



Genome Size Variation: Consequences and Evolution

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Genome size variation: consequences and evolution

- (i) How genome size varies across plants
- (ii) What are the consequence of this variation
- (iii) How did such variation evolve

Early genome size studies in plants



First genome size of a plant:
Lilium longiflorum

Ogur M et al. 1951. *Exp. Cell Res.* **2**: 73-89.

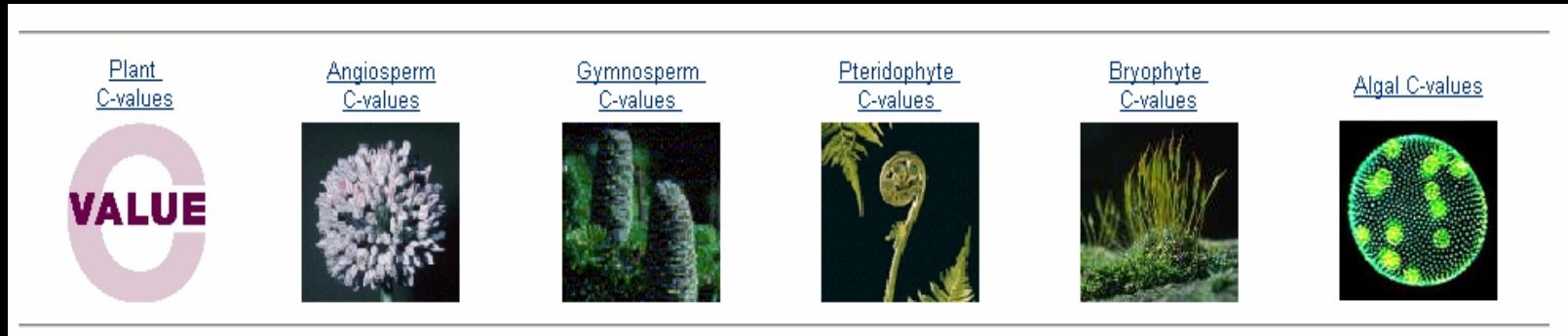


Concept of C-value:

DNA amount in unreplicated
gametic nucleus

Swift H. 1950. *Proc. Natl. Acad. Sci. USA* **36**: 643-654.

Plant DNA C-values database



www.kew.org/genomesize/homepage.html

5150 species

Land plants

4427 angiosperms

207 gymnosperms

87 pteridophytes

176 bryophytes

Algae

91 Chlorophyta

44 Phaeophyta

118 Rhodophyta

C-values in angiosperms range nearly 2000-fold



*Genlisea
margaretae*

1C = 0.065 pg



*Utricularia
gibba*

1C = 0.091 pg



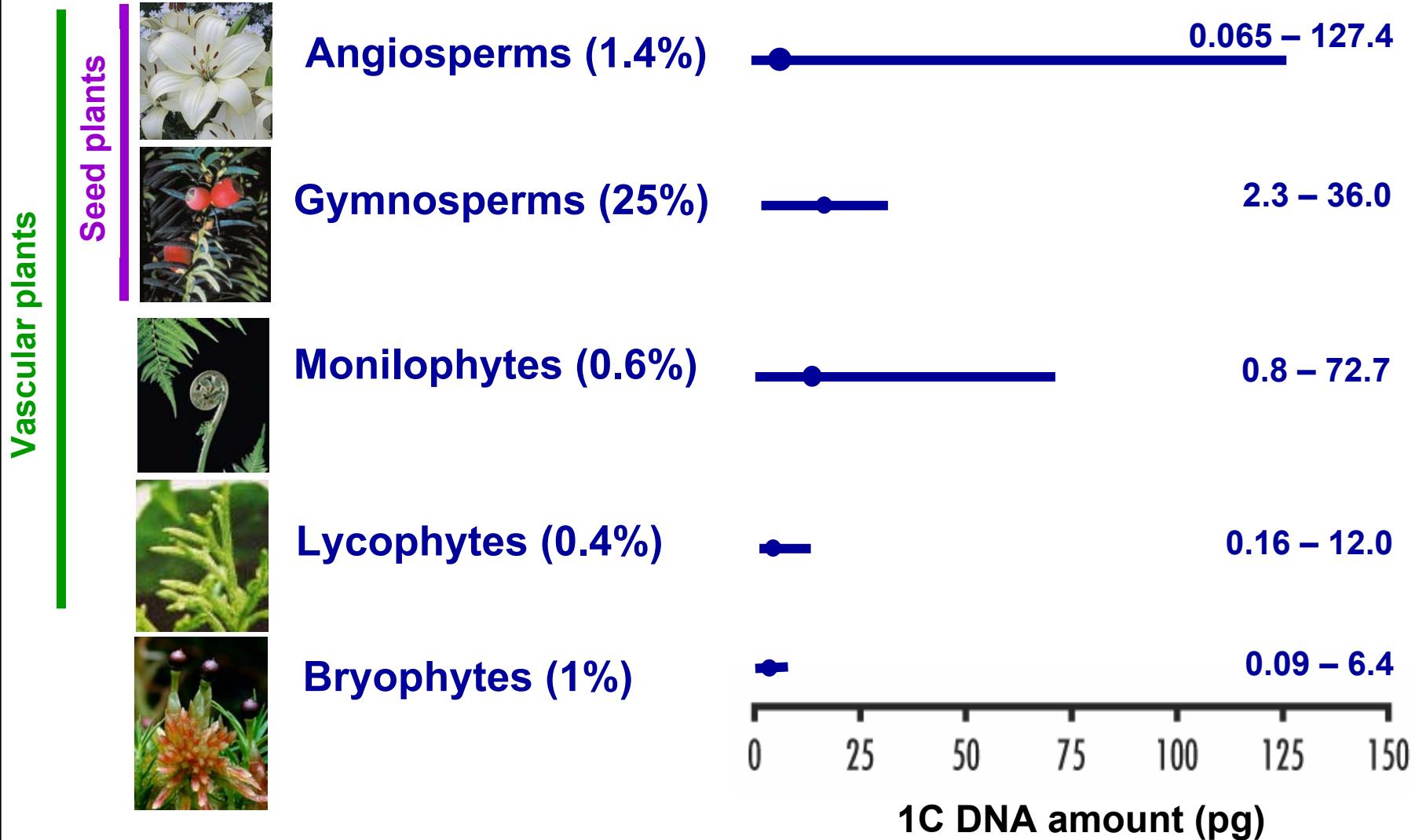
*Fritillaria
assyriaca*

1C = 127.4 pg

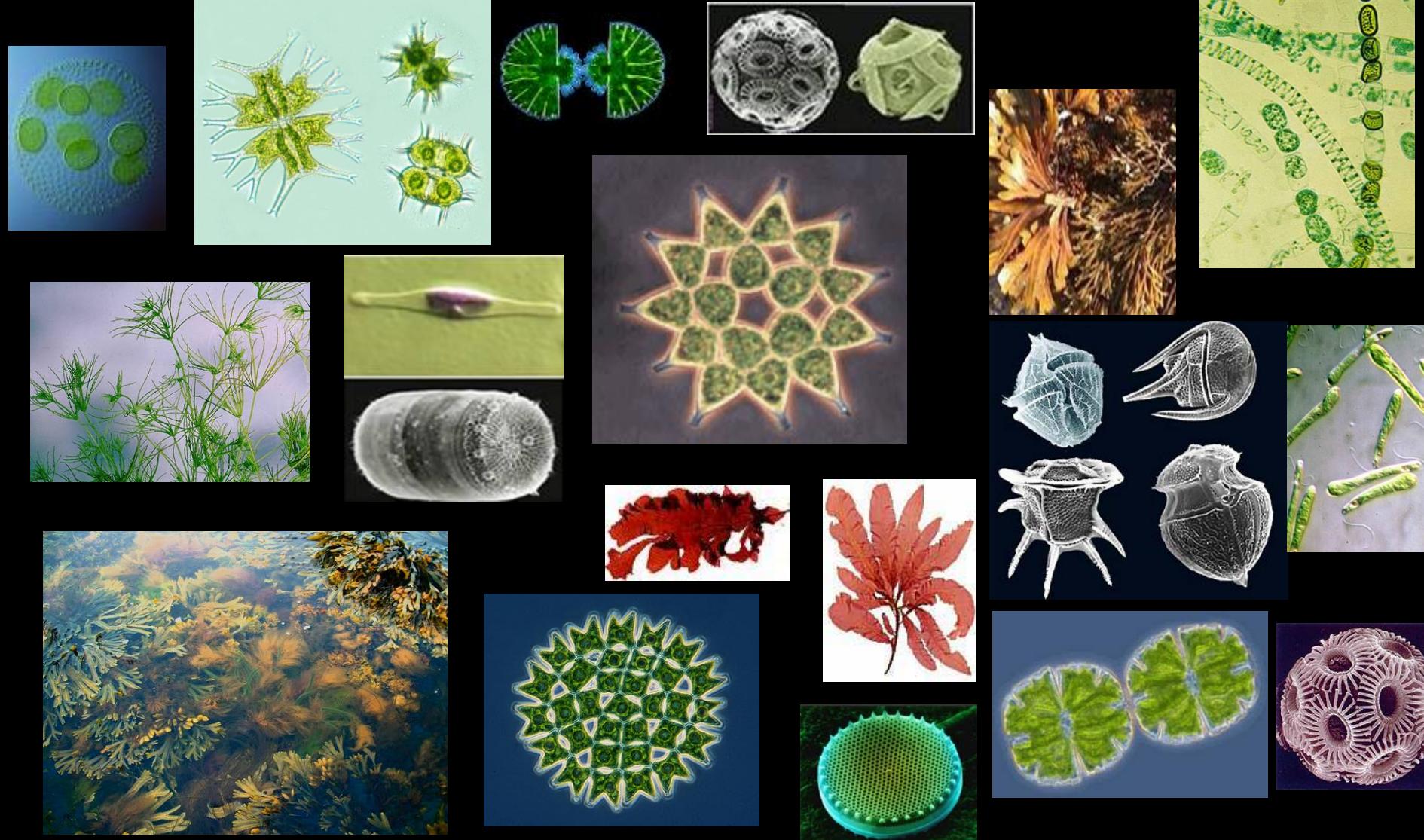
Greilhuber *et al.* 2006. Greilhuber *et al.* 2006.
Plant Biology Plant Biology
8: 770-777 8: 1331-1338

Bennett. 1972.
Proc. Roy. Soc. Lond. B
181: 109-135.

Range of DNA amounts in land plants



DNA amount in algae



DNA amount in algae



Phaeophyta
44 species



Rhodophyta
118 species



Chlorophyta
153 species

Kapraun DF. 2005.
Annals of Botany **95:** 7-44.

Kapraun DF. 2007.
Annals of Botany **99:** 677-701

Range of DNA amounts in algae



Angiosperms

0.065 – 127.4

Gymnosperms

2.3 – 36.0

Monilophytes

0.8 – 72.7

Lycophytes

0.16 – 12.0

Bryophytes

0.09 – 6.4

Phaeophyta (2.9%)

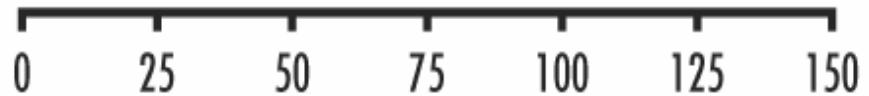
0.1 – 0.9

Rhodophyta (1.8%)

0.017 – 1.4

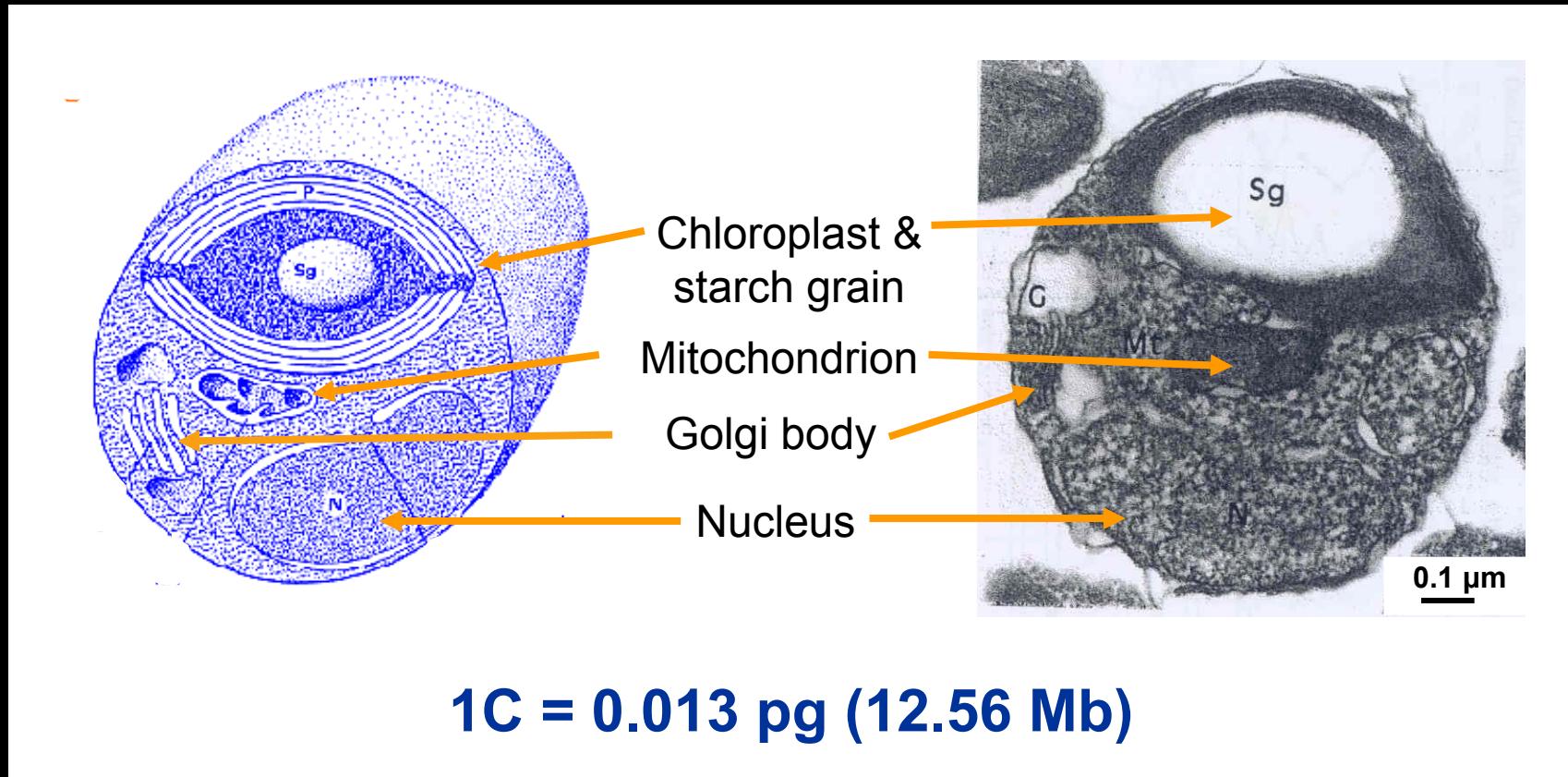
Chlorophyta (1.3%)

0.013 – 23.4



1C DNA amount (pg)

Ostreococcus tauri (Prasinophyta)



$$1C = 0.013 \text{ pg (12.56 Mb)}$$

Derelle et al. 2006.

Genome analysis of the smallest free-living eukaryote *Ostreococcus tauri* unveils many unique features.

Proc Natl Acad Sci 103: 11647-11652.

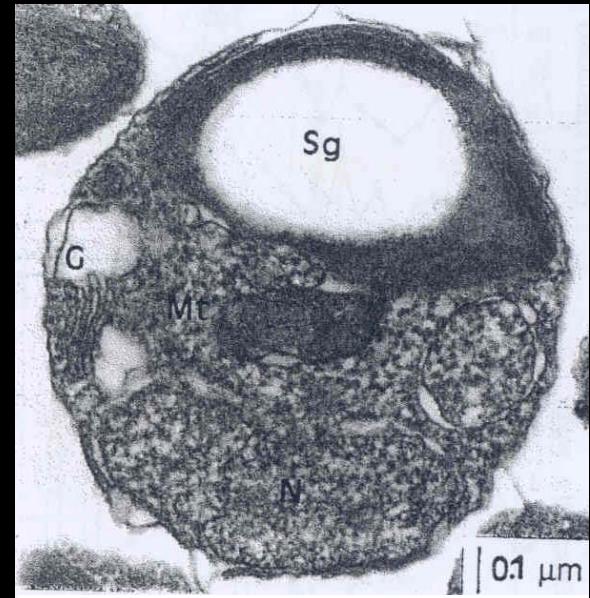
Genome size variation



Fritillaria assyriaca
1C = 127.4 pg



Genlisea margaretae
1C = 0.065 pg



Ostreococcus tauri
1C = 0.01 pg



C-value paradox

Thomas CA. 1971.

The genetic organization of chromosomes.

Annual Review of Genetics 5: 237-256.



‘why the lowly liverwort
has 18 times as much DNA as we have,
and the slimy, dull salamander
known as *Amphiuma* has 26 times our
complement of DNA’.



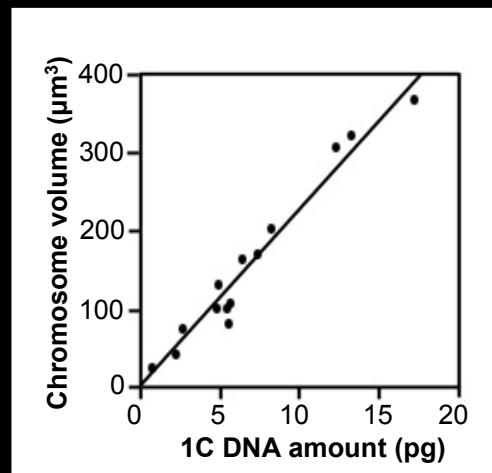
Comings DE. 1972.

Advances in Human Genetics 3: 237-431.

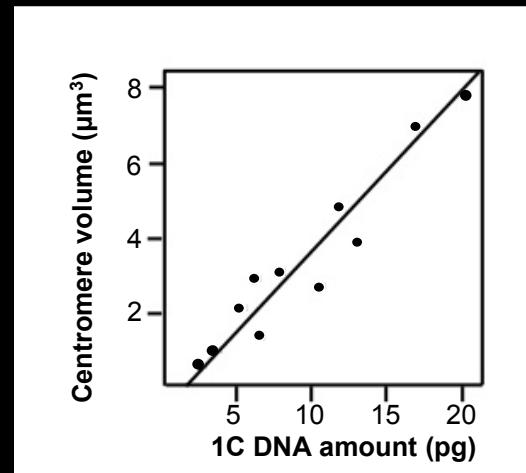
C-value enigma

Gregory TR. 2001. Coincidence, co-evolution, or causation? DNA content, cell size, and the C-value enigma. *Biological Reviews* **76**: 65-101.

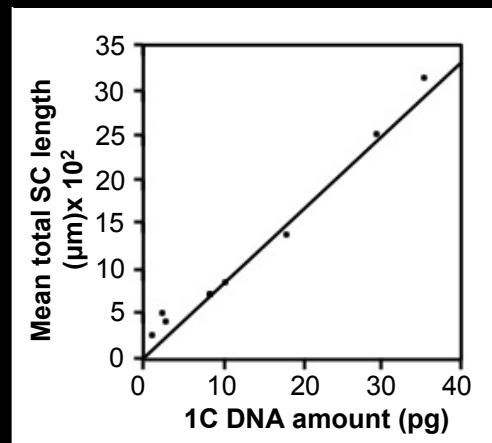
Variation of genome size: Consequences at nuclear level



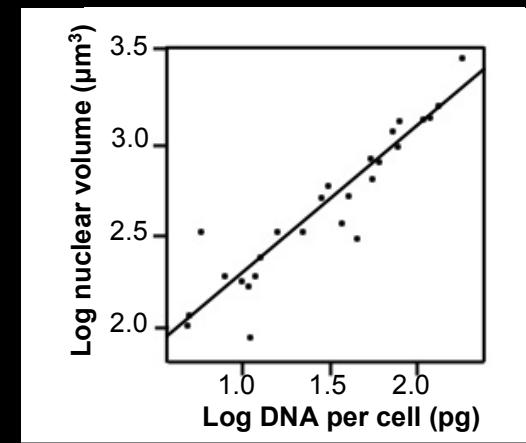
Bennett et al. 1983.
J. Cell Sci. **63**: 173-179.



Bennett et al. 1981.
J. Cell Sci. **47**: 91-115.

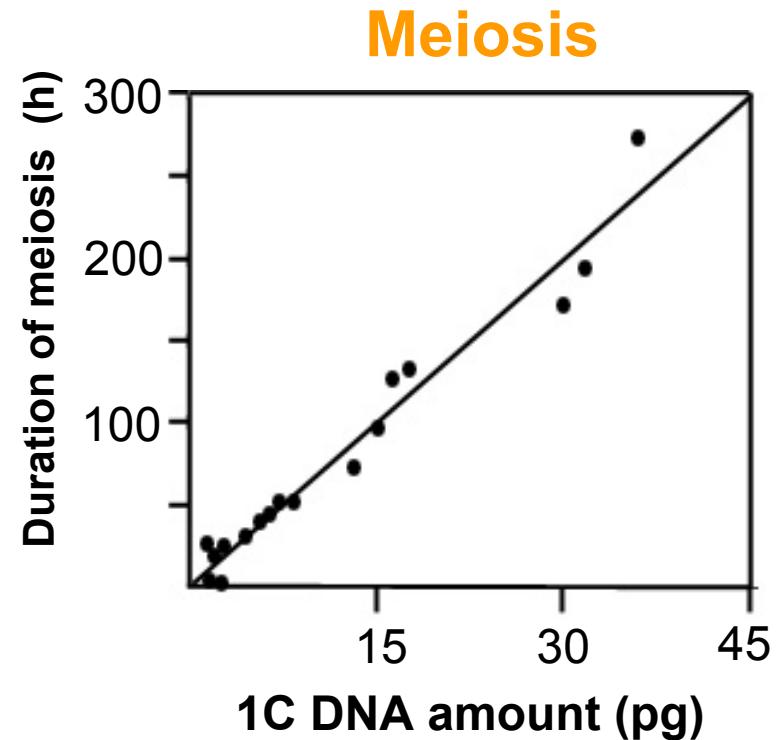
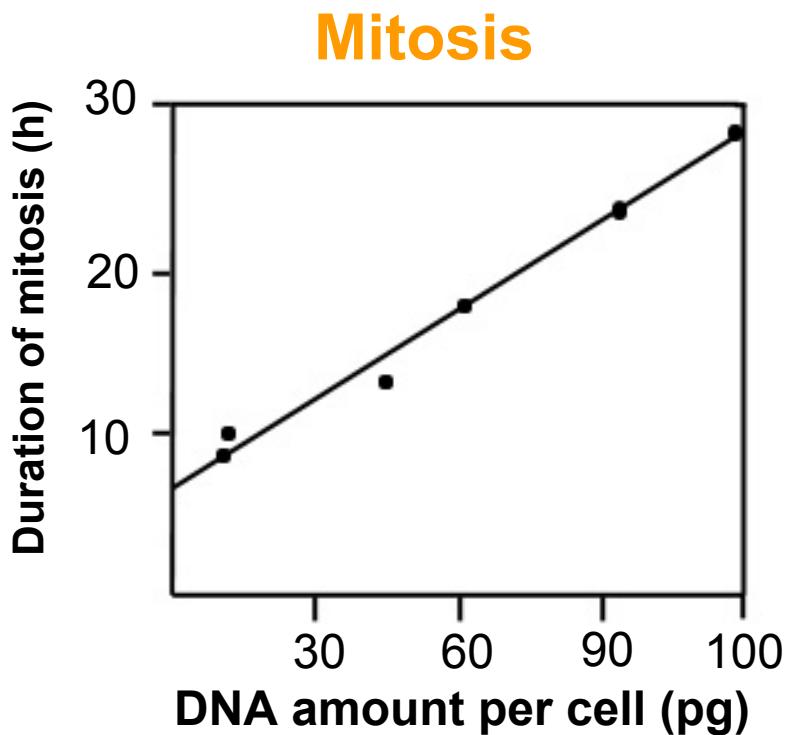


Anderson et al. 1985.
Exp. Cell Res. **156**: 367-378.



Baetcke et al. 1967.
Proc. Natl. Acad. Sci. USA **58**: 533-540.

Variation of genome size: Consequences of timing



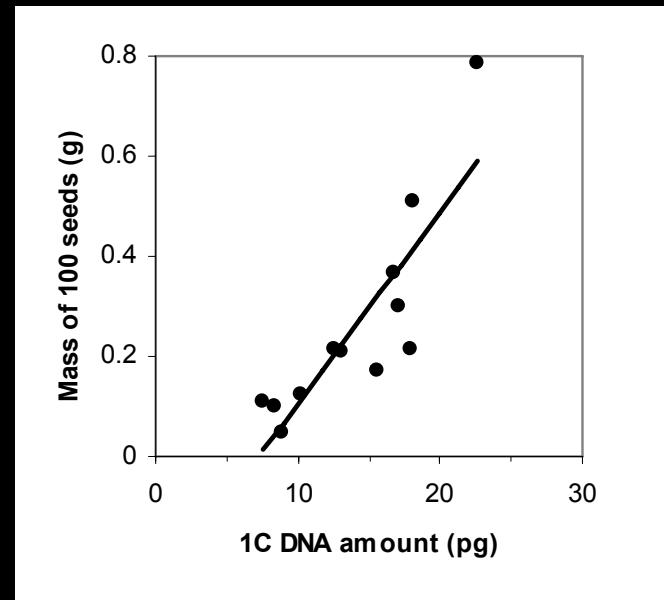
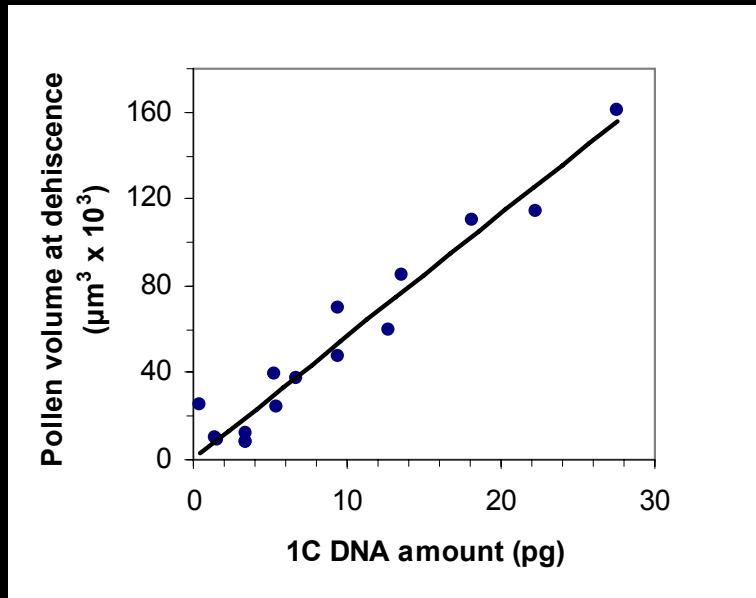
Van't Hof & Sparrow AH. 1963.

Proc. Natl. Acad. Sci. USA 49: 897-902.

Bennett MD. 1977.

Phil. Trans. Roy. Soc. B 277: 201-277.

Variation of genome size: Consequences at cell and tissue level



Relationship between pollen volume and DNA amount in 16 grass species.

Bennett *et al.* 1972



Relationship between seed weight and DNA amount in 12 *Allium* species.

Bennett *et al.* 1972

Consequences of variation in DNA amount

Whole plant level

- a) Life cycle options
- b) Life strategy options
- c) Ecology options
- d) Coping with environmental change

Consequences of variation in DNA amount

Whole plant level

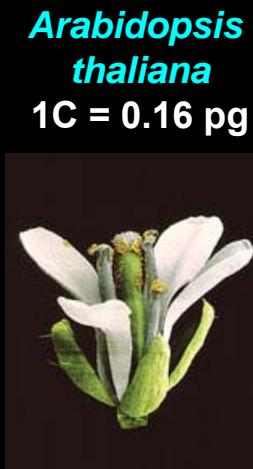
a) Life cycle options

Bennett MD. 1972.

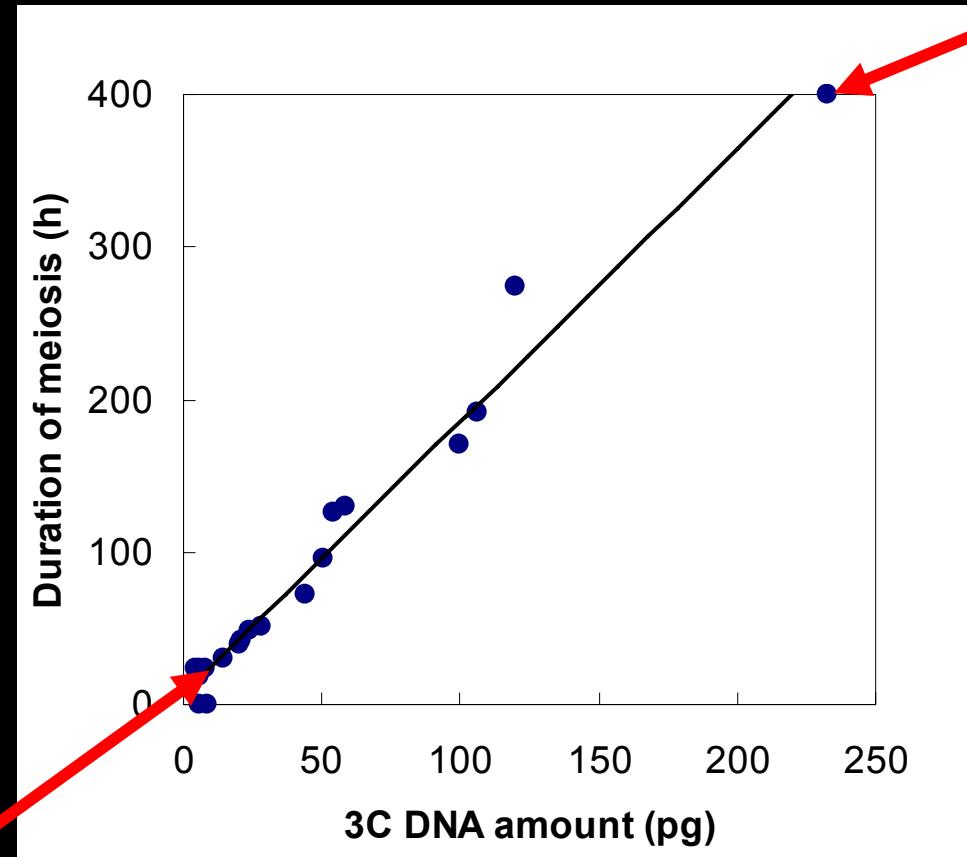
Nuclear DNA content and minimum generation time in herbaceous plants.

Proceedings of the Royal Society of London Series B-Biological Sciences 181: 109-135.

Consequences: life cycle options



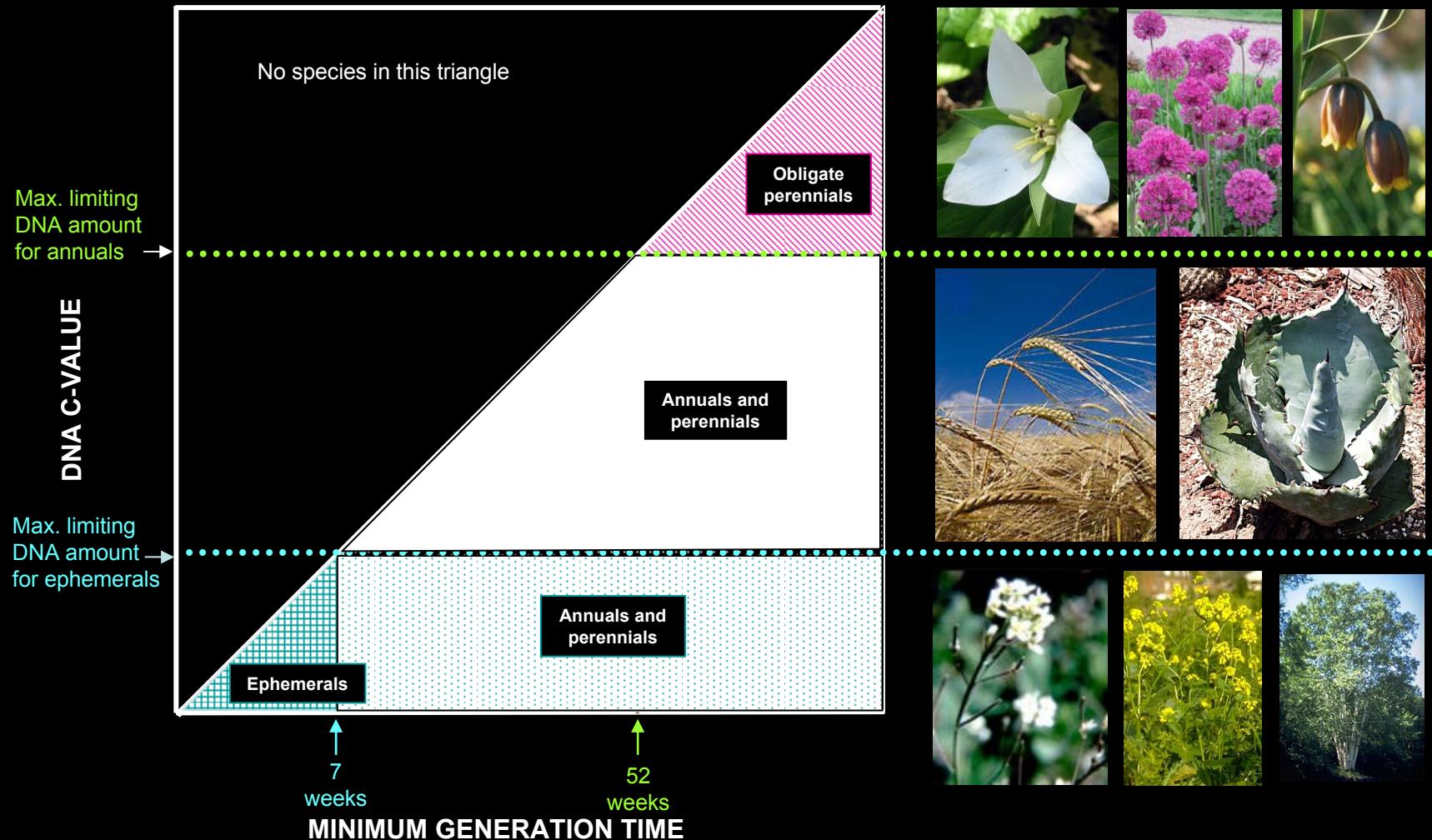
Arabidopsis thaliana
1C = 0.16 pg



Fritillaria meleagris
1C = 70.7 pg

Bennett MD. 1977.
Phil. Trans. Roy. Soc. B 277: 201-277.

Consequences: life cycle options



Consequences of variation in DNA amount

Life cycle options:

Conclusions

- DNA amount can impose limits on the type of life cycle a species can display
- Species with small genomes may be ephemerals, annuals or perennials
- Species with large genomes are restricted to being obligate perennials

Consequences of variation in DNA amount

Whole plant level

- a) Life cycle options
- b) Life strategy options**
- c) Ecology options
- d) Coping with environmental change

Consequences of variation in DNA amount

Whole plant level

b) Life strategy options:

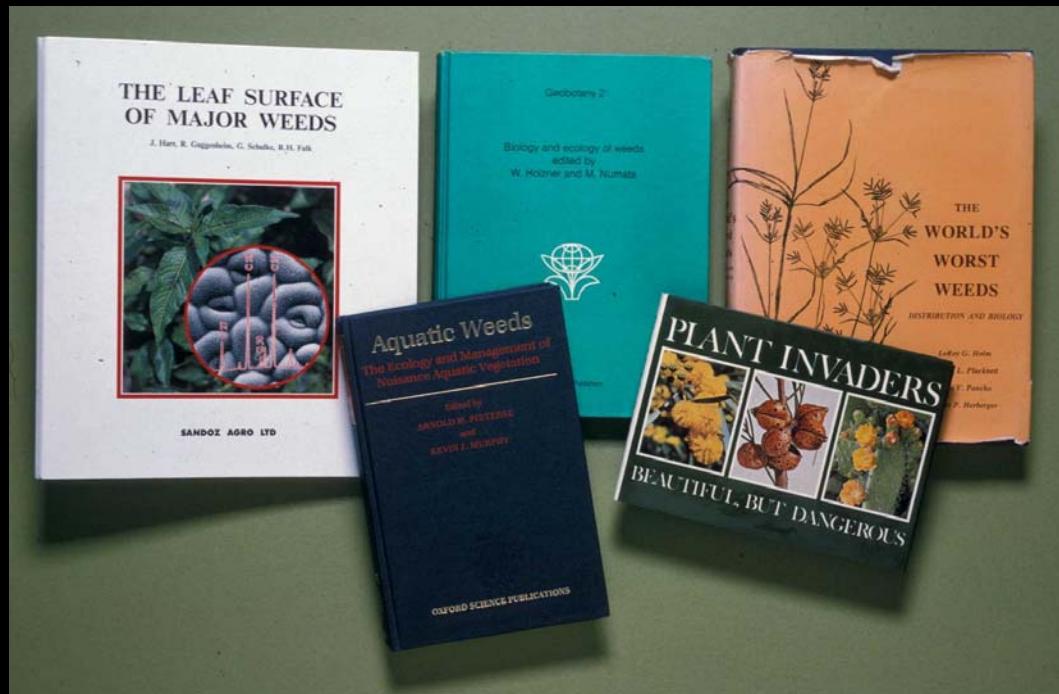
Potential to become a weed

Bennett, Leitch & Hanson. 1998.

DNA amounts in two samples of angiosperm weeds.

Annals of Botany 82: 121-134.

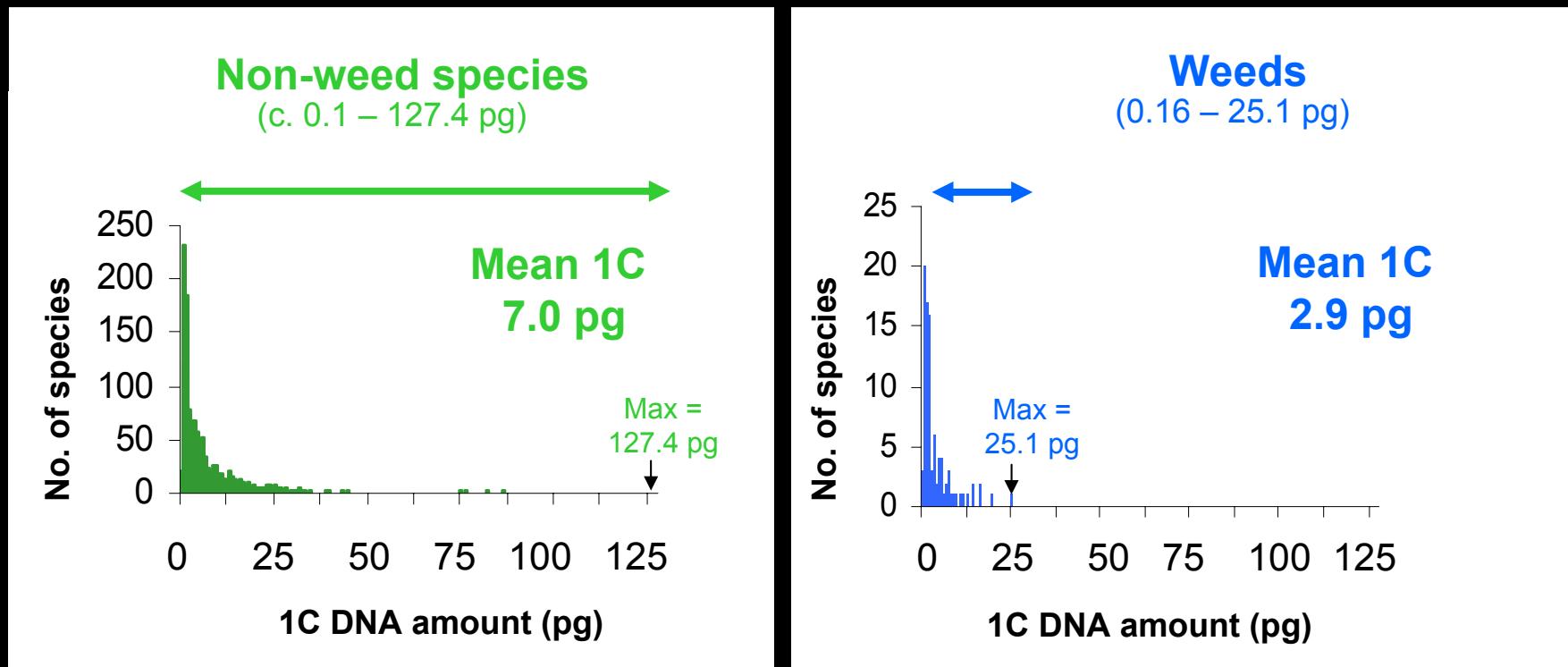
Consequences: option to be a weed



Method

DNA amounts for 156 angiosperms
recognised as weeds compared with
2685 non-weed species

Consequences: option to be a weed



Bennett, Leitch & Hanson. 1998.

DNA amounts in two samples of angiosperm weeds.

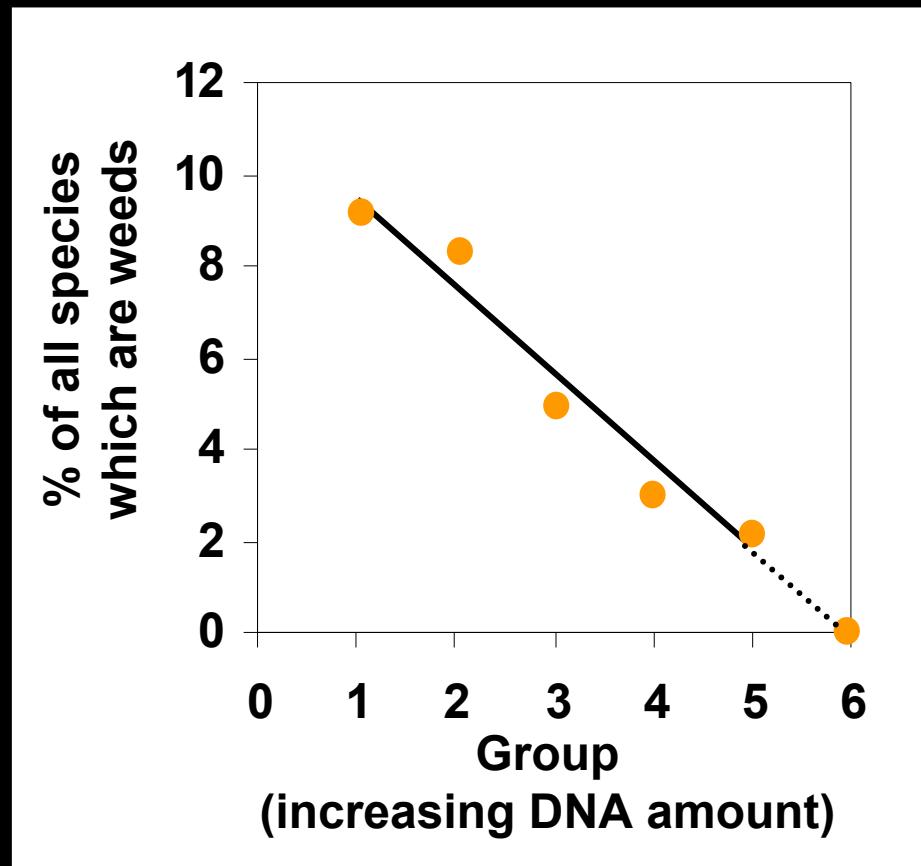
Annals of Botany 82: 121-134.

Success of an invasive weed



- Rapid establishment or completion of reproductive development
- Short generation time
- Rapid production of many small seeds

Consequences: option to be a weed



Consequences of variation in DNA amount

Whole plant level

- a) Life cycle options
- b) Life style options
- c) **Ecology options**
- d) Coping with environmental change

Genome size and latitude

Pop.	Several <i>Picea sitchensis</i>	Miksche 1967, 1971
Sp.	Tropical vs. temperate grasses	Avdulov 1931
Sp.	329 tropical vs. 527 temperate plants	Levin and Funderburg 1979
Sp.	17 Poaceae and 15 Fabaceae crops	Bennett 1976
Pop.	24 <i>Berberis</i> in Patagonia	Bottini <i>et al.</i> 2000



+ correlation

Consequences: ecology options

401 species
in the state of
California

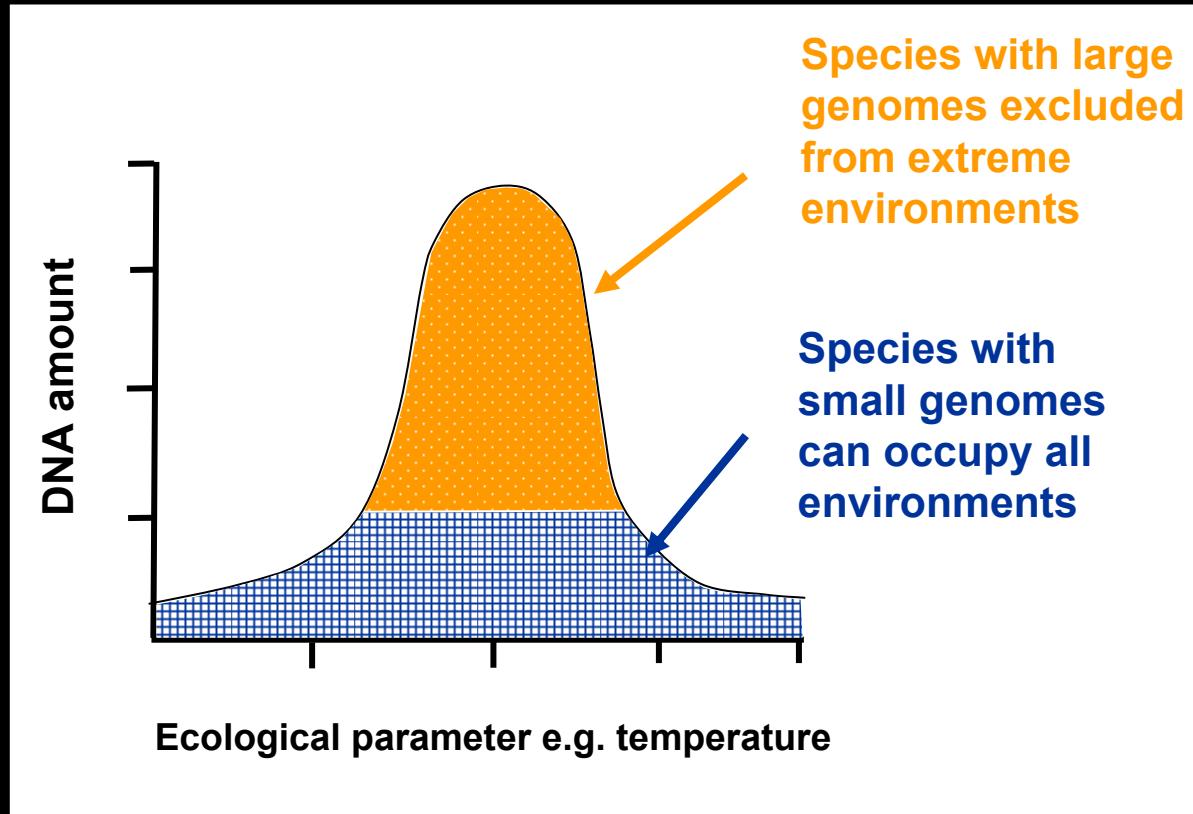


Knight & Ackerly. 2002.

Variation in nuclear DNA content across environmental gradients:
a quantile regression analysis.

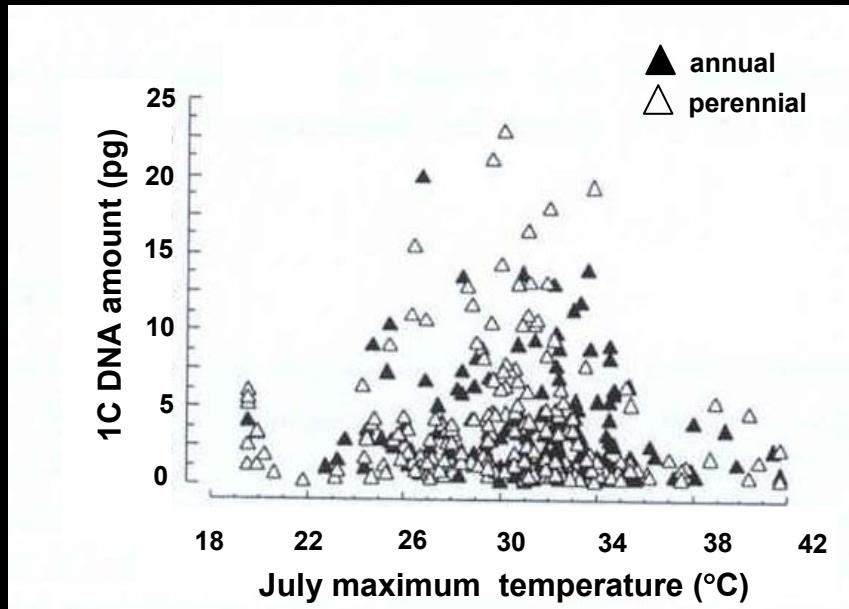
Ecology Letters 5: 66-76.

Consequences: ecology options



Knight & Ackery. 2002.
Ecology Letters 5: 66-76.

Consequences: ecology options

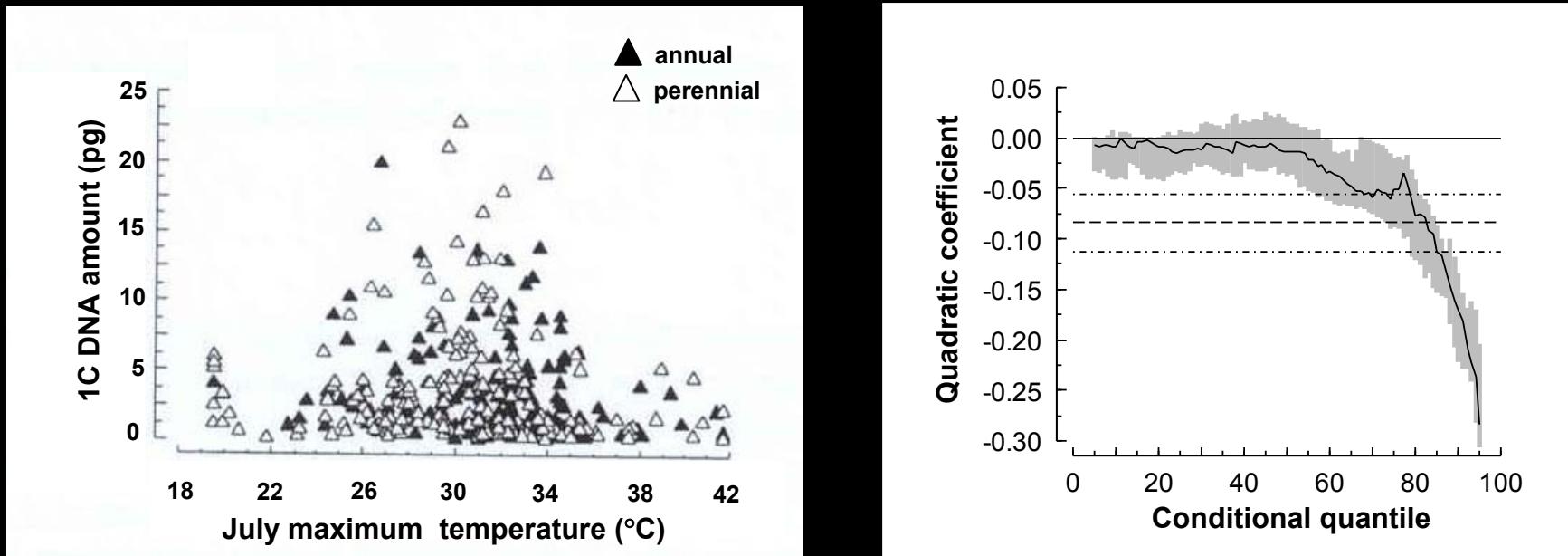


Knight & Ackerly. 2002.

Variation in nuclear DNA content across environmental gradients:
a quantile regression analysis.

Ecology Letters 5: 66-76.

Consequences: ecology options



Knight & Ackerly. 2002.

Variation in nuclear DNA content across environmental gradients:
a quantile regression analysis.

Ecology Letters 5: 66-76.

Consequences: ecology options

Summary

- The relationship between genome size and environmental factors is not uniform but appears to be stronger for species with large genomes
- Species with large genomes are excluded from extreme environments

Consequences of variation in DNA amount

Whole plant level

- a) Life cycle options
- b) Life style options
- c) Ecology options
- d) **Coping with environmental change**
 - (i) Pollution
 - (ii) Threat of extinction

Consequences: *Coping with environmental change*

Pollution: The question

What effect does genome size have on the survival of plants in lead polluted soils?

B. Vilhar, T. Vidic and J. Greilhuber

Consequences: Genome size and pollution

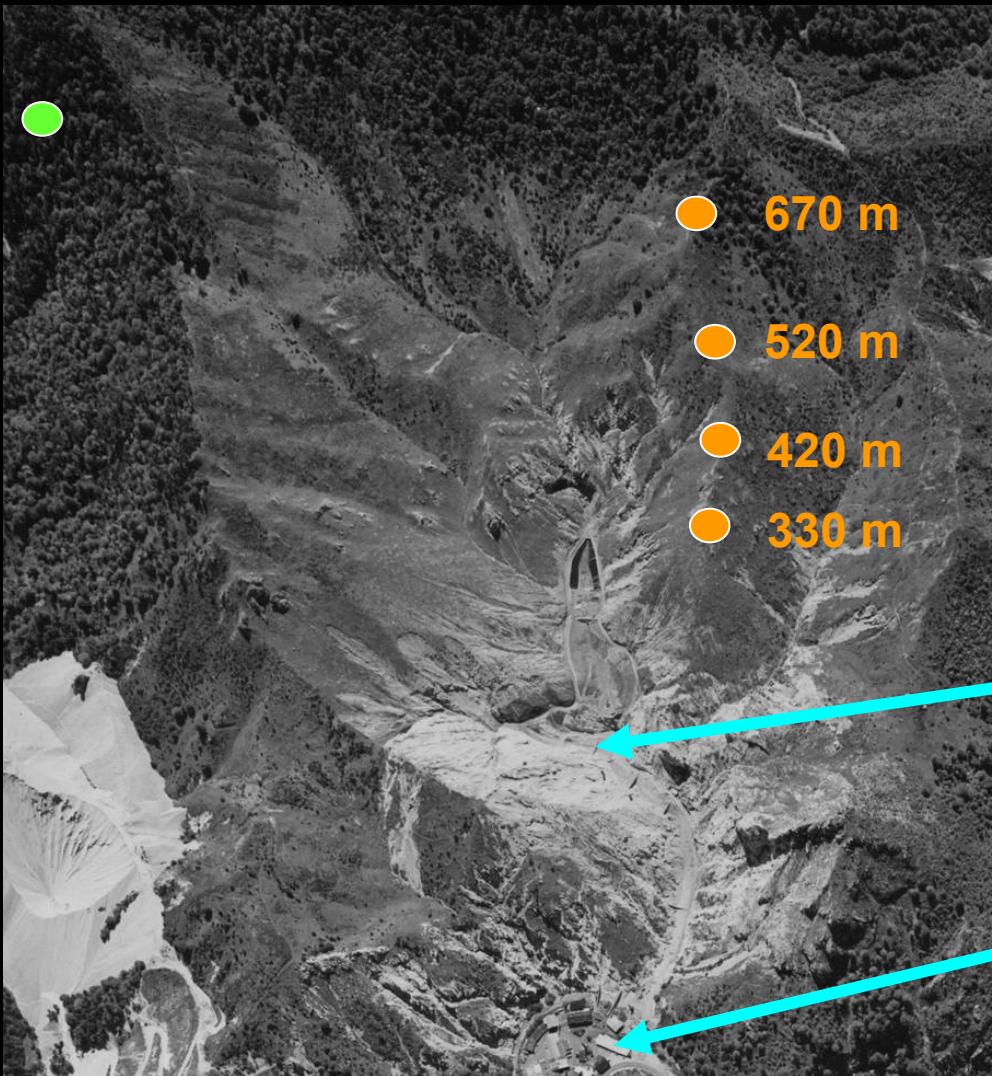


Dolina smrti in Slovenia

Consequences: Genome size and pollution

Reference
plot

Conc. lead in
soil = 0.1%



Conc. of
lead in soil

0.7%

1.5%

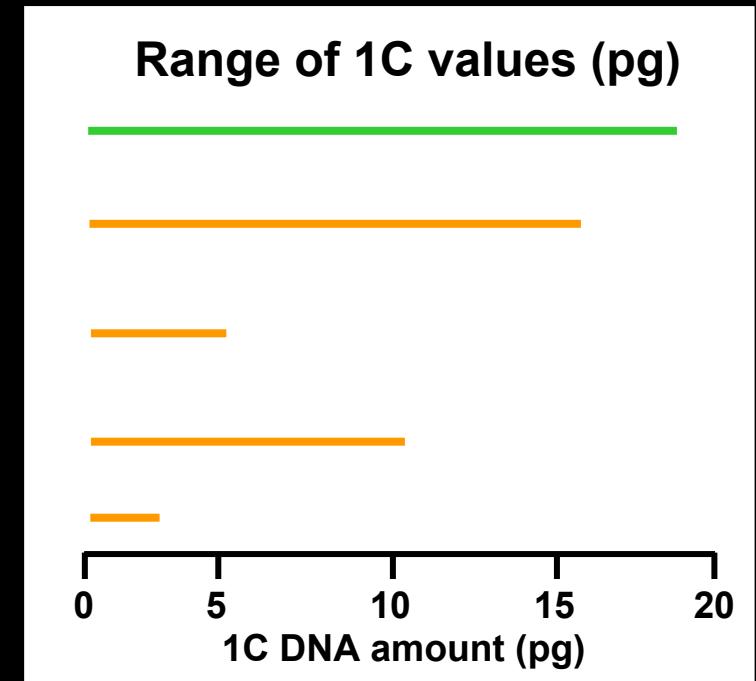
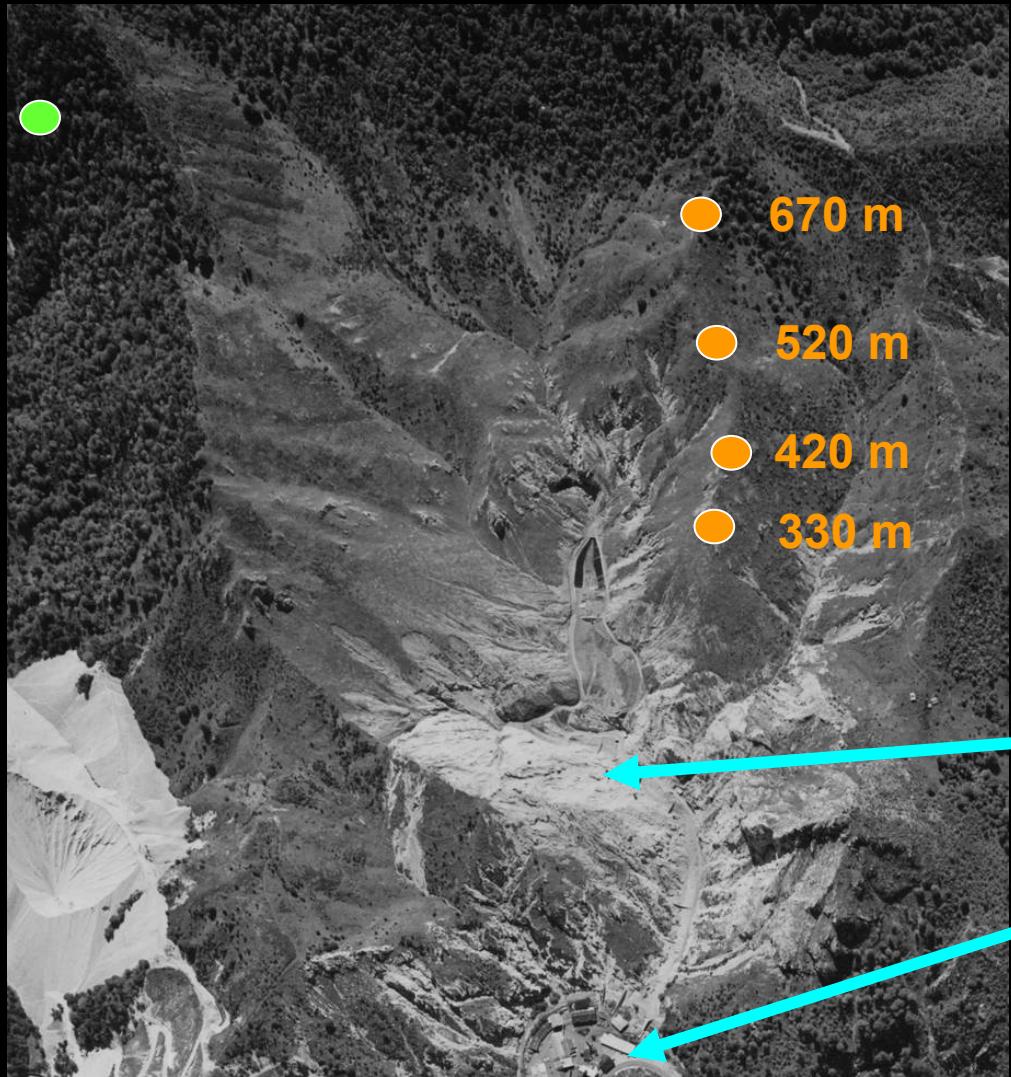
2.0%

3.3%

Smelter
chimney

Lead
smelter

Consequences: Genome size and pollution



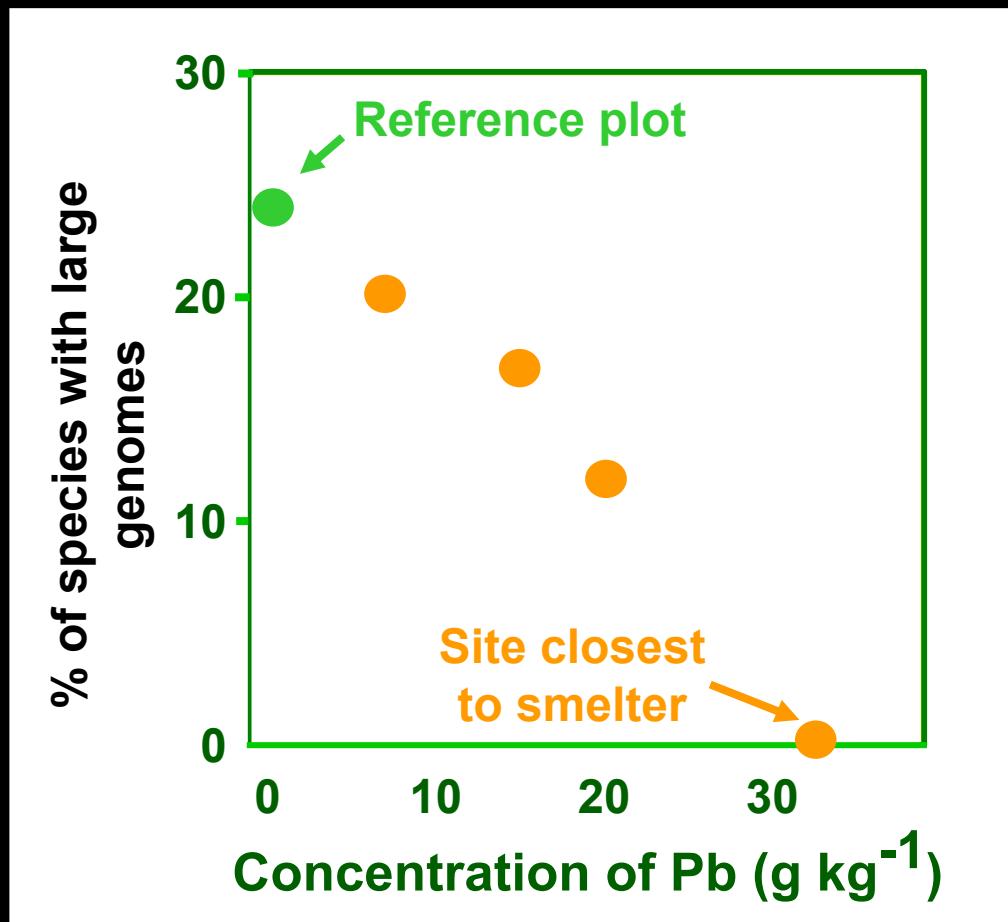
Smelter

chimney

Lead
smelter

Consequences: Genome size and pollution

Percentage of species with large genomes in individual plots



Consequences: Genome size and pollution

Conclusions

Species with large genomes are at selective disadvantage in extreme environmental conditions induced by pollution.

Consequences of variation in DNA amount

Whole plant level

- a) Life cycle options
- b) Life style options
- c) Ecology options
- d) **Coping with environmental change**
 - (i) Pollution
 - (ii) Threat of extinction

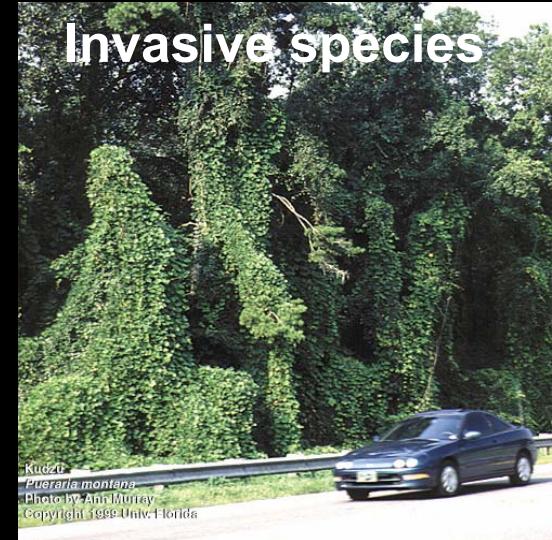
Consequences: Genome size and threat of extinction



Habitat loss



Pollution



Invasive species

Is genome size important?

Vinogradov AE. 2003.

Selfish DNA is maladaptive: evidence from the plant Red List.
Trends in Genetics 19: 609-614.

Consequences: Genome size and threat of extinction

Data and analysis



→ 3036 species →



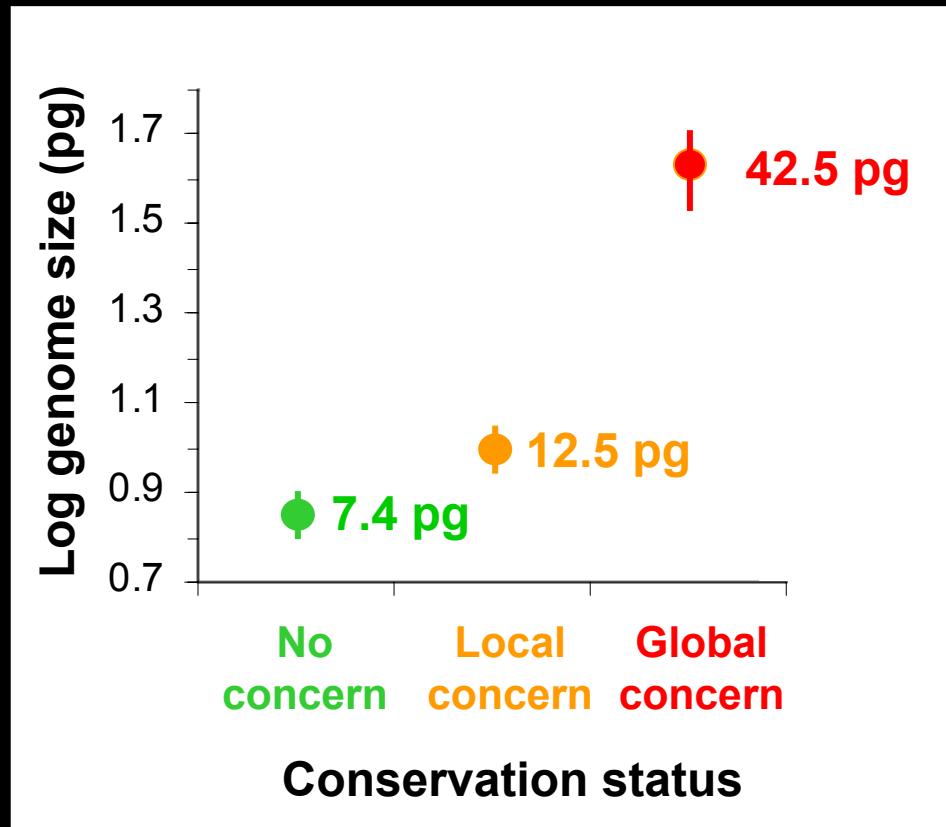
- Global concern = 305
- Local concern = 1329
- No concern = 1402

Vinogradov AE. 2003.

Selfish DNA is maladaptive: evidence from the plant Red List.
Trends in Genetics 19: 609-614.

Consequences: Genome size and threat of extinction

Results



Vinogradov AE. 2003.
Trends in Genetics 19: 609-614.

Consequences: Genome size and threat of extinction

Analysis within families

$$\text{Genome size contrast} = \frac{\text{Genome size for species}}{\text{Mean genome size of family}}$$



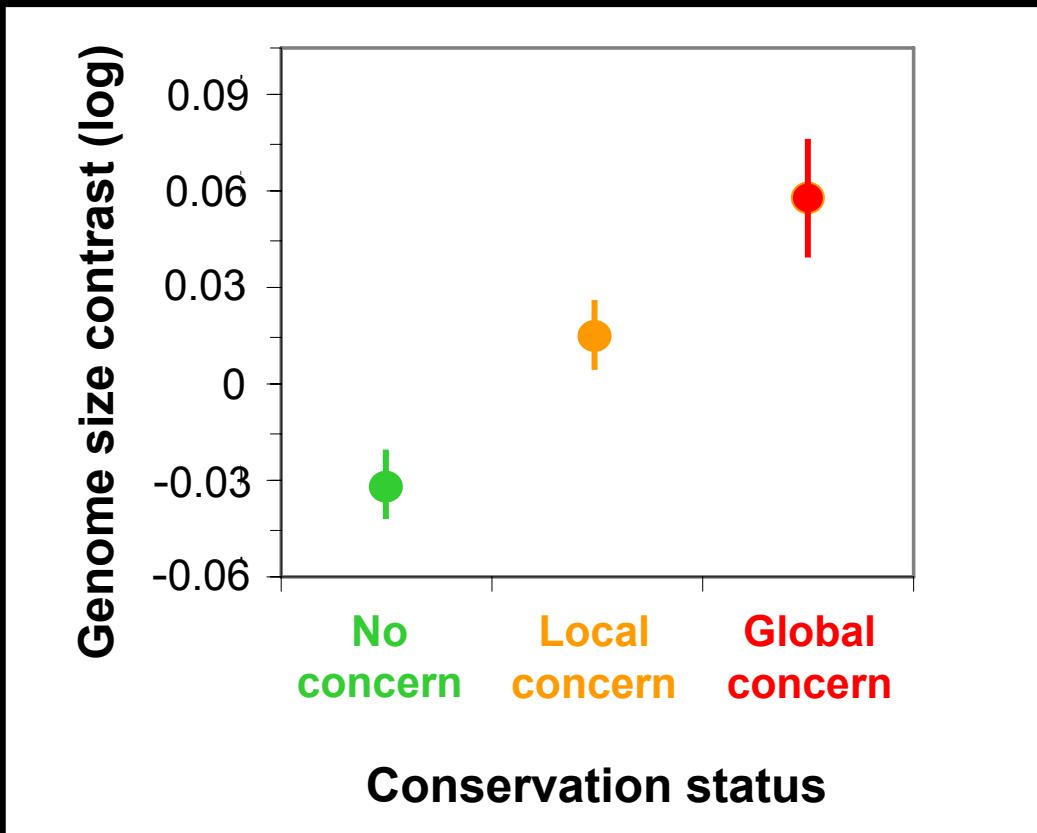
$$\text{Genome size contrast} = \frac{32.4}{7.7} = 4.2$$



$$\text{Genome size contrast} = \frac{1.2}{4.3} = 0.3$$

Consequences: Genome size and threat of extinction

Results



Vinogradov AE. 2003.
Trends in Genetics 19: 609-614.

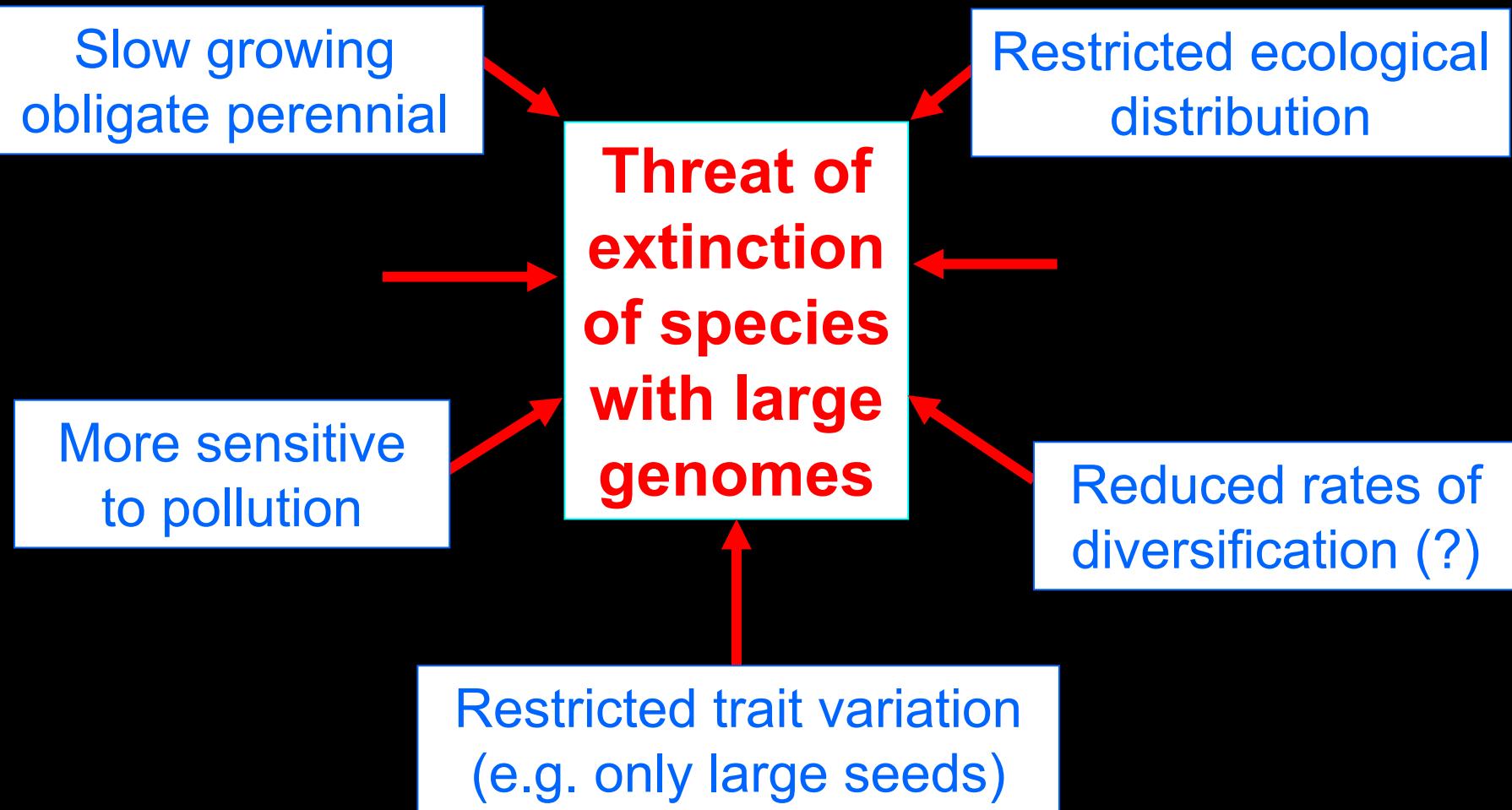
Consequences: Genome size and threat of extinction

Conclusions

Species with large genomes are at greater risk of extinction than those with small genomes.

- Independent of life cycle type (at least partially)
- Independent of polyploidy

Consequences: Genome size and threat of extinction

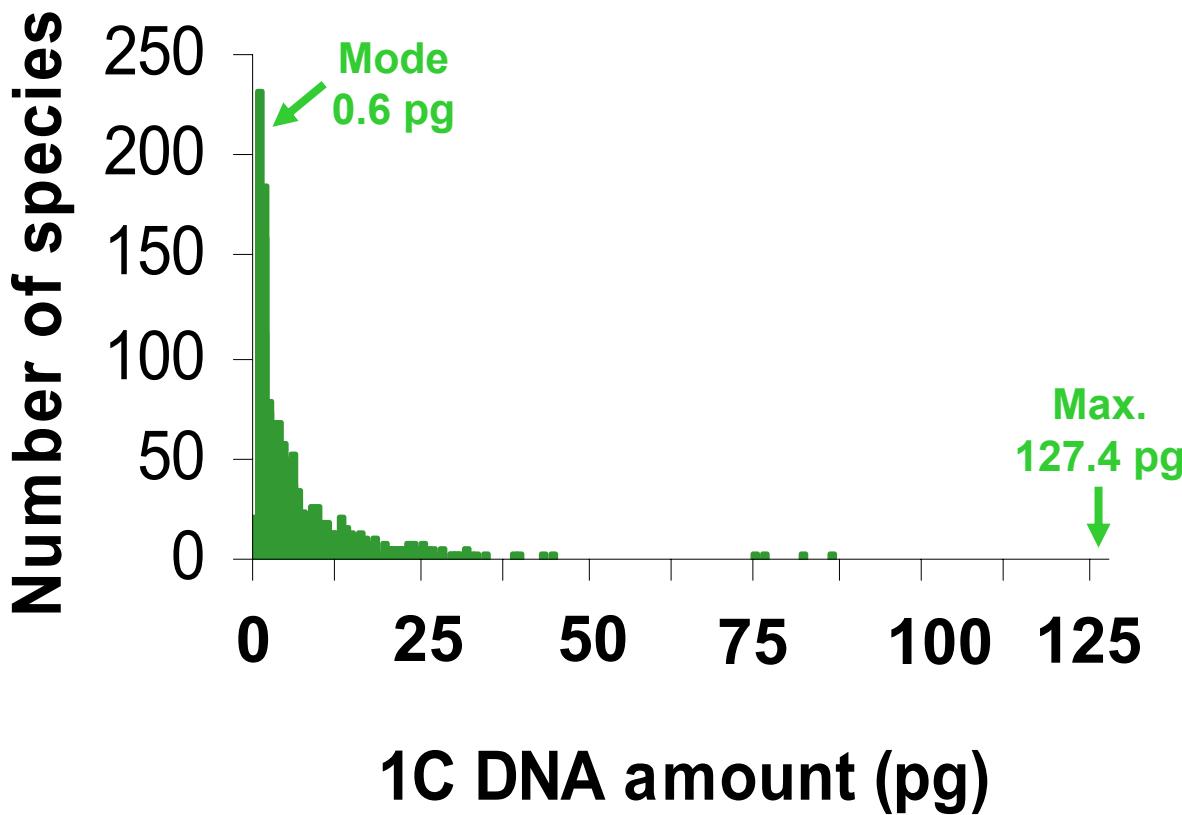


DNA amount variation and consequences

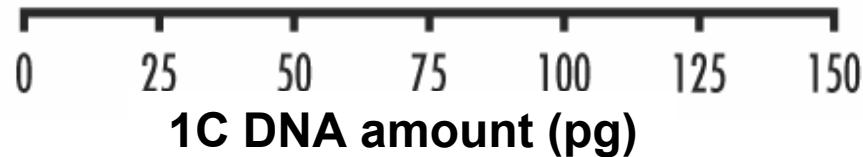
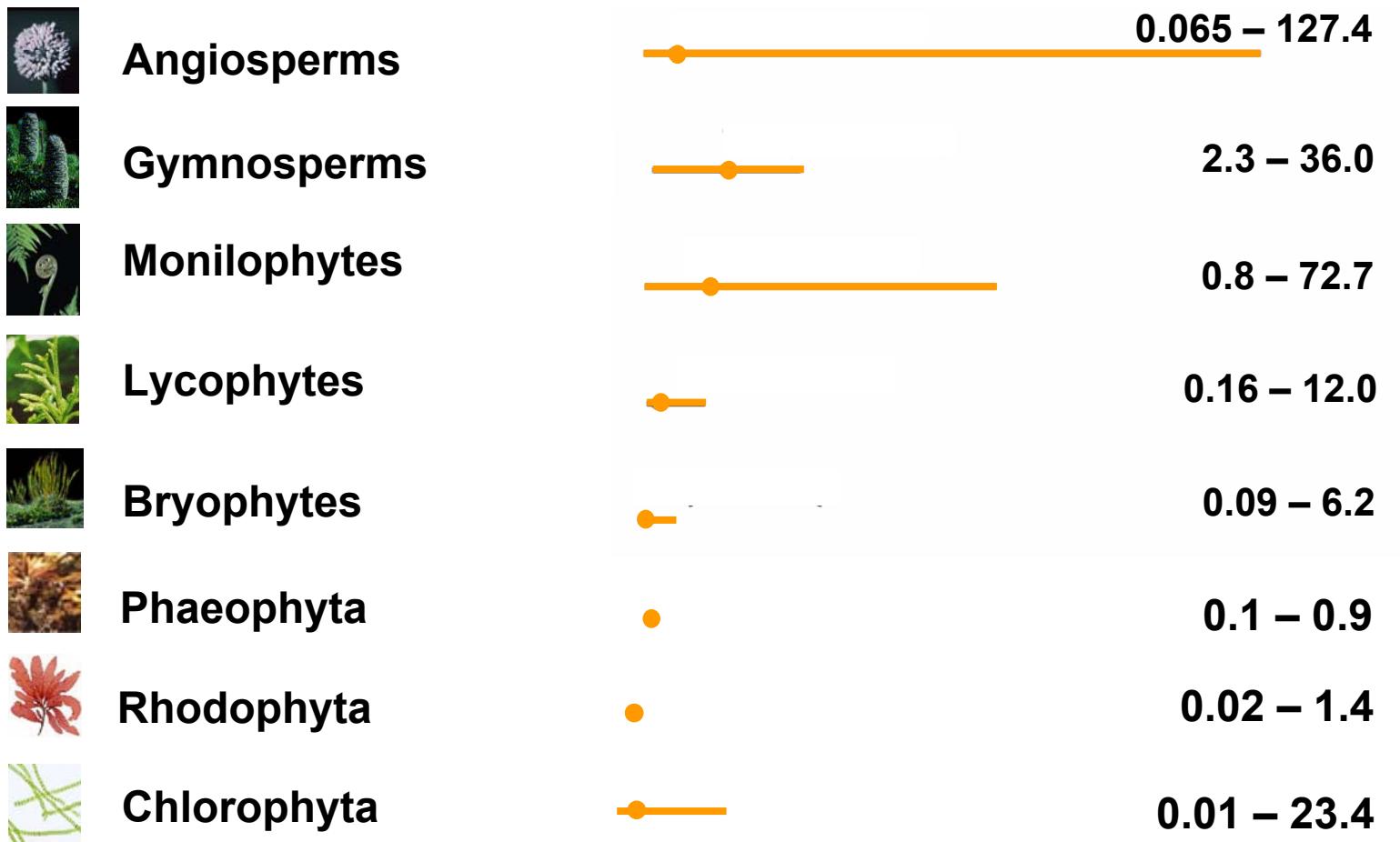
Summary

- Huge variation in DNA amount in plants
- Consequences of this variation visible at:
 - Cellular level
 - Tissue level
 - Whole organism level
- Possession of large genomes appear to impose constraints which operate at:
 - Functional level
 - Ecological level
 - Evolutionary level

DNA amount variation in angiosperms



Range of DNA amounts

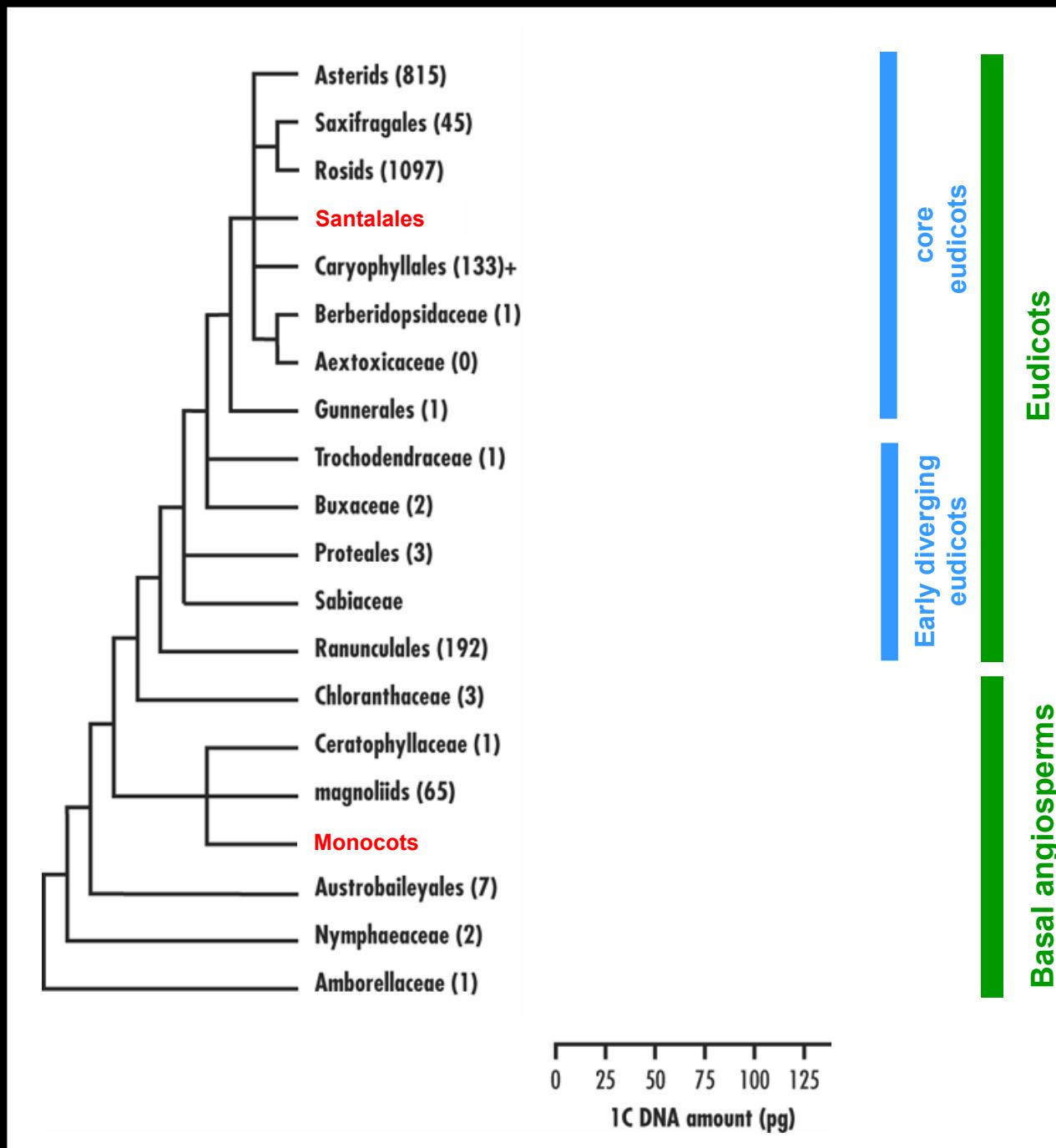


Variation of genome size

1. Consequences of genome size variation in plants
2. **Evolution of genome size variation**

Phylogenetic tree of angiosperms and C-value data

Modified from:
**Leitch, Chase,
Bennett MD. 1998.**
Annals of Botany
82: 85-94.



Angiosperms with 'very large' genomes (≥ 35 pg)

MONOCOTS

- **Liliales**
 - Liliaceae
 - Melanthiaceae
- **Asparagales**
 - Alliaceae
 - Alstroemeriaceae
 - Orchidaceae
 - Xanthorrhoeaceae
- **Commelinids**
 - Commelinaceae



CORE EUDICOTS

- **Santalales**
 - Santalaceae
 - Viscum*



Large scale analysis of genome size evolution in angiosperms

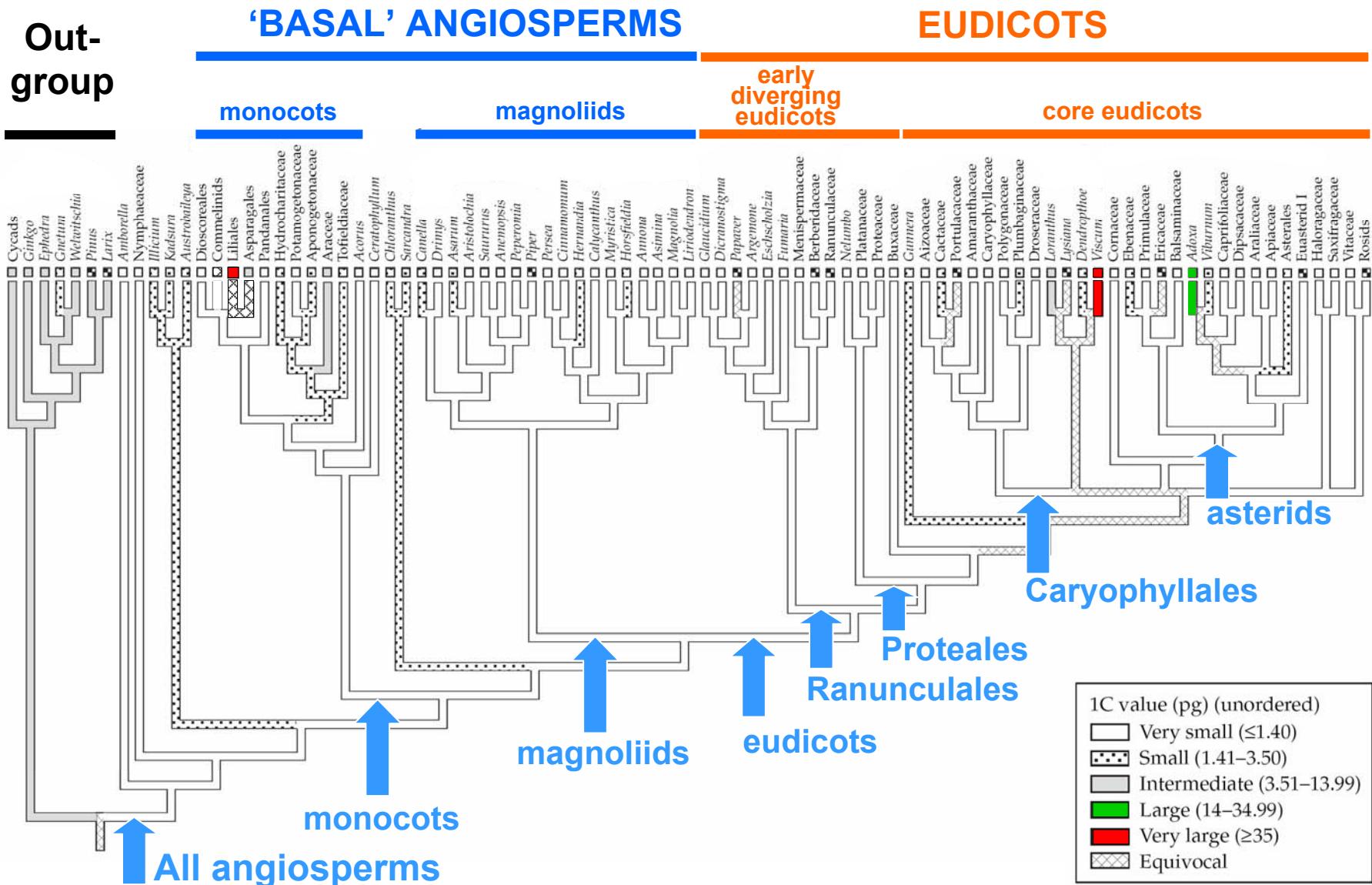
Data: Genome sizes for 4,119 species

Method: The ‘All most parsimonious states’ resolving option of MacClade

C-value range	Description
$\leq 1.4 \text{ pg}$	Very small
$\leq 3.5 \text{ pg}$	Small
$3.51 - 13.99 \text{ pg}$	Intermediate
$\geq 14 \text{ pg}$	Large
$\geq 35 \text{ pg}$	Very large

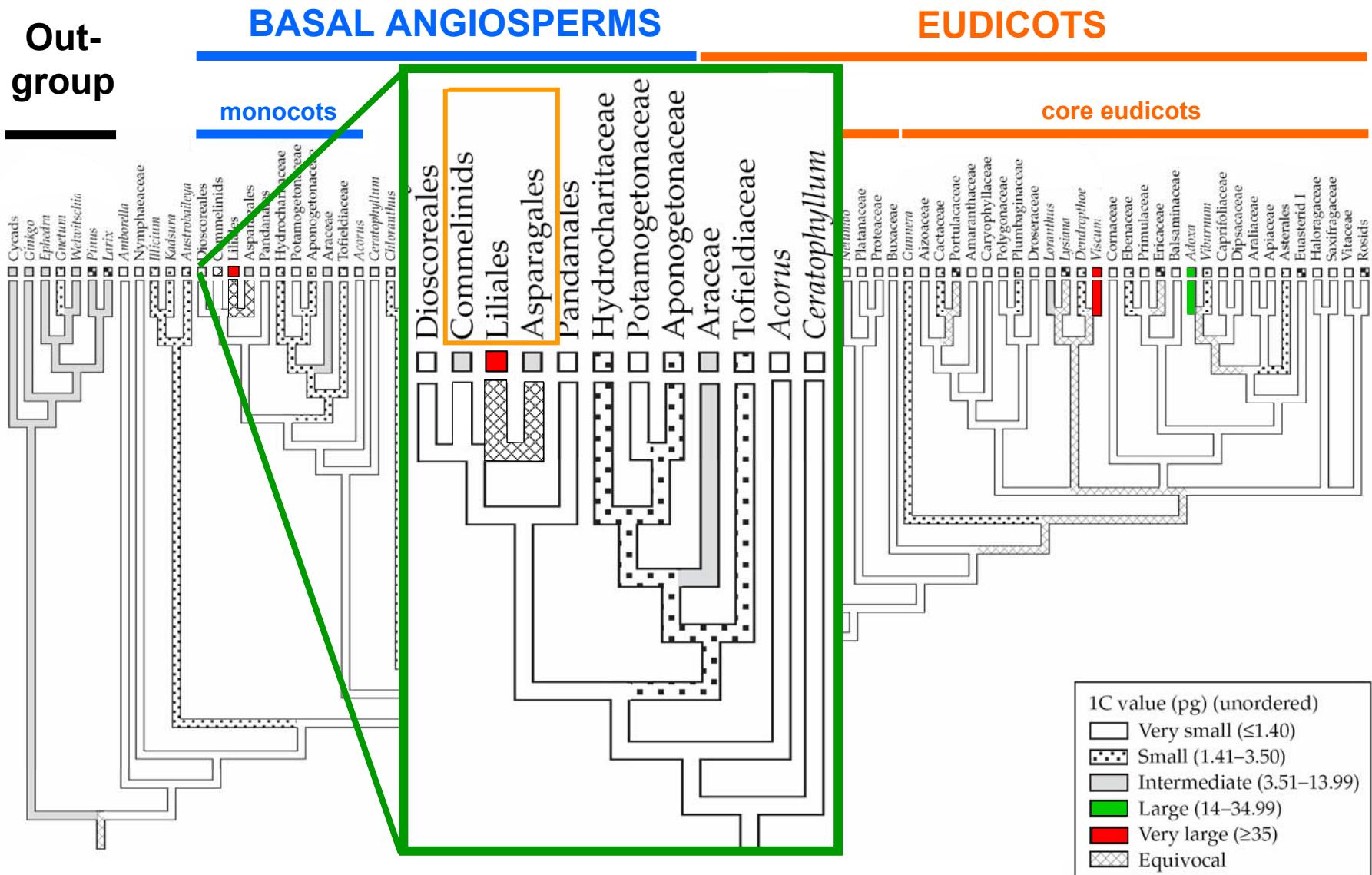
Large scale analysis of genome size evolution in angiosperms

Out-group



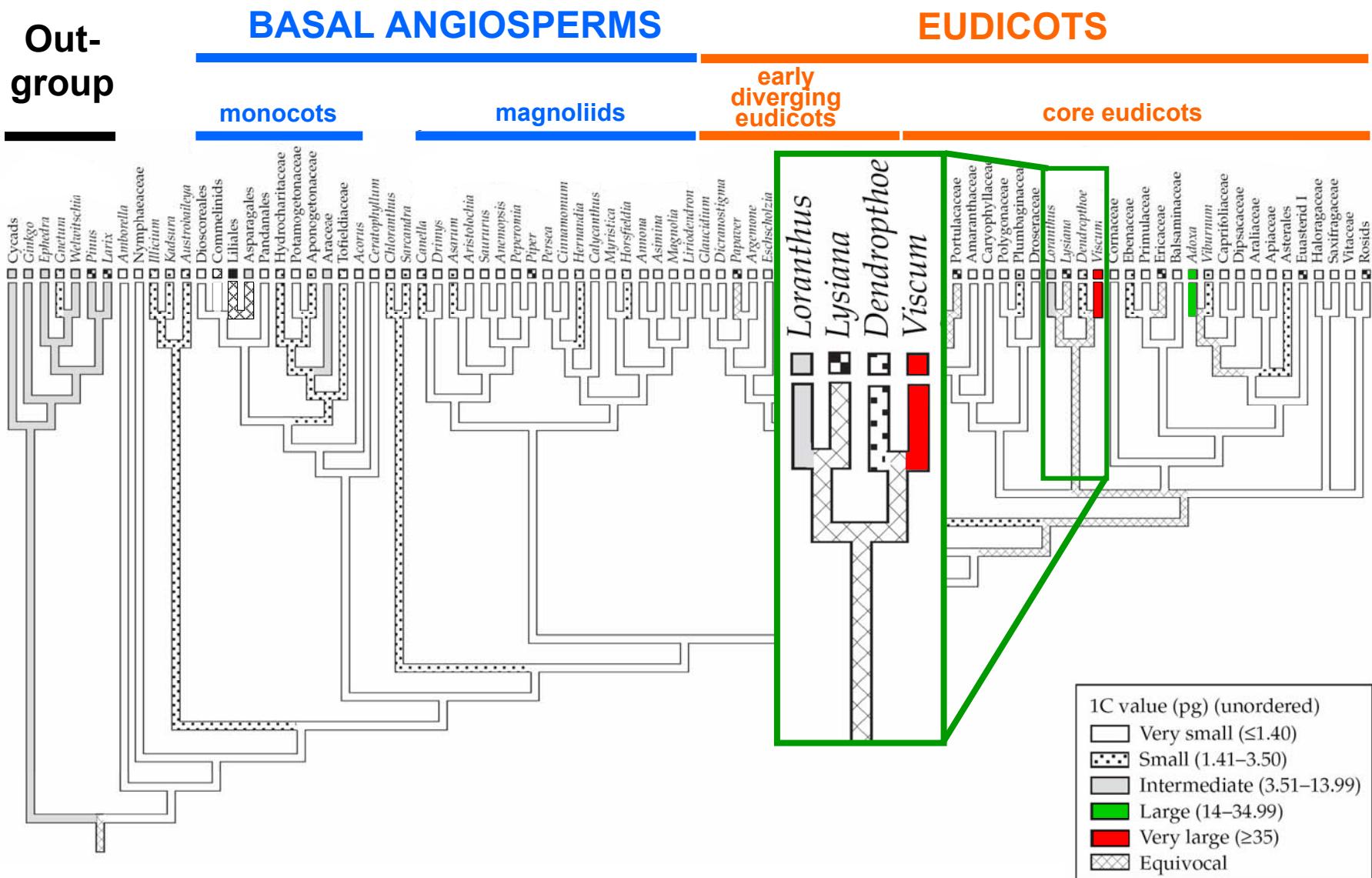
Reconstruction of *C*-value diversification across angiosperms

Out-group

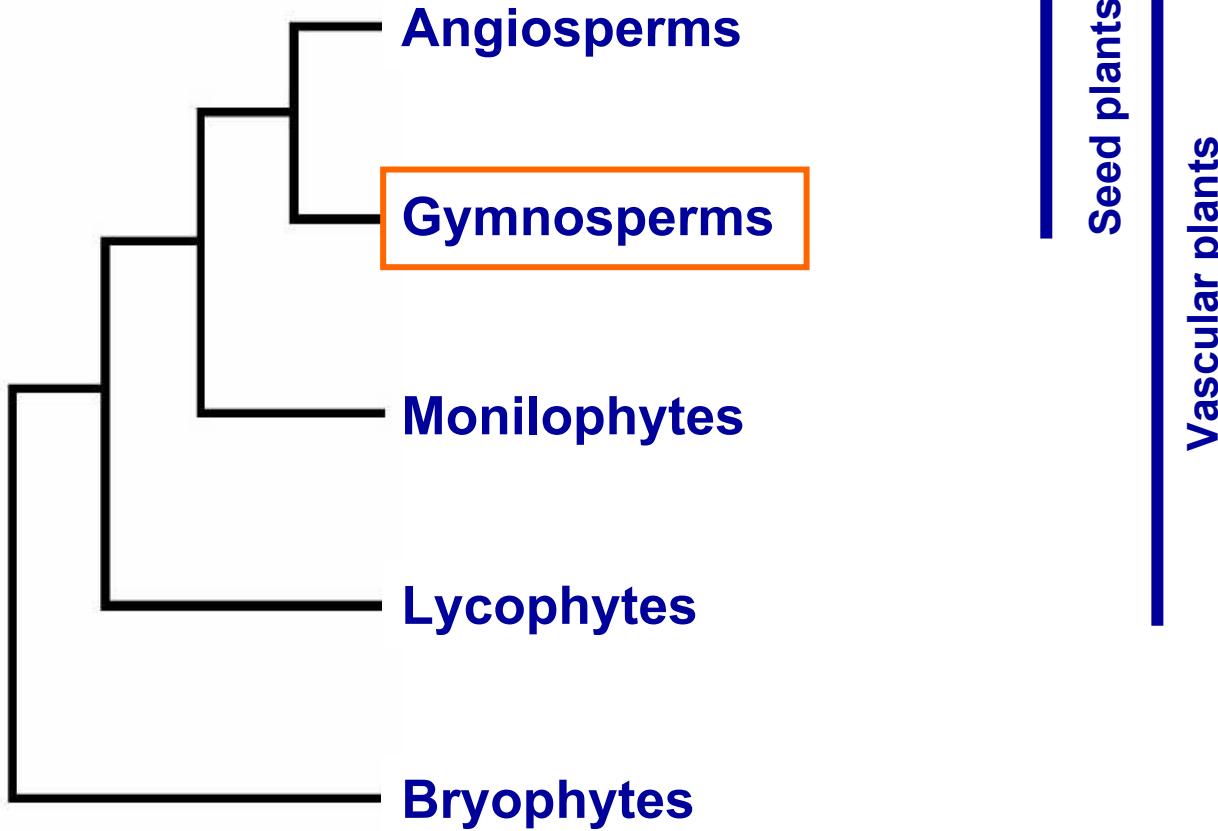


Reconstruction of C-value diversification across angiosperms

Out-group



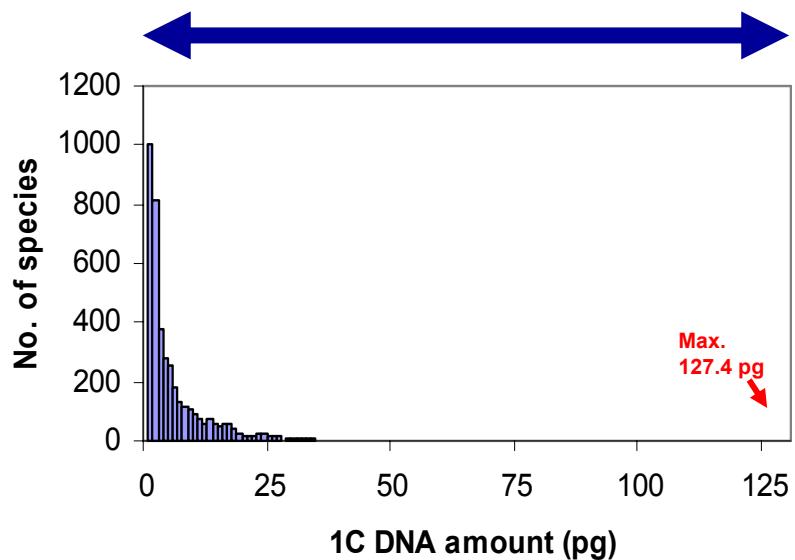
Land plant phylogeny



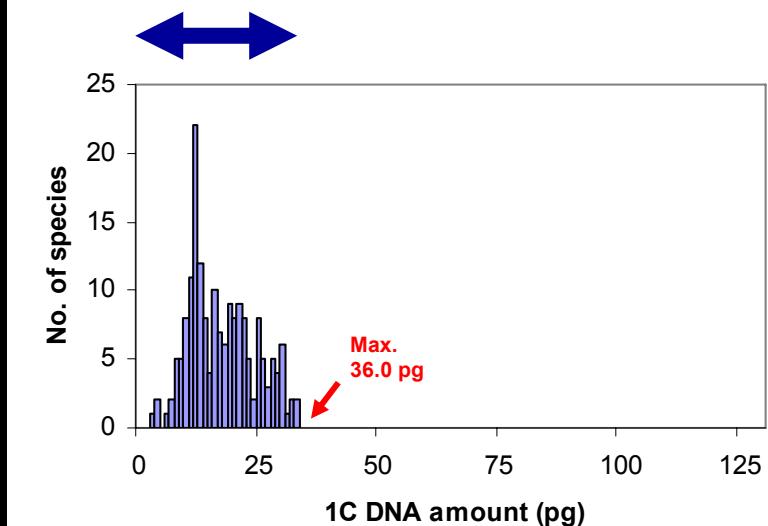
SEED PLANTS



Angiosperms



Gymnosperms



Mode: 0.6 pg

Mean: 6.13 pg

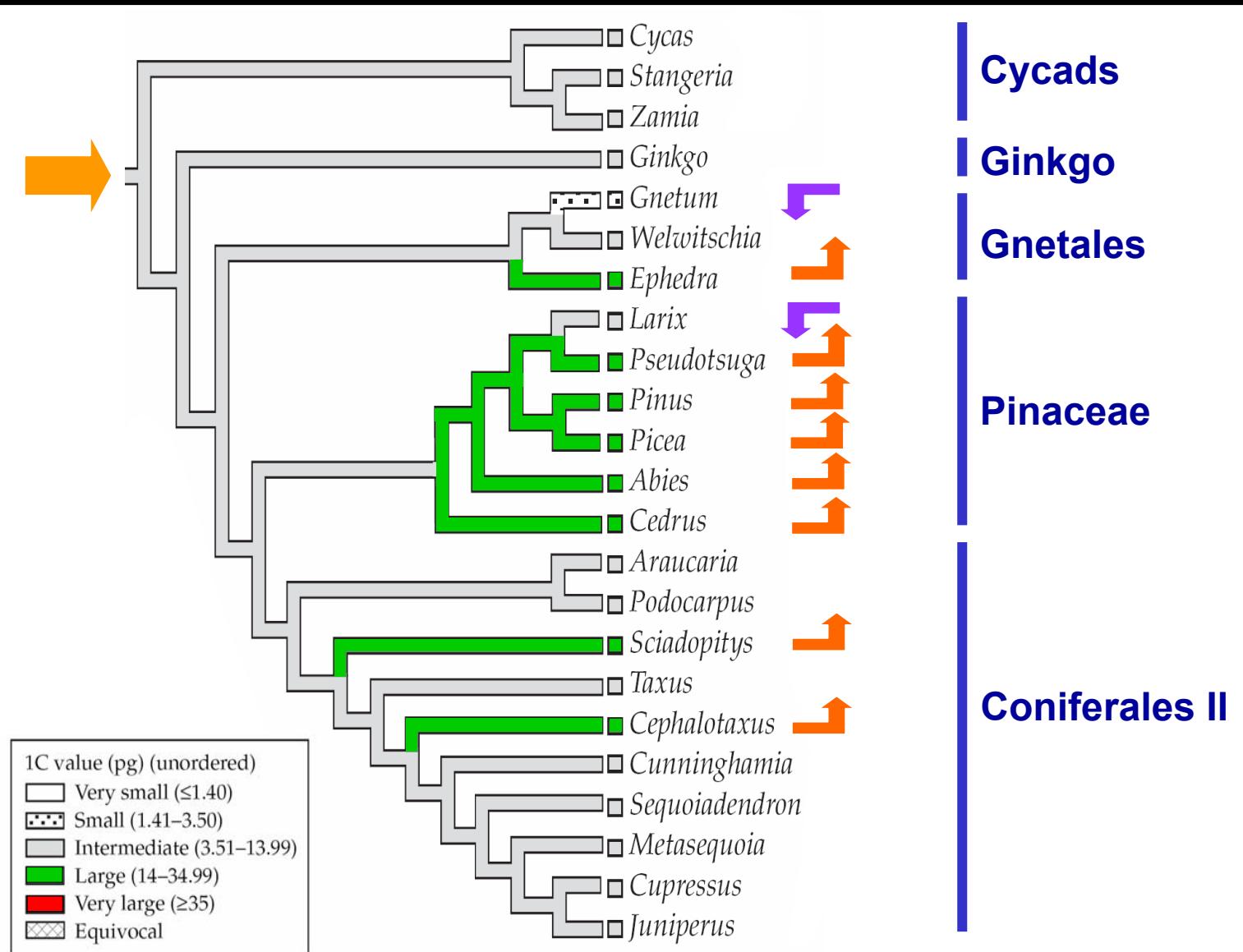
Range: 0.065 – 127.4 pg

Mode: 12 pg

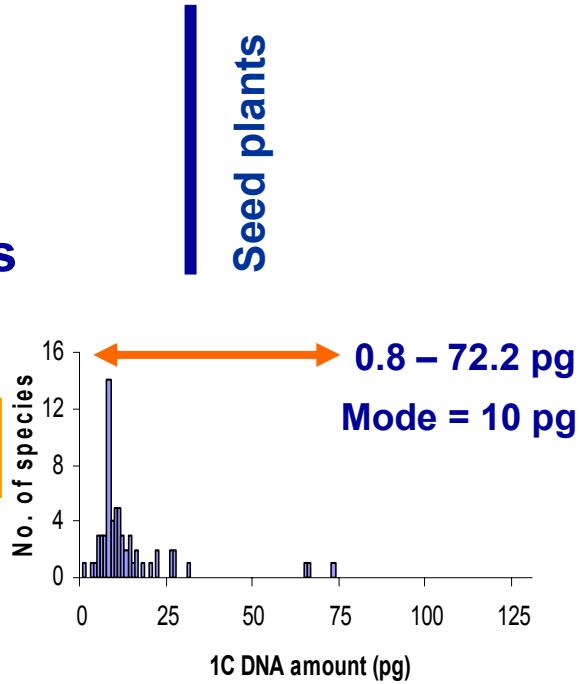
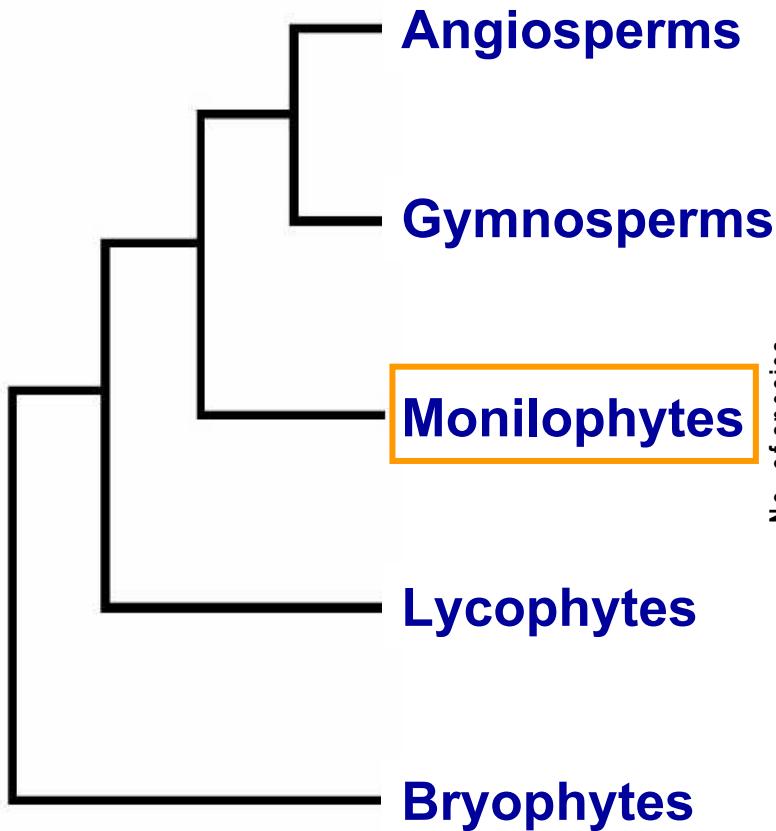
Mean: 17.0 pg

Range: 2.25 – 36.0 pg

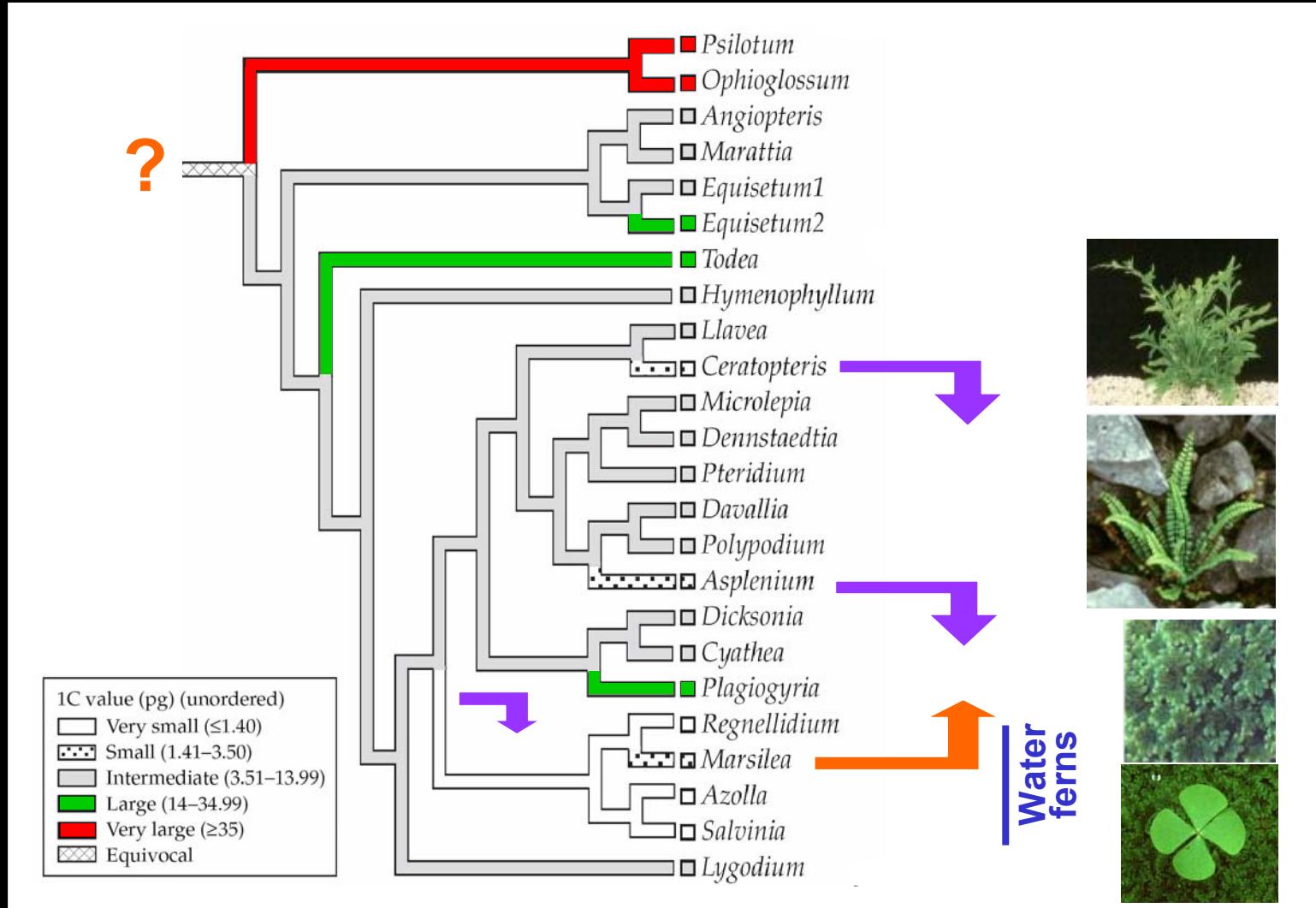
Reconstruction of genome size diversification across gymnosperms



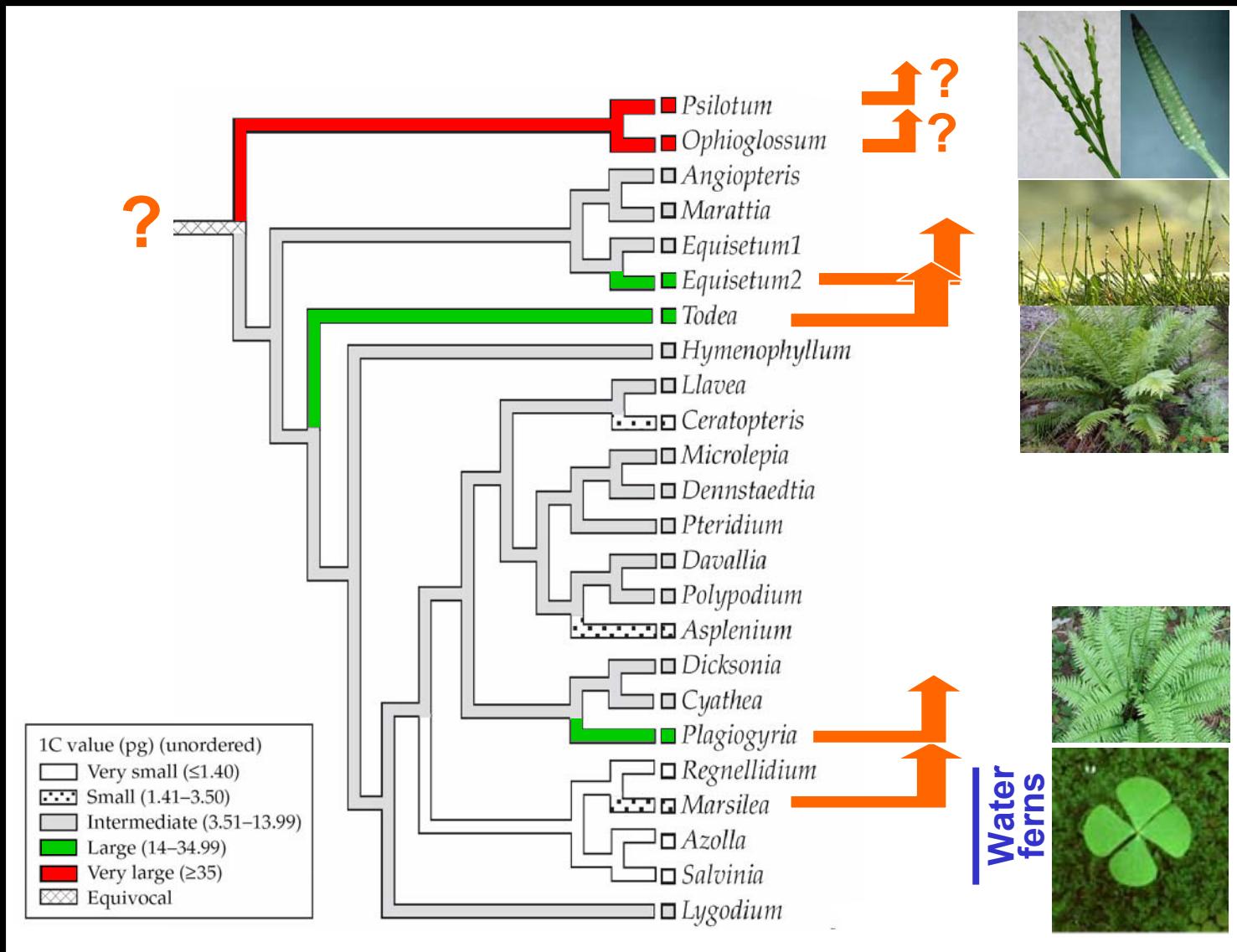
Land plant phylogeny



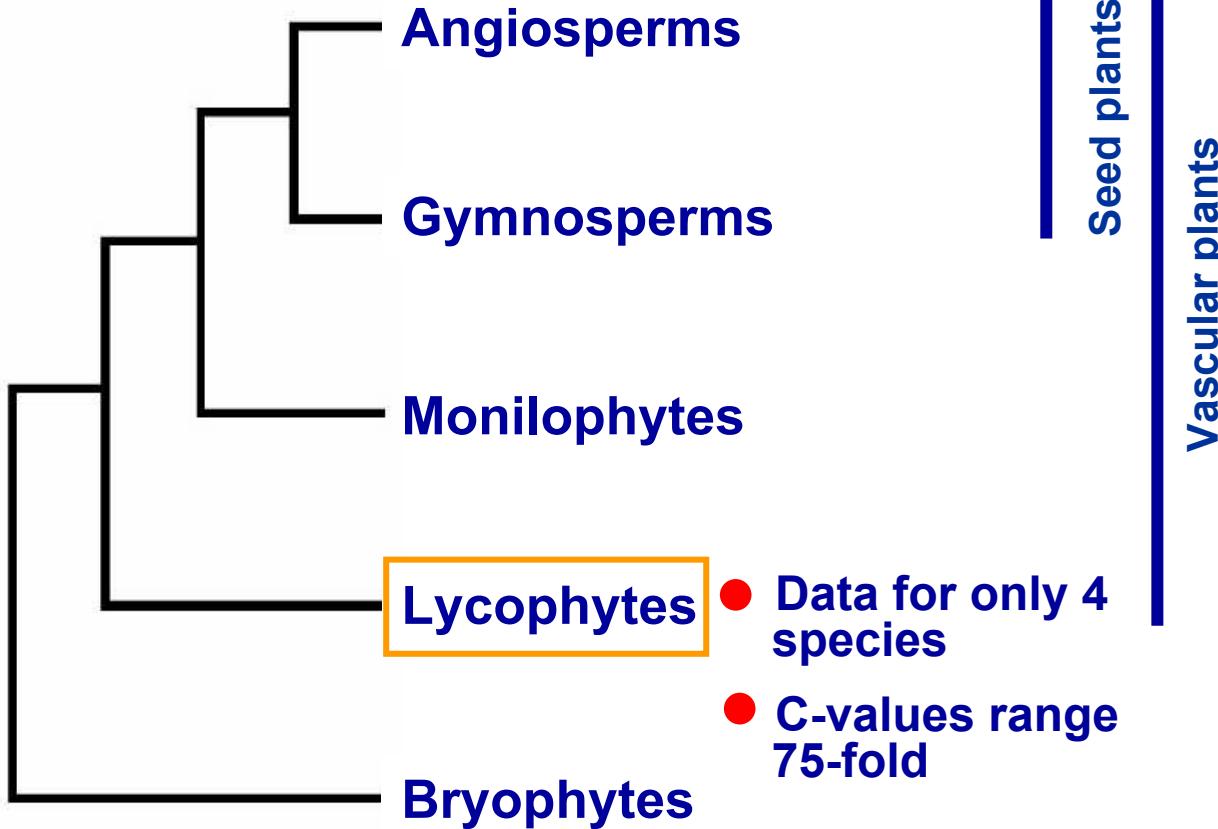
Reconstruction of genome size diversification across monilophytes



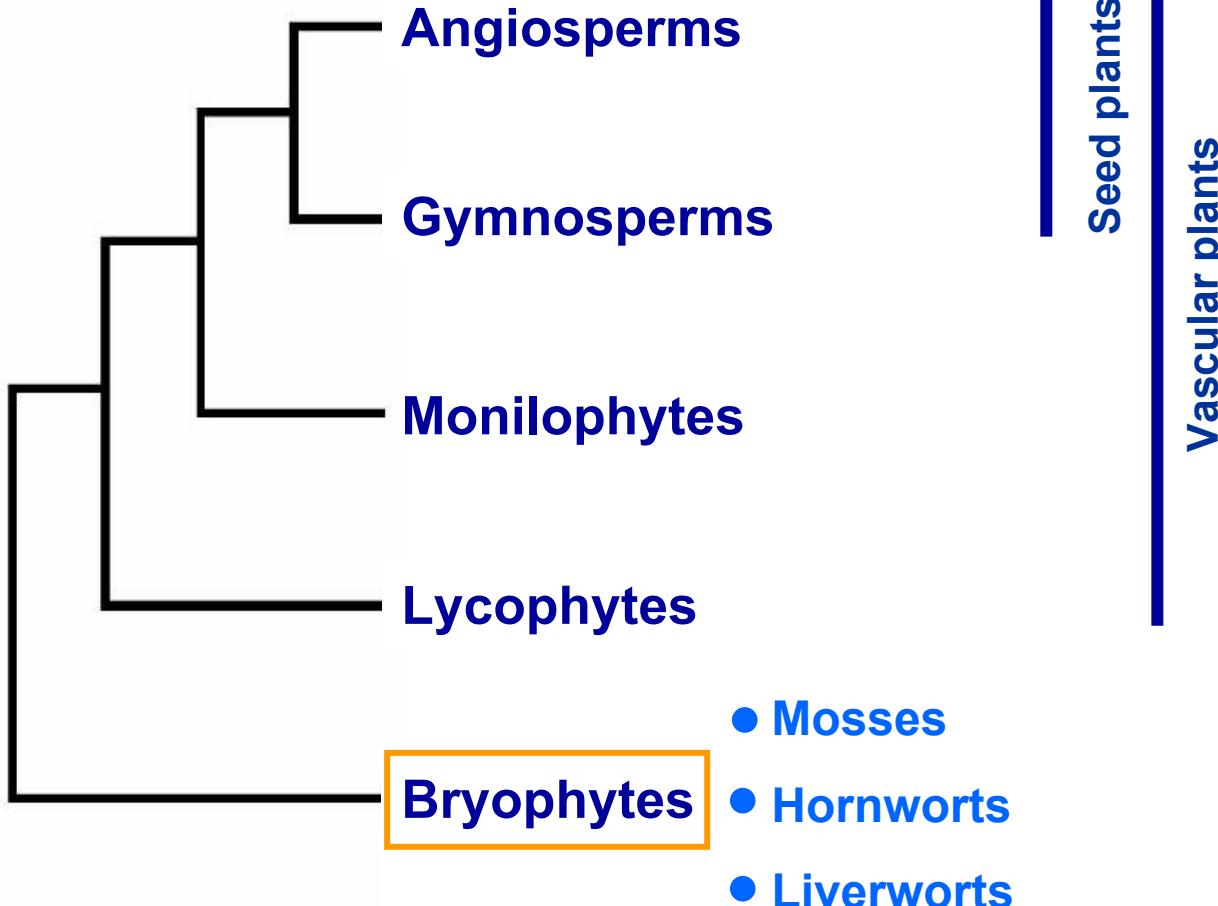
Reconstruction of genome size diversification across monilophytes



Land plant phylogeny



Land plant phylogeny



C-values in mosses

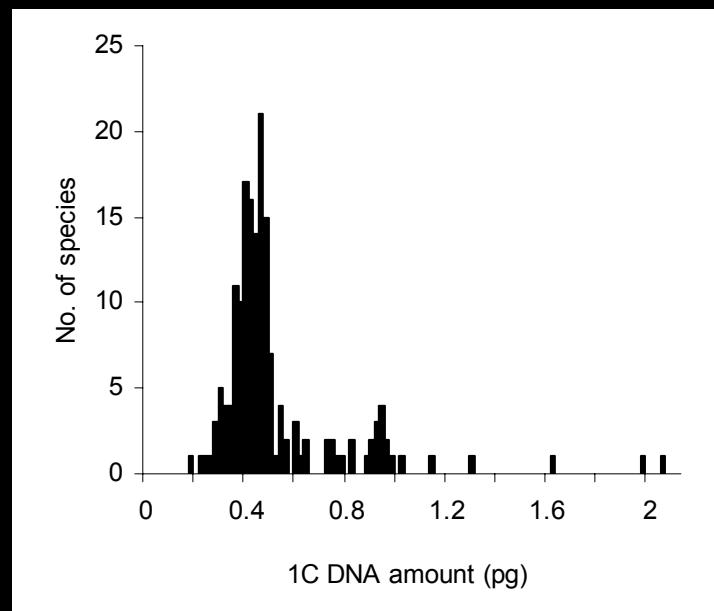
No. Moss species with data = 176

Range: c. 12-fold

Min.: 0.17 pg in *Holomitrium arboreum*

Max.: 2.01 pg in *Mnium marginatum*

Mode: 0.45 pg



Data from: Voglmayr H. 2000. *Annals of Botany* 85: 531-546.

C-values in hornworts



Anthoceros agrestis

1C = 0.087 pg

C-values in liverworts



Pellia endiviifolia

1C = c. 3.3 & 7.1 pg



Plagiochila asplenoides 1C = c. 1.4 & 3.1 pg



Mylia taylorii

1C = 6.4 pg

Genome size evolution across land plants

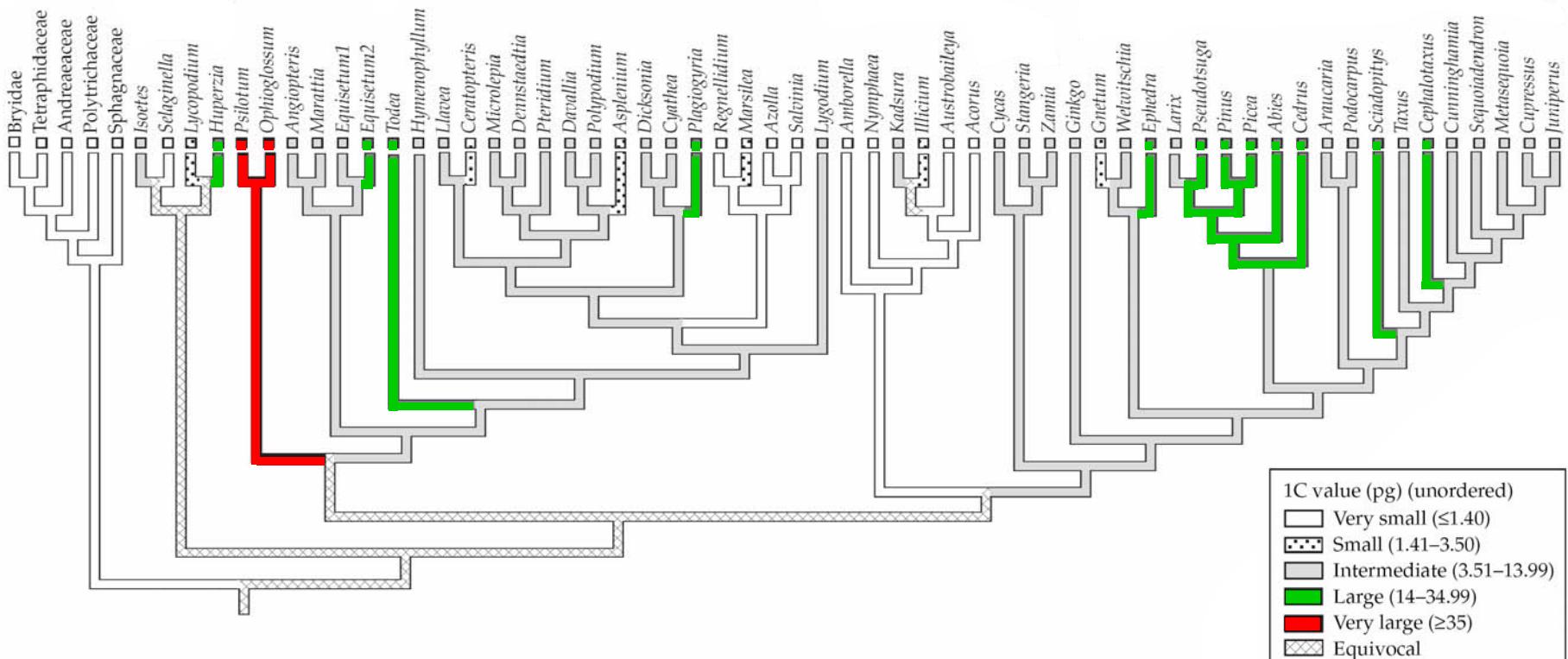


Mosses **Lyc.**

Monilophytes

Angios.

Gymnosperms



Modified from Leitch *et al.* 2005. Ann Bot 95: 207–217.

Analysis of genome size as a continuously varying character

‘Continuous’

- Mode (punctuated or gradual)
- Tempo (recent or adaptive radiation)
- Ancestral genome size reconstructed

Pagel M. 1999. *Nature* 401: 877-844.

.....

‘Analysis of traits’ (AOT) in Phylocom

- Identifies nodes in phylogenetic tree which contribute significantly to observed pattern of genome size evolution

Ackerly DD. 2006. <http://www.phyldiversity.net/phylocom>

Analysis of genome size as a continuously varying character

GENOME SIZE EVOLUTION IN LILIACEAE

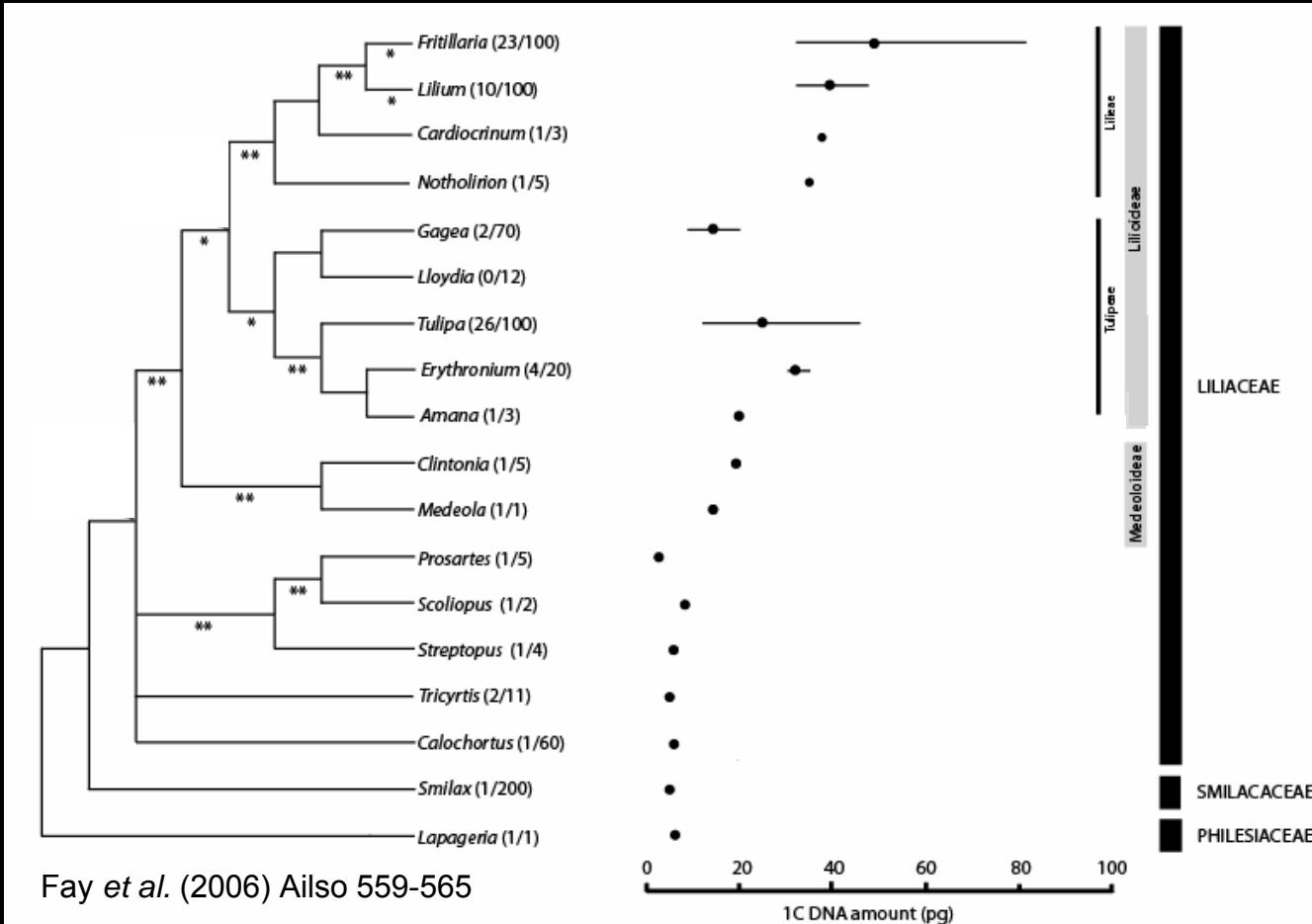
Data:

32 new C-value estimates

46 estimates from the Plant DNA C-values database

Leitch IJ, Beaulieu JM, Cheung K, Hanson L, Lysak MA & Fay MF
Punctuated genome size evolution in Liliaceae.
J Evol Biol (online 2007)

Genome size evolution in Liliaceae



Tempo of evolution:

Accelerated rather than slow

Genome size evolution in *Orobanche*



Weiss-Schneeweiss H, Greilhuber J,
Schneeweiss GM. 2005.

Genome size evolution in holoparasitic *Orobanche* (Orobanchaceae) and related genera.

American Journal of Botany 93: 148-156.

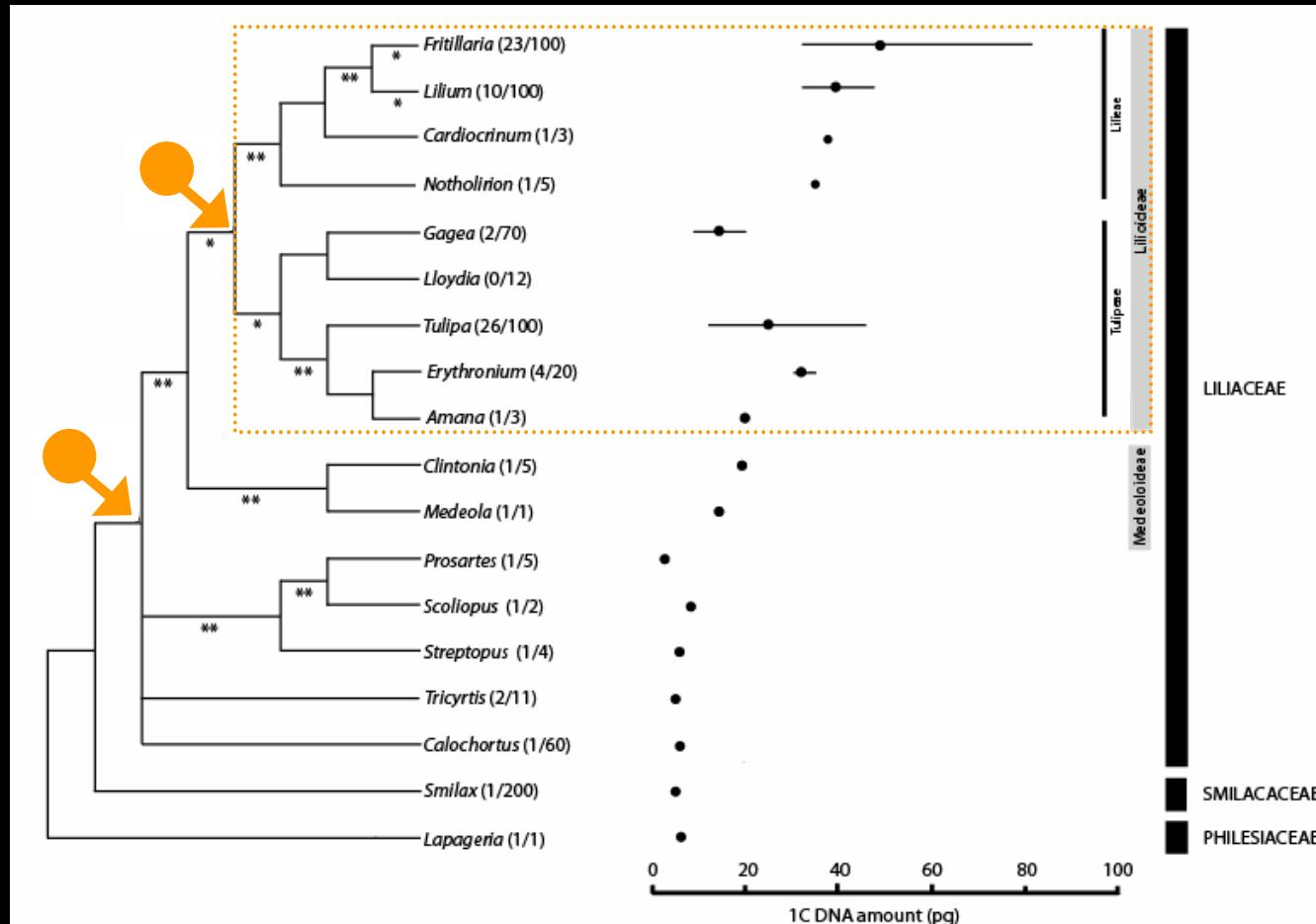
Mode of evolution:

Punctuated rather than gradual

Tempo of evolution:

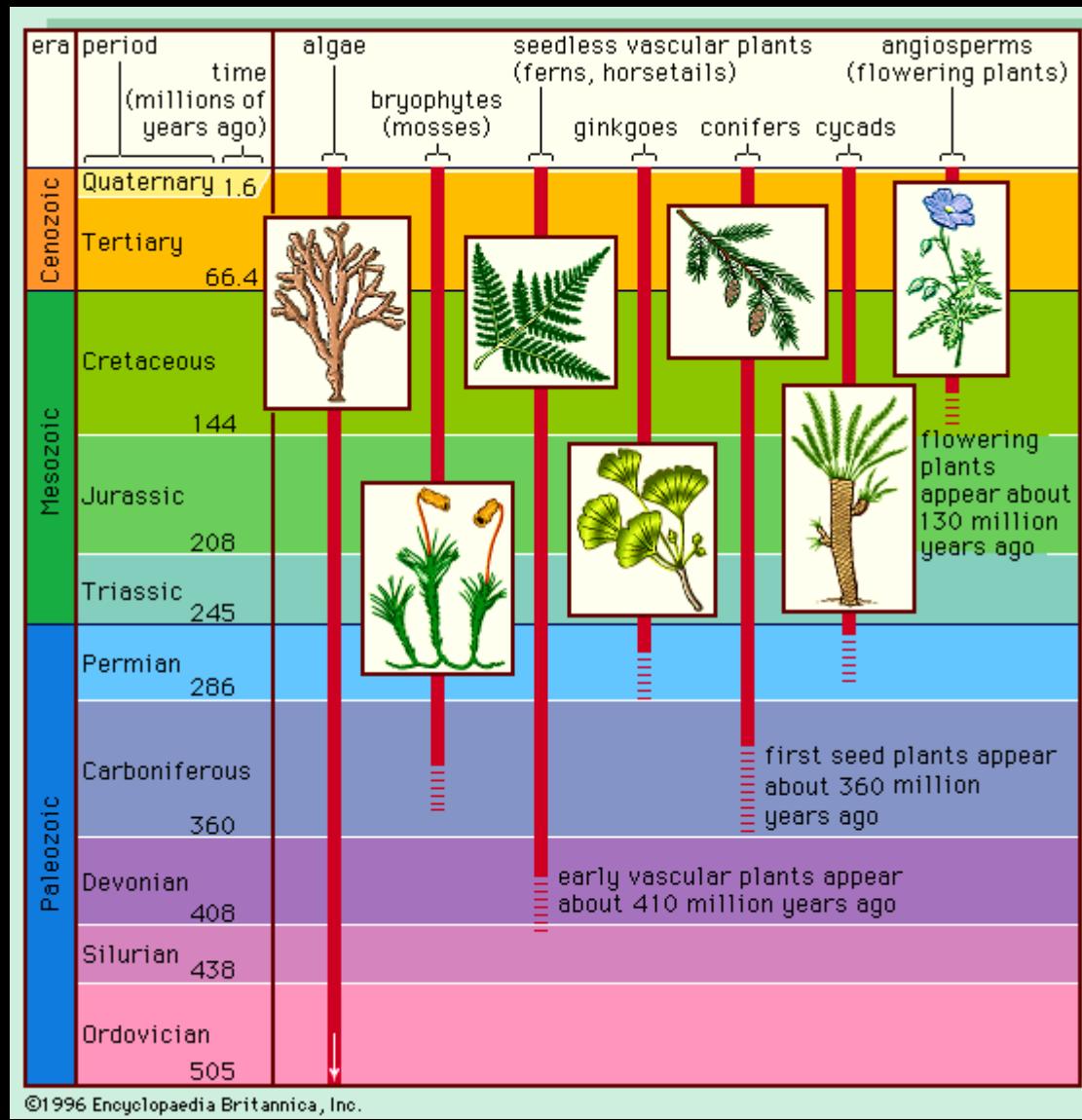
Slow rather than accelerated

Genome size evolution in Liliaceae

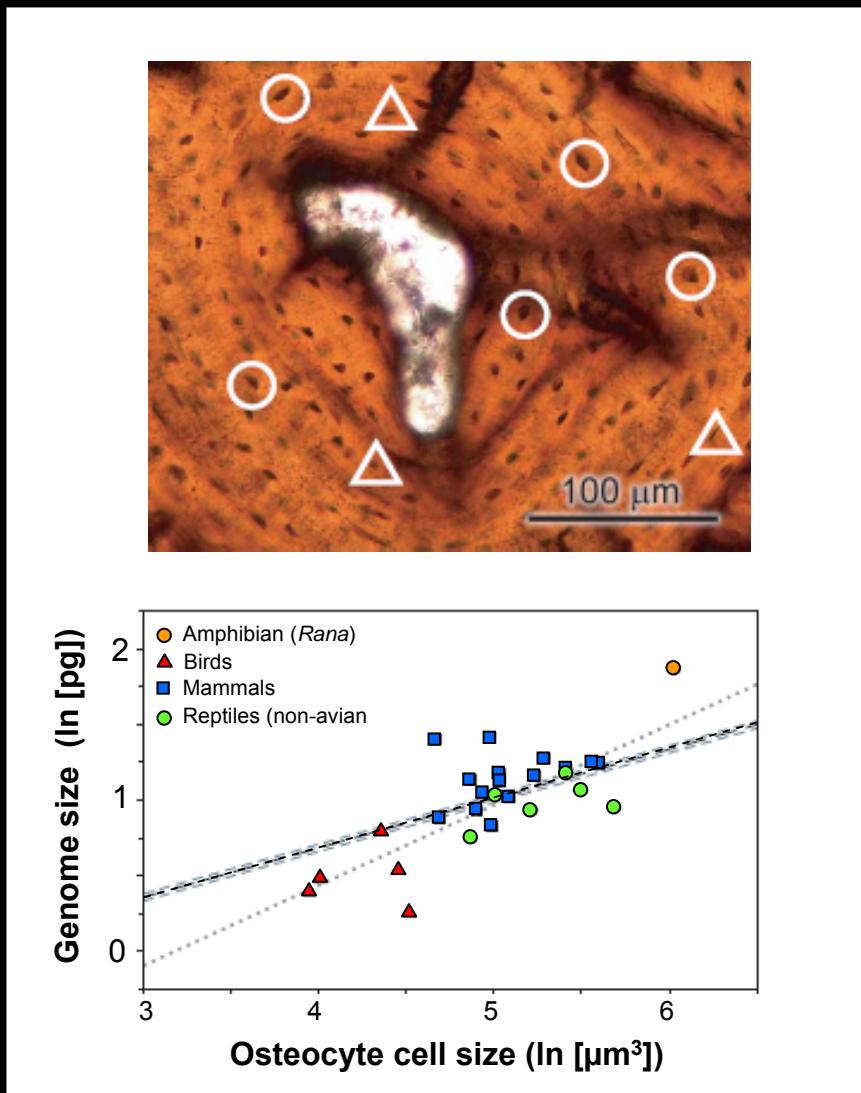


‘Analysis of traits’ module in Phylocom

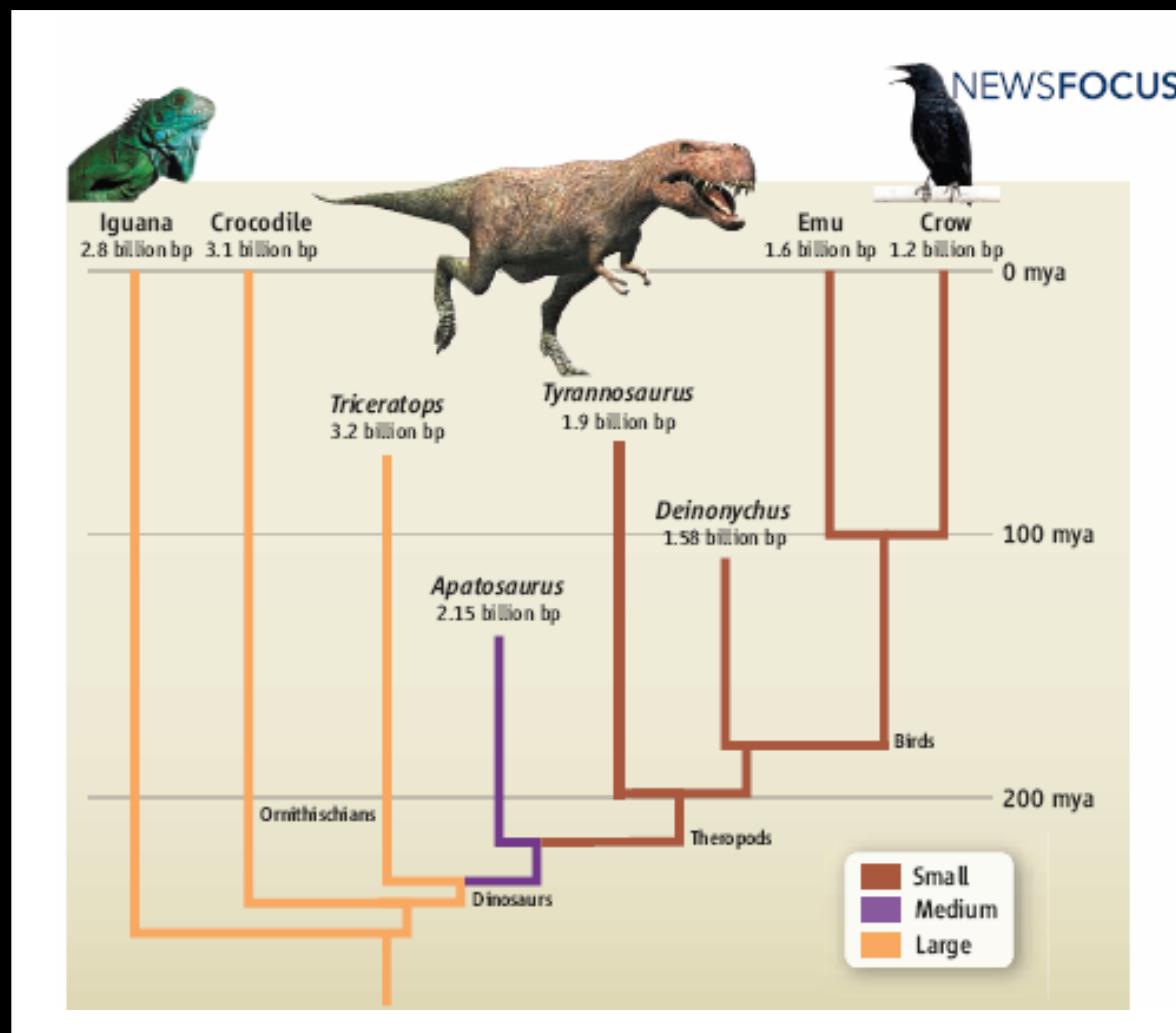
Genome size evolution across land plants



Tracking genome size evolution in fossils

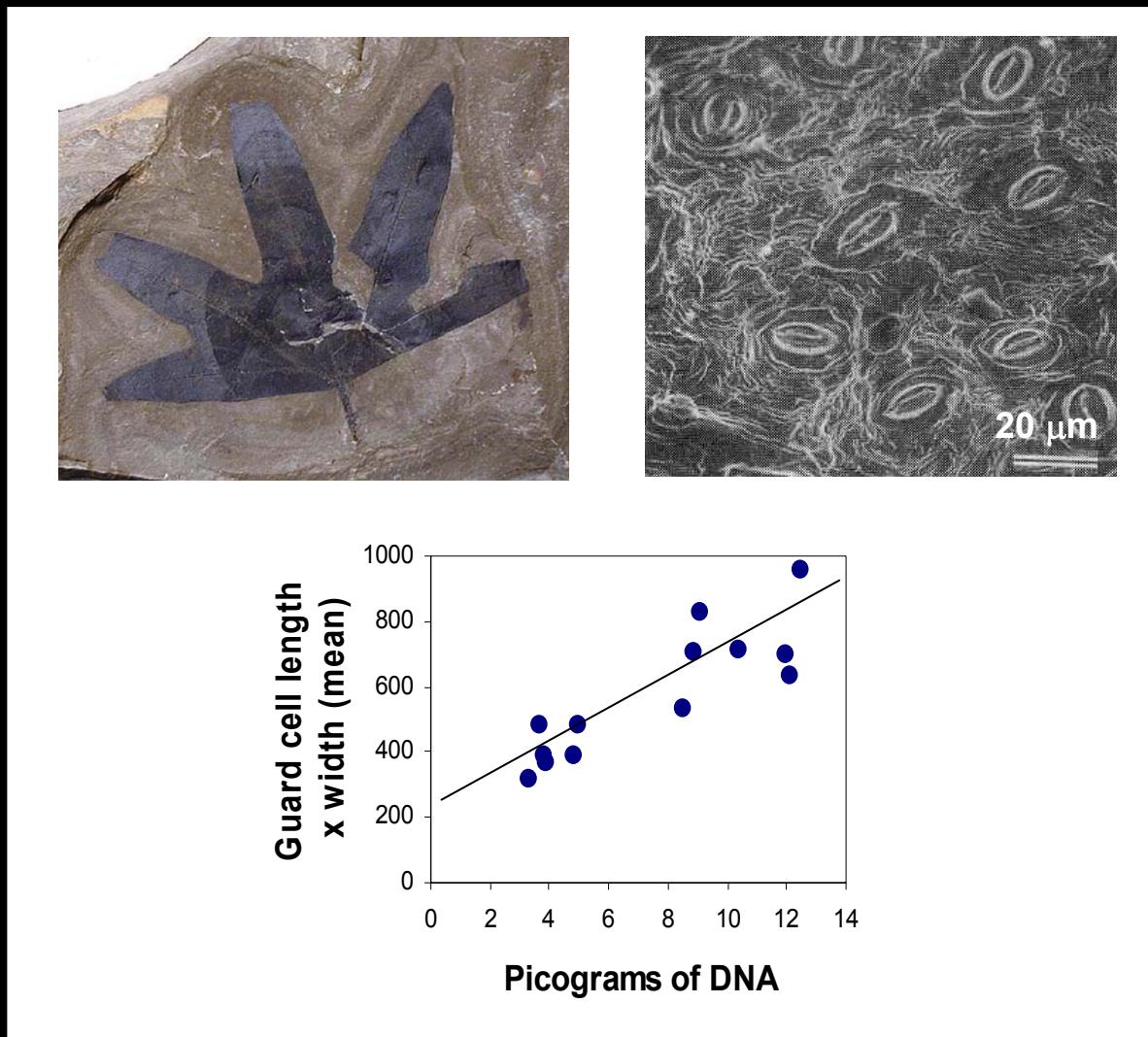


Tracking genome size evolution in fossils



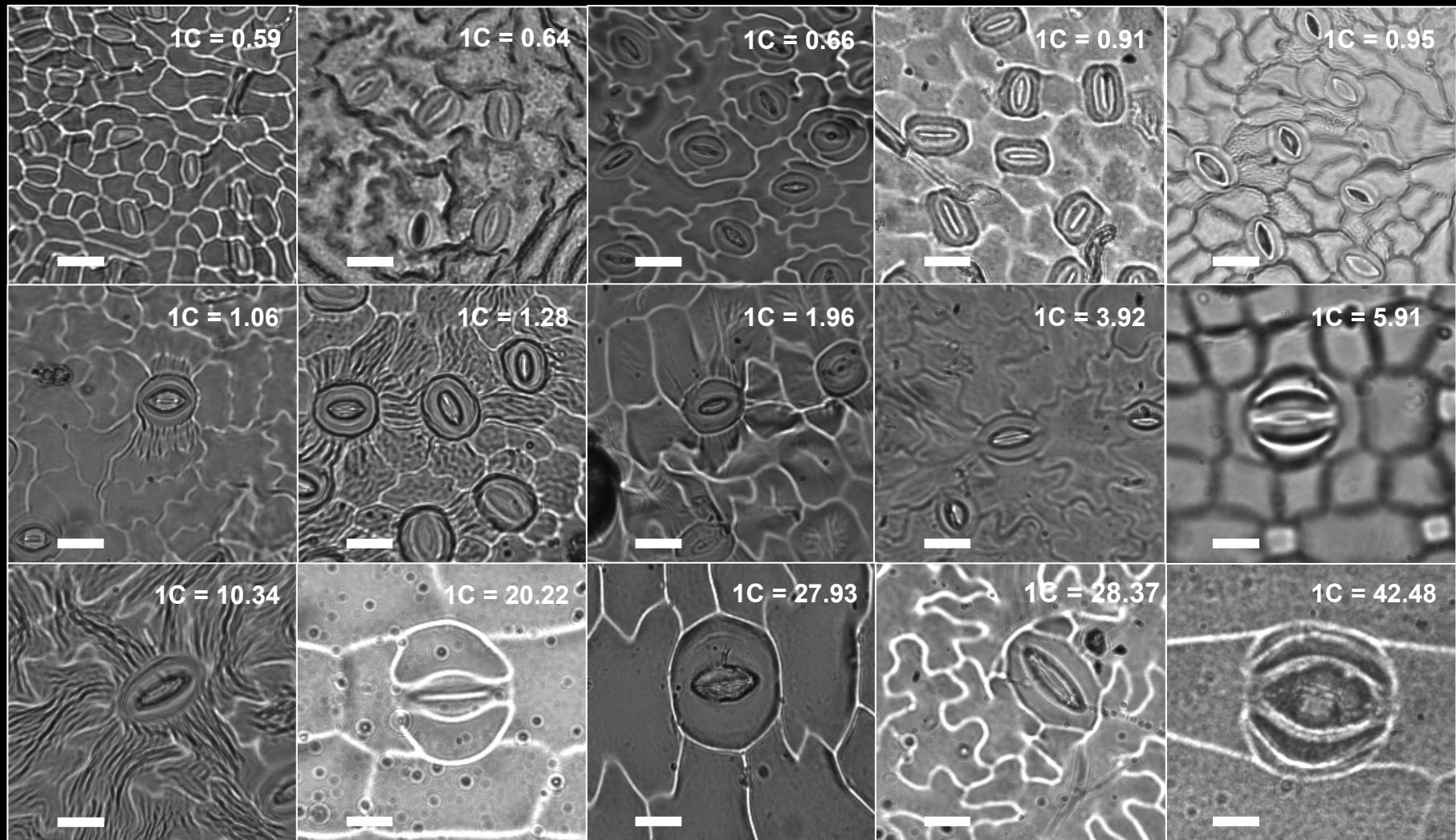
Modified from Organ *et al.* 2007. Nature 446: 180-184

Tracking genome size evolution in fossils



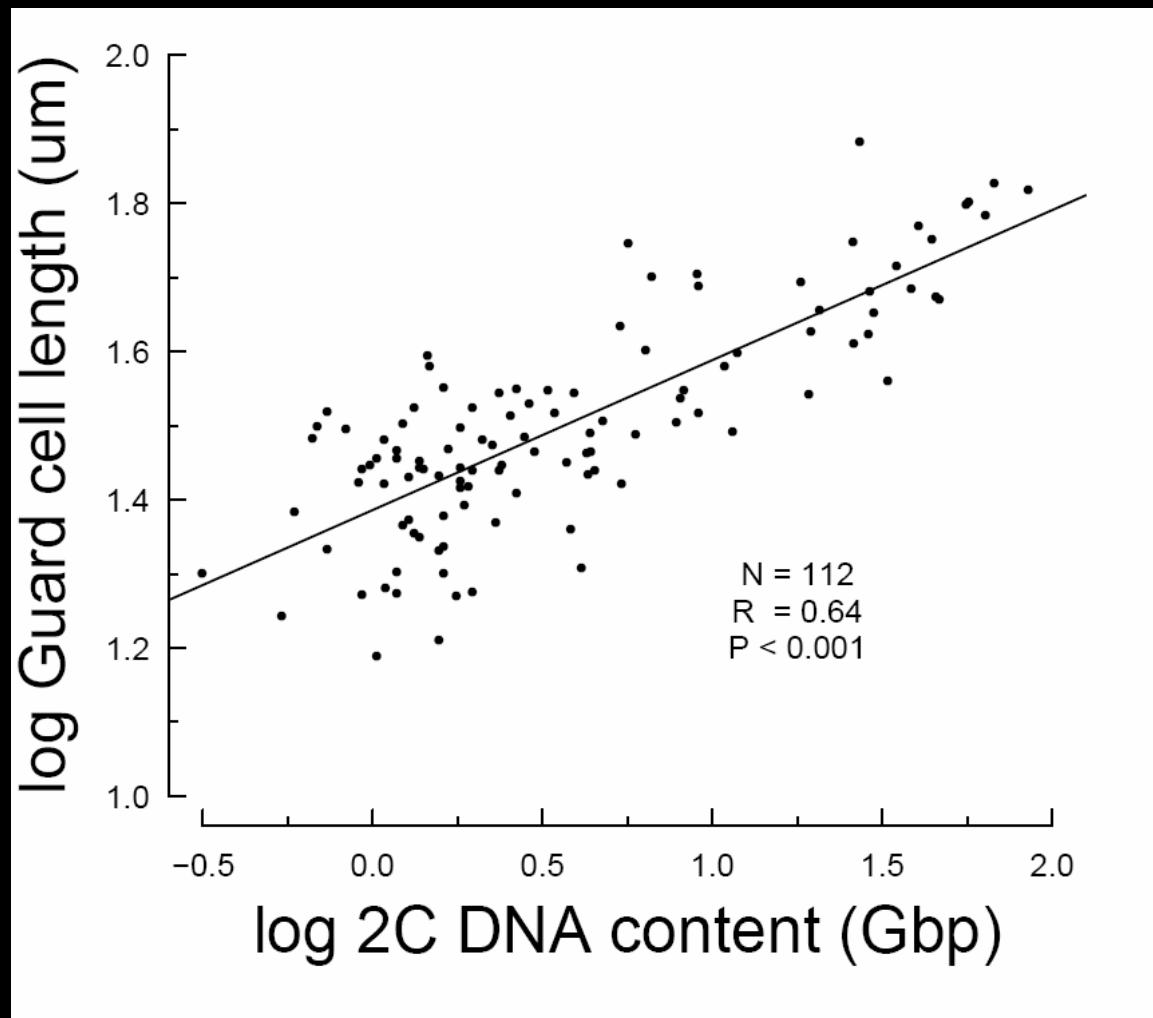
From: Masterson J. 1994. Stomatal size in fossil plants - evidence for polyploidy in majority of angiosperms. *Science*, **264**: 421-424

Tracking genome size evolution



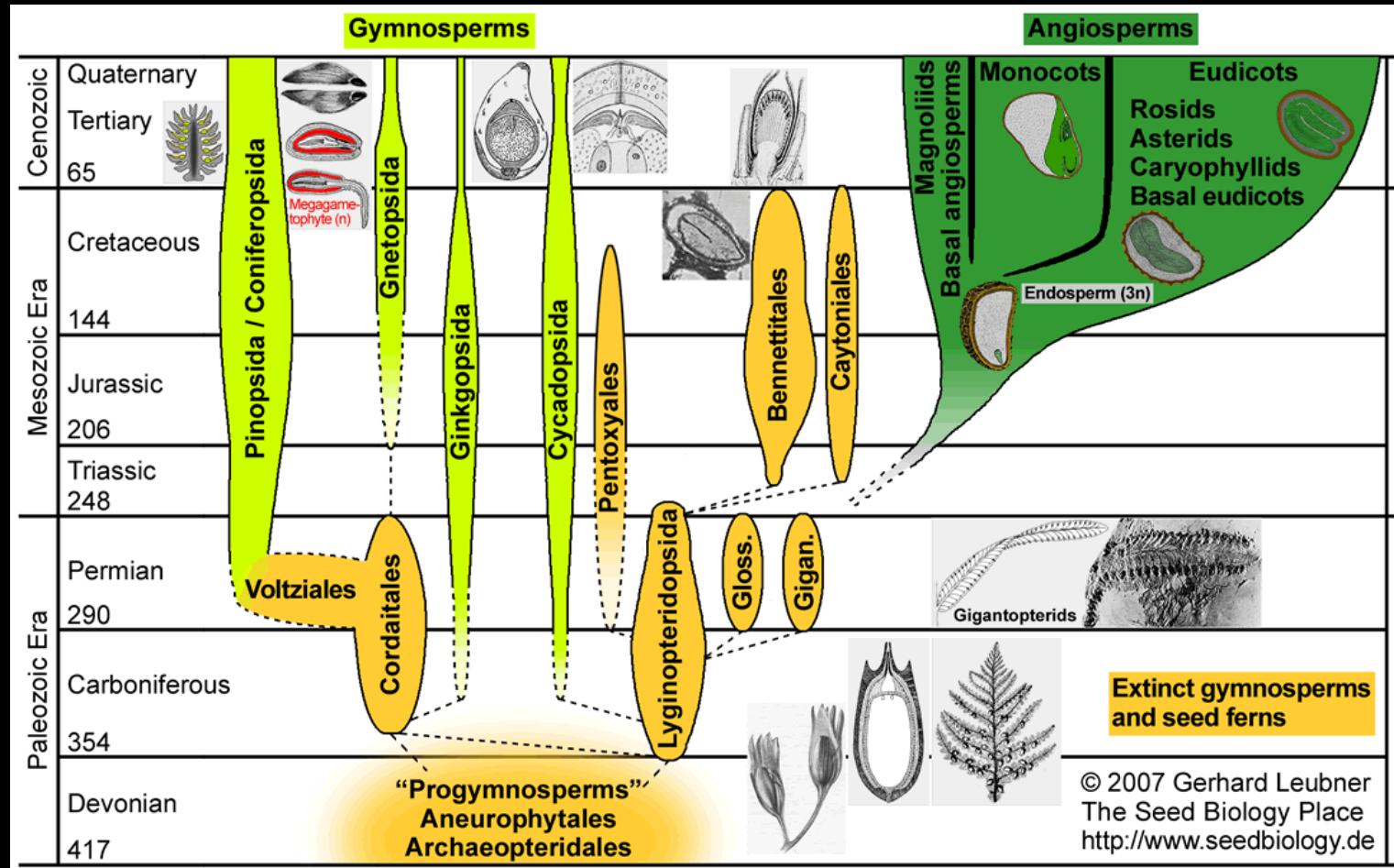
Unpublished data from Beaulieu, Knight and Leitch

Tracking genome size evolution

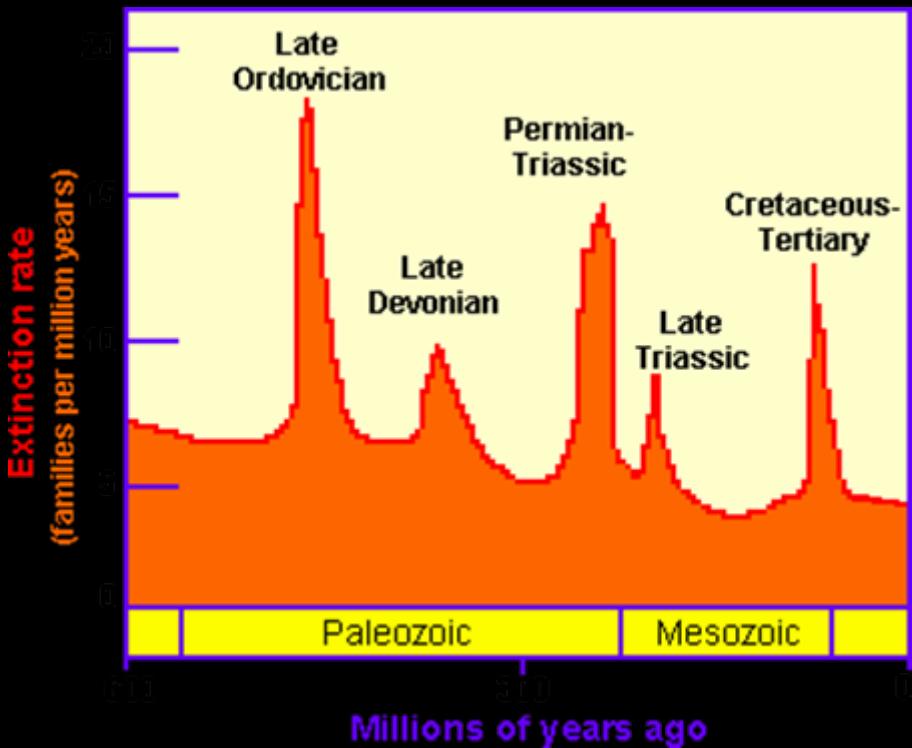


Unpublished data from Beaulieu, Knight and Leitch

Tracking genome size over land plant evolution



Tracking genome size over mass extinctions



Acknowledgements

Jodrell Laboratory, Royal Botanic Gardens, Kew, UK

Mike Bennett

Mike Fay

Lynda Hanson

Masaryk University, Brno, Czech Republic

Martin Lysak

California Polytechnic State University, USA

Charley Knight

Arjun Pendharkar

Biological Sciences, Yale University, USA

Jeremy Beaulieu