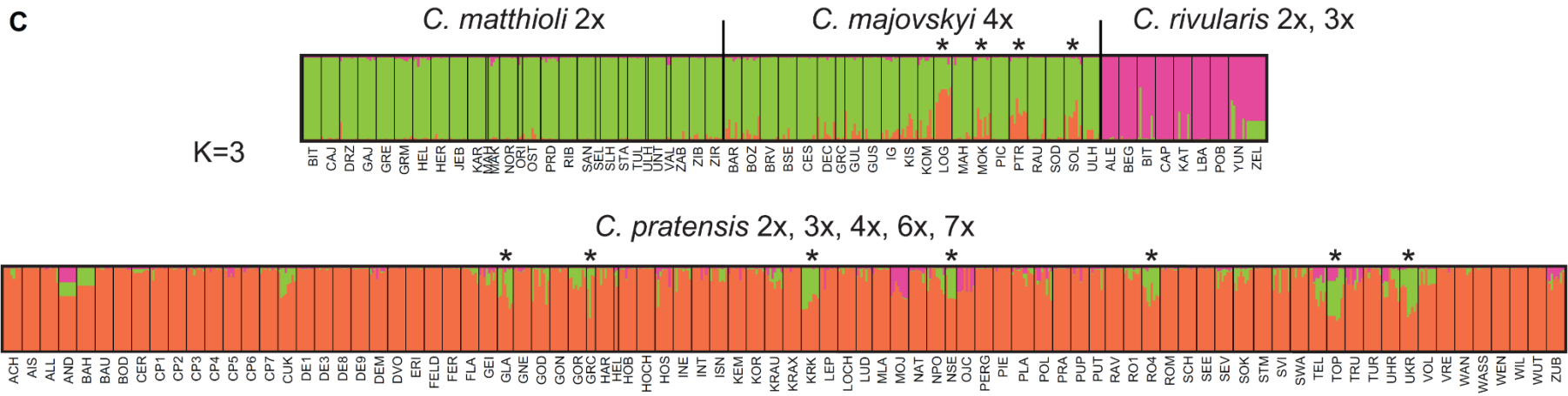
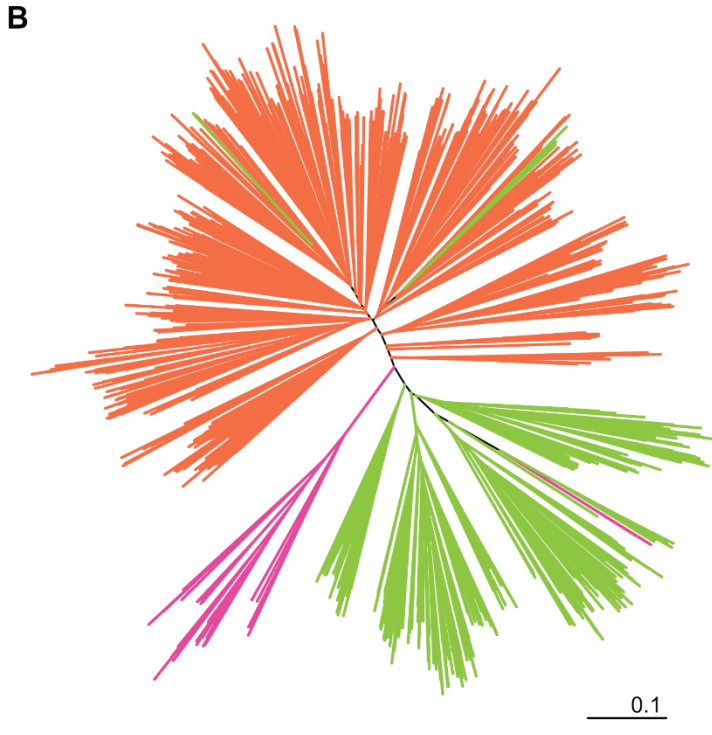
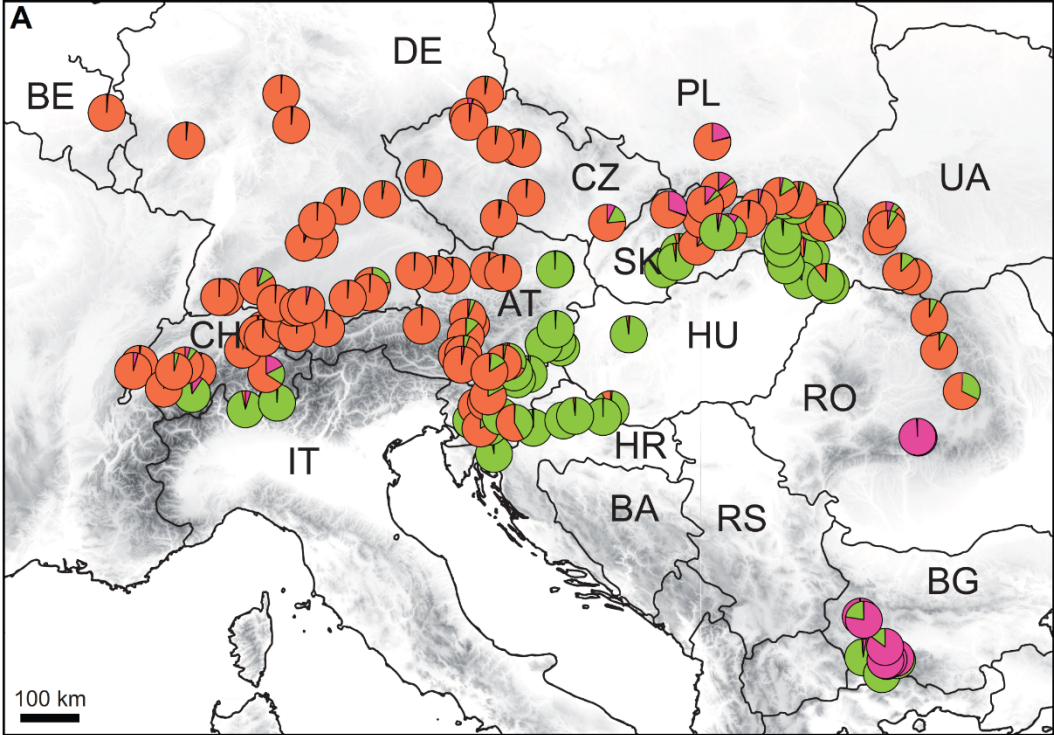


C. pratensis

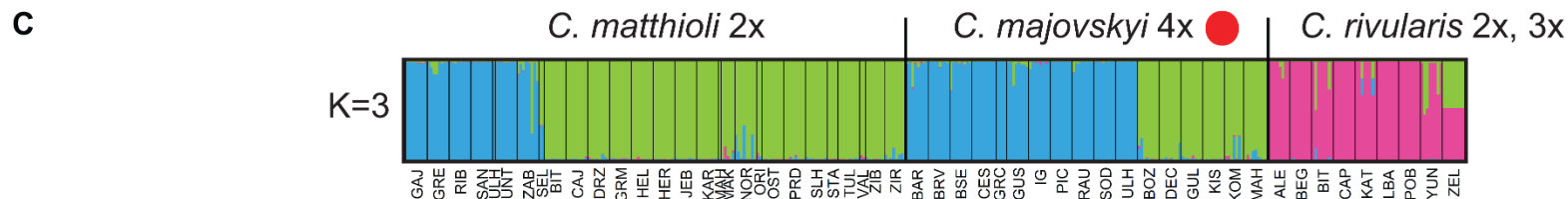
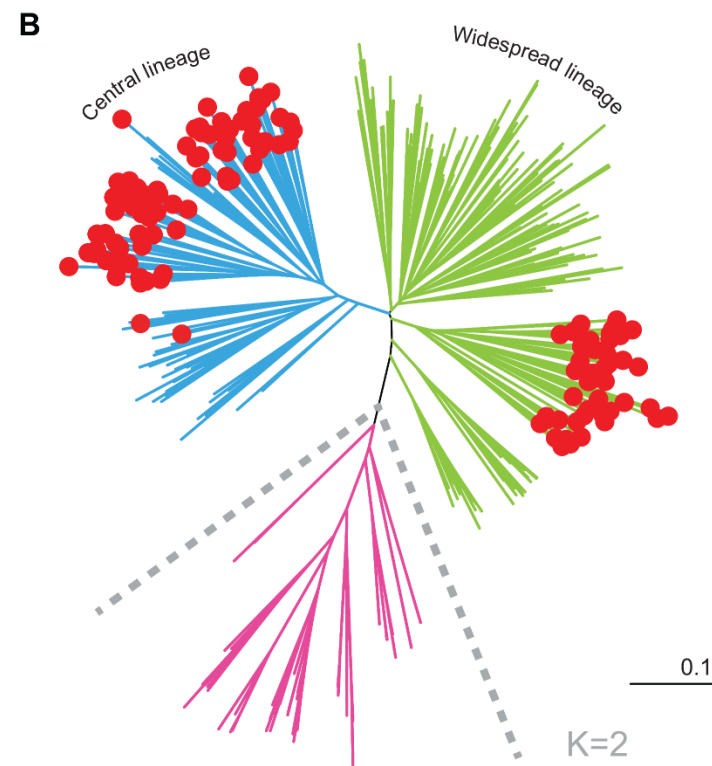
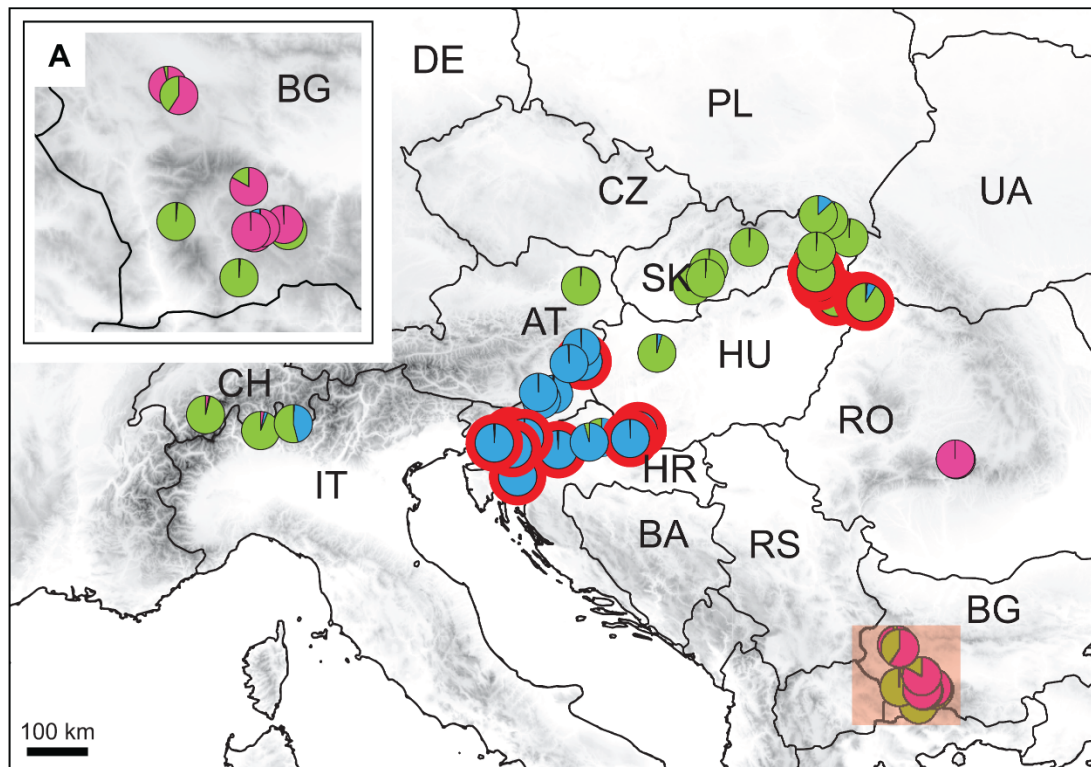
– fusion of chromosomes



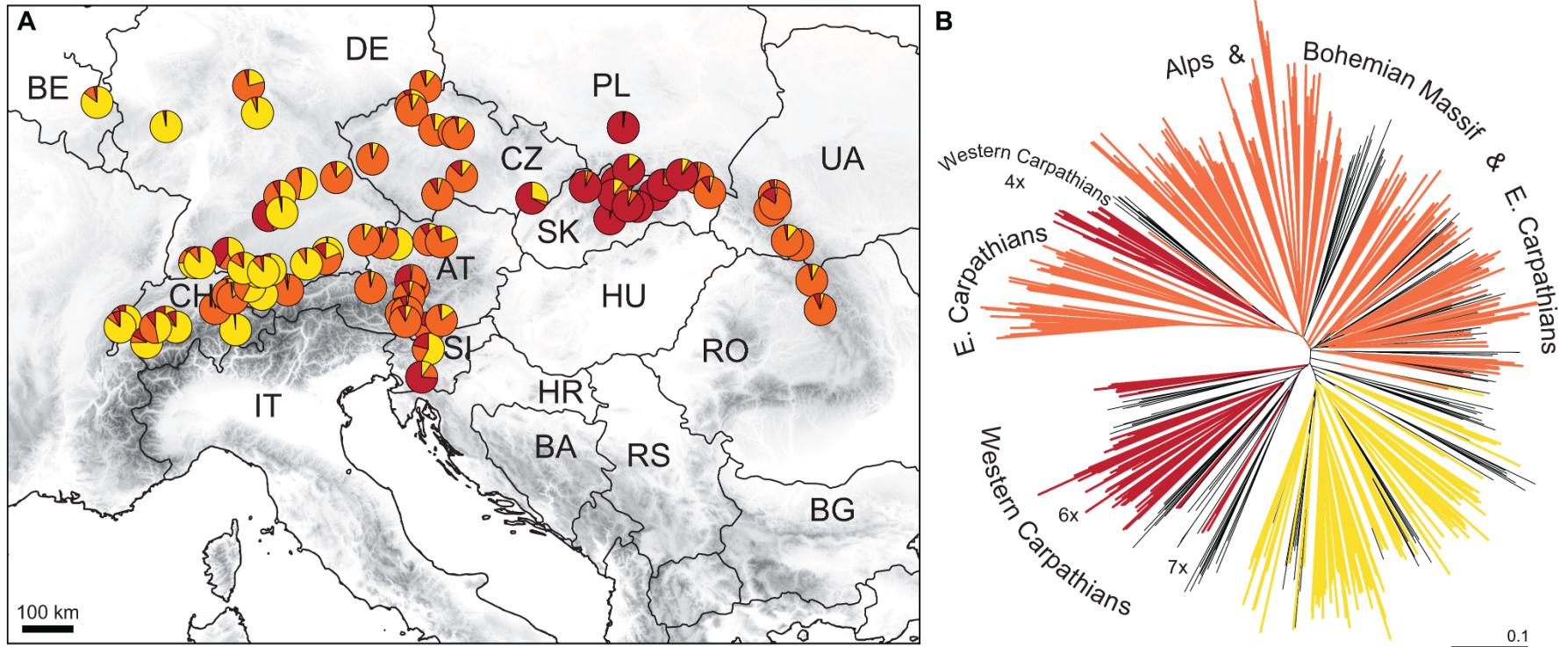
Genetic structure of all species studied, *C. matthioli*, *C. majovskyi*, *C. rivularis*, and *C. pratensis*, as inferred from microsatellite data analyses



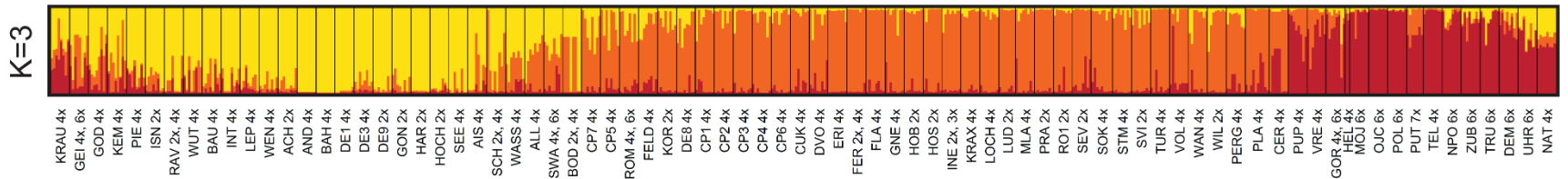
Genetic structure of *Cardamine matthioli*, *C. majovskyi*, and *C. rivularis* inferred from microsatellite data analyses



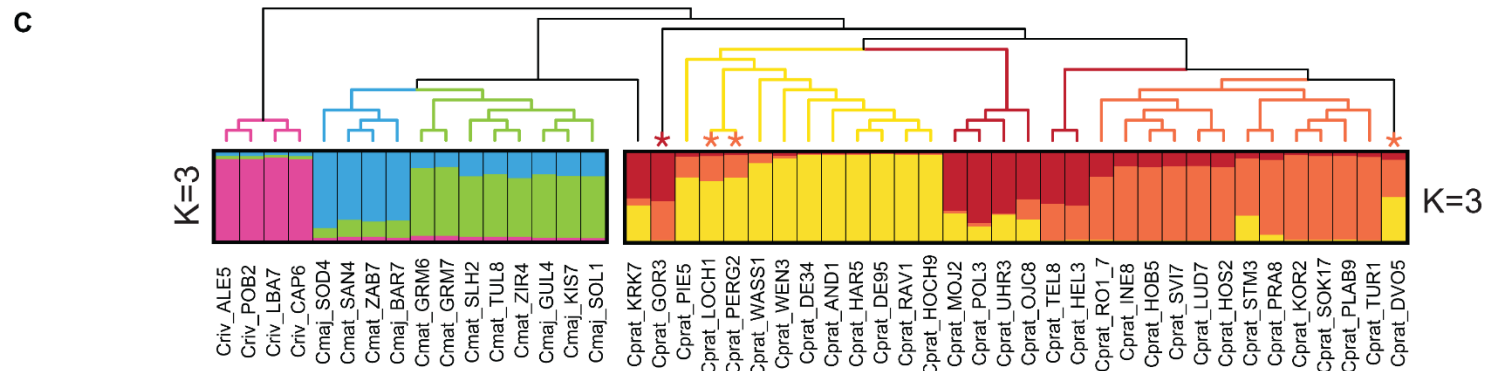
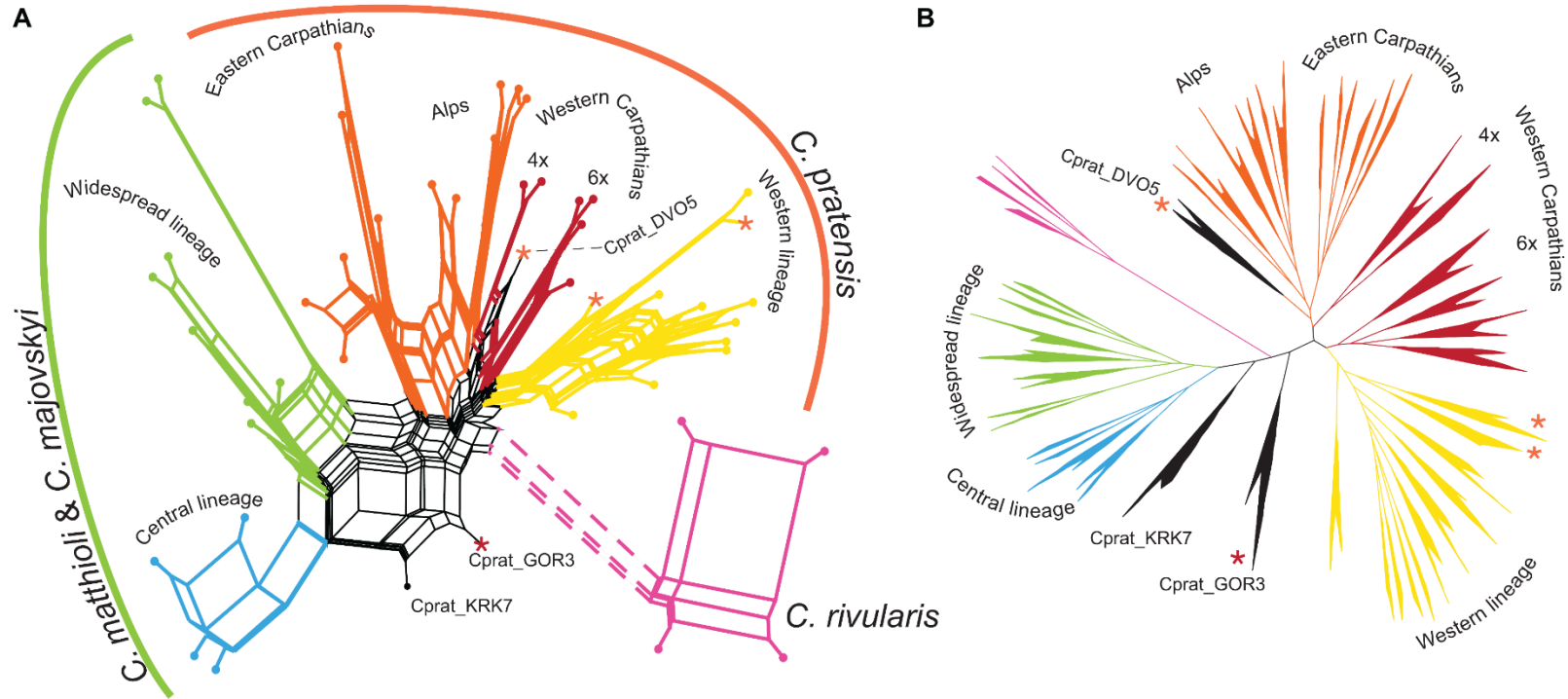
Genetic structure of *Cardamine pratensis* inferred from microsatellite data analyses



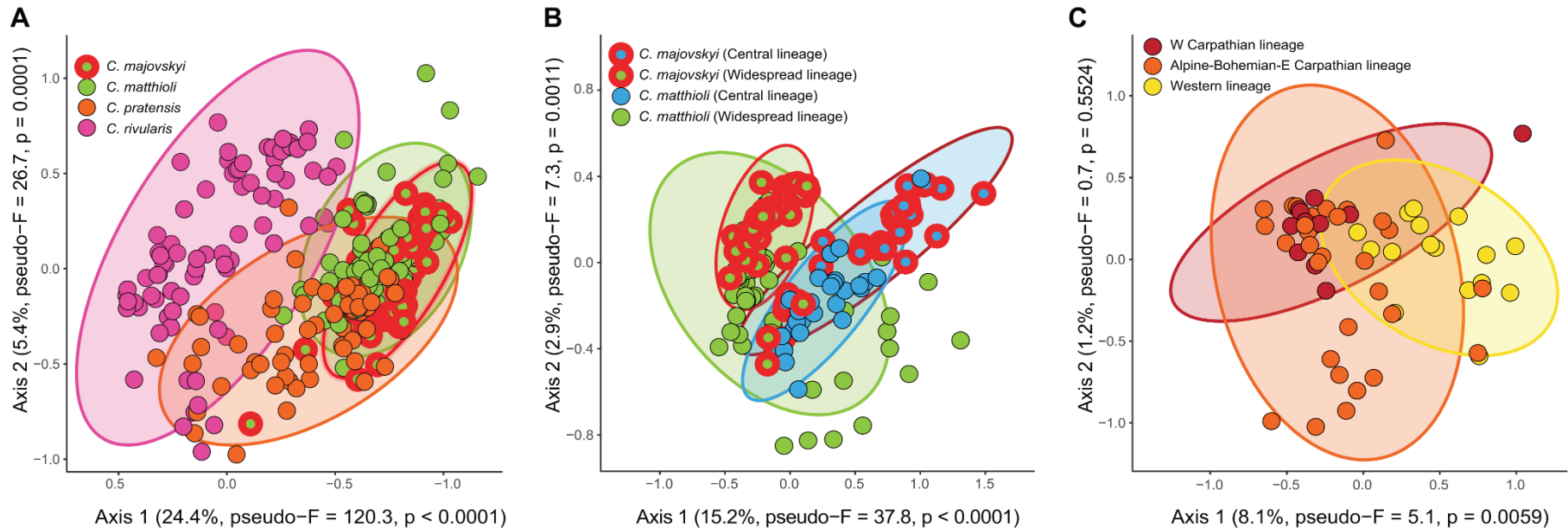
C *C. pratensis* 2x, 3x, 4x, 6x, 7x



Genetic structure of *C. matthioli*, *C. majovskyi*, *C. rivularis*, and *C. pratensis* inferred from Hyb-Seq data analyses. **A** - Supernet network representation of quartets generated in SuperQ, derived from 499 most informative ML gene trees. **B** - ML tree constructed from concatenated allele sequences obtained by read-backed phasing from all 963 genes in RAXML-NG



Results of RDA showing significant differences in the environmental niches of the four analyzed *Cardamine* species (A), genetic lineages within *C. matthioli* and *C. majovskyi* (B), and three genetic lineages within *C. pratensis* (C). Ellipses define regions expected to contain 95% of all populations of the species or lineages.



**Melichárková et al., *Frontiers in Plant Science* 1:588856, 2020.
 doi: 10.3389/fpls.2020.588856**