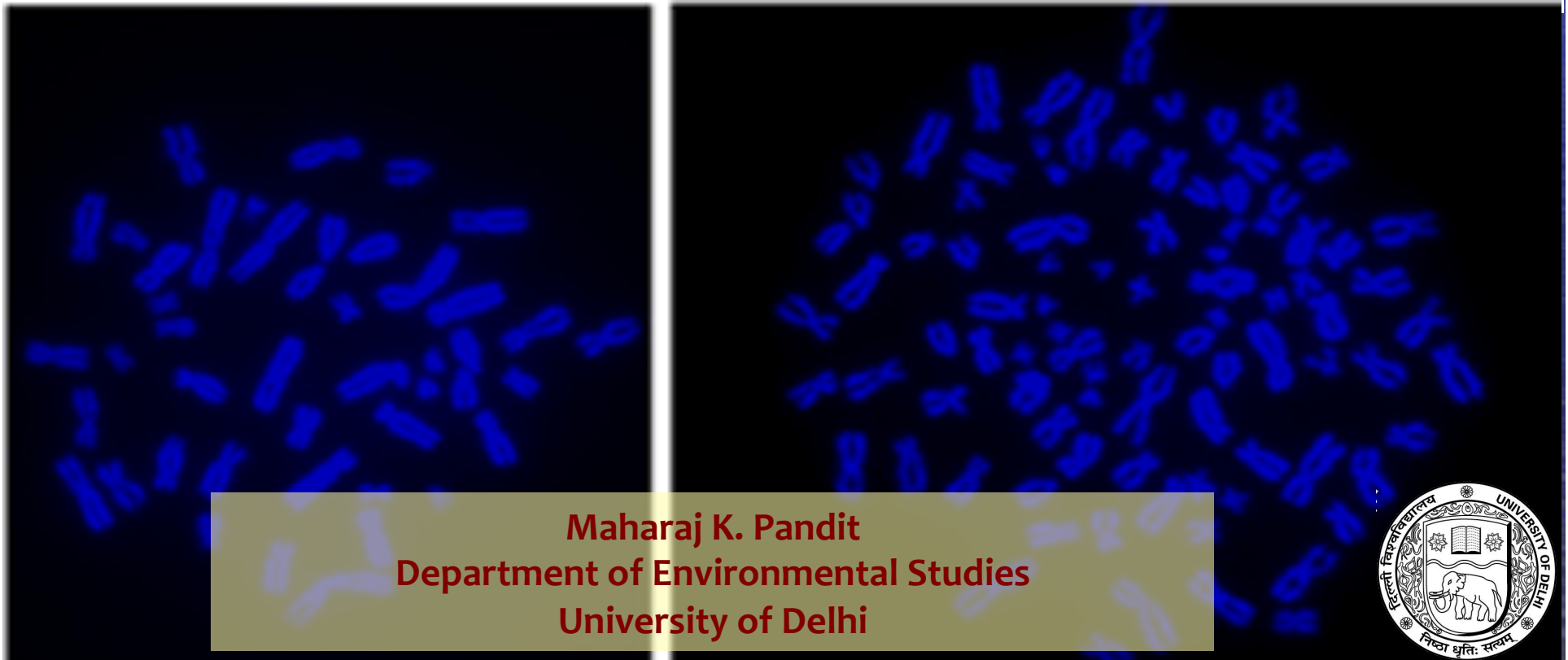
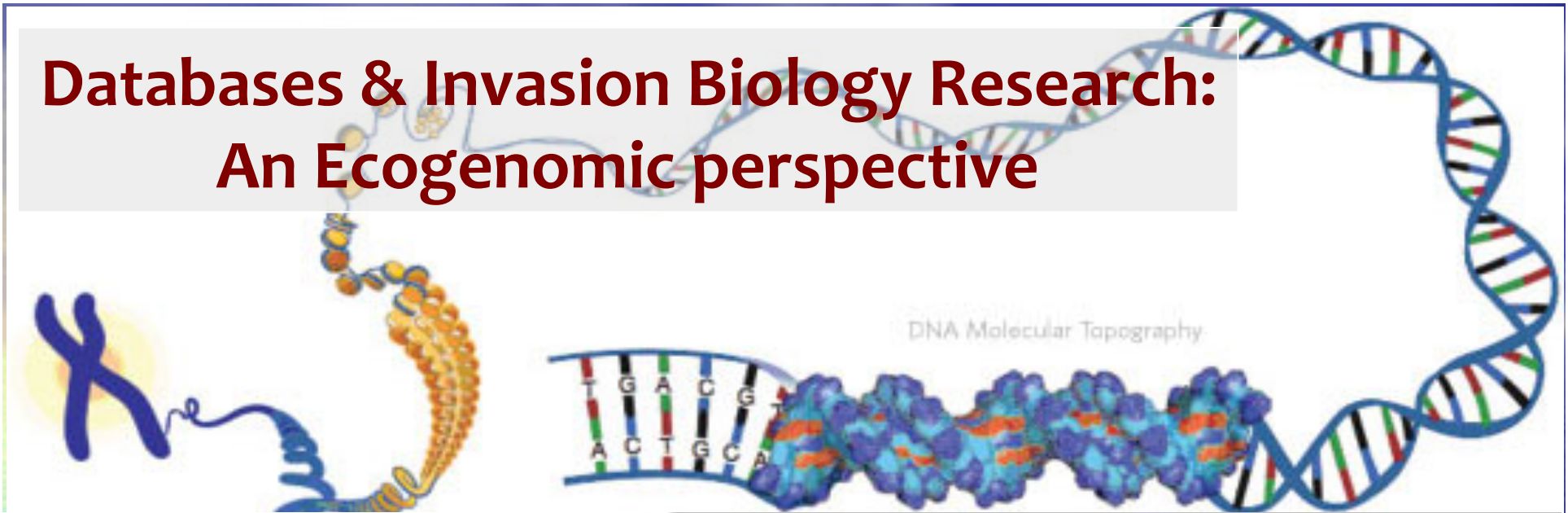


Databases & Invasion Biology Research: An Ecogenomic perspective



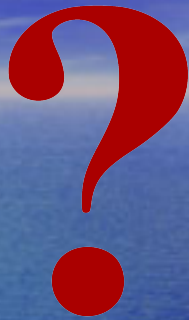
Maharaj K. Pandit
Department of Environmental Studies
University of Delhi



The Outline

- Why database?
- I had a Question for myself?
- Phylogenetic and Ecological
- The present approach
- The genetic & genomic traits
- Results – General Theory
- Databases – Research & Policy

First Bioinformatics Crisis!



“Taxonomy, the classification of living things, has its origins in ancient Greece and in its modern form dates back nearly 250 years, to when Linnaeus [1707 – 1778] introduced the binomial classification still used today. Linnaeus, of course, hugely underestimated the number of plants and animals on Earth. As subsequent workers began to describe more and more species, often in ignorance of each others’ work, the resulting confusion and chaos threatened to destroy the whole enterprise while still in its infancy. In today’s jargon, we might call this the first bioinformatics crisis.”

H. Charles J. Godfray, 2002

Second Bioinformatics Crisis!

commentary

Challenges for taxonomy

The discipline will have to reinvent itself if it is to survive and flourish.

H. Charles J. Godfray

NATURE | VOL 417 | 2 MAY 2002 | www.nature.com

GenBank Management

File Search Help

GenBank Feature Search

Accession: NC_05298

Organism: mitochondrion Saccopharynx leventbergi (Leven...)

Sequence Type: CDS

Gene/Product: ND1, ND2, ND5, ATP8, COX1, COX2

Path:

Strand Type: all

Export Feature Sequences ...

Export Protein Sequences ...

Apply Filter

Reset Filter

Accession Id	Gene Id	Organism	Sequence Type	Gene/Product	Start Position	End Position	Strand Type
1 NC_05298	39841620	mitochondrion Saccopharynx leventbergi (Leven...	CDS	ND1	2845	3813	normal
2 NC_04386	25057347	mitochondrion Hypotherina tsurugae (cobaltcap...	CDS	ND1	2861	3835	normal
3 NC_05513	40804706	mitochondrion Auxis rochei (bullet tuna)	CDS	ND1	3955	4000	normal
4 NC_04386	25057347	mitochondrion Hypotherina tsurugae (cobaltcap...	CDS	ND2	4048	5094	normal
5 NC_05298	39841620	mitochondrion Saccopharynx leventbergi (Leven...	CDS	ATP8	4098	4265	normal
6 NC_05298	39841620	mitochondrion Saccopharynx leventbergi (Leven...	CDS	ATP8	4256	4937	normal
7 NC_05513	40804706	mitochondrion Auxis rochei (bullet tuna)	CDS	ND2	4883	5928	normal
8 NC_04386	25057347	mitochondrion Hypotherina tsurugae (cobaltcap...	CDS	COX1	5483	7033	normal
9 NC_05513	40804706	mitochondrion Auxis rochei (bullet tuna)	CDS	COX1	6317	7967	normal
10 NC_05298	39841620	mitochondrion Saccopharynx leventbergi (Leven...	CDS	ND5	6826	8679	normal
11 NC_04386	25057347	mitochondrion Hypotherina tsurugae (cobaltcap...	CDS	COX2	7206	7896	normal
12 NC_04386	25057347	mitochondrion Hypotherina tsurugae (cobaltcap...	CDS	ATP8	7971	8138	normal
13 NC_05513	40804706	mitochondrion Auxis rochei (bullet tuna)	CDS	COX2	8023	8713	normal
14 NC_04386	25057347	mitochondrion Hypotherina tsurugae (cobaltcap...	CDS	ATP8	8129	8812	normal
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19 NC_04386	25057347	mitochondrion Hypotherina tsurugae (cobaltcap...	CDS	ND5	11969	13807	normal
20 NC_05513	40804706	mitochondrion Auxis rochei (bullet tuna)	CDS	ND5	12790	14628	normal
21 NC_05298	39841620	mitochondrion Saccopharynx leventbergi (Leven...	CDS	COX2	13749	14439	normal

1777p5rLC AGACTAAAGCAAAGCTTGGATTCAAAGCTGGTGTAAAGATTACAAATTCGATTATTATATCTCTAACTATGAAACCAAGATACGATATCTTGGCAGCATTCGAGTAACTCTT

1780p3rLC AGACTAAAGCAAAGCTTGGATTCAAAGCTGGTGTAAAGATTACAAATTCGATTATTATATCTCTAACTATGAAACCAAGATACGATATCTTGGCAGCATTCGAGTAACTCTT

1804p3rLC AGACTAAAGCAAAGCTTGGATTCAAAGCTGGTGTAAAGATTACAAATTCGATTATTATATCTCTAACTATGAAACCAAGATACGATATCTTGGCAGCATTCGAGTAACTCTT

1777p5rLC AGACTAAAGCAAAGCTTGGATTCAAAGCTGGTGTAAAGATTACAAATTCGATTATTATATCTCTAACTATGAAACCAAGATACGATATCTTGGCAGCATTCGAGTAACTCTT

1752p5rLC AGACTAAAGCAAAGCTTGGATTCAAAGCTGGTGTAAAGATTACAAATTCGATTATTATATCTCTAACTATGAAACCAAGATACGATATCTTGGCAGCATTCGAGTAACTCTT

1743p5rLC AGACTAAAGCAAAGCTTGGATTCAAAGCTGGTGTAAAGATTACAAATTCGATTATTATATCTCTAACTATGAAACCAAGATACGATATCTTGGCAGCATTCGAGTAACTCTT

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1780p3rLC CACGAAAAATCAATTTATTGCTTATGACCTTATCCTTTAGACCTTTTGAAGAAAGCTTCAGTTACTAACATGTTTACTTCCATTGCGGTAATGTTTTTGGGTTCAAAGCCCTGCG

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1777p5rLC CACGAAAAATCAATTTATTGCTTATGACCTTATCCTTTAGACCTTTTGAAGAAAGCTTCAGTTACTAACATGTTTACTTCCATTGCGGTAATGTTTTTGGGTTCAAAGCCCTGCG

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1804p3rLC CACGAAAAATCAATTTATTGCTTATGACCTTATCCTTTAGACCTTTTGAAGAAAGCTTCAGTTACTAACATGTTTACTTCCATTGCGGTAATGTTTTTGGGTTCAAAGCCCTGCG

A Game that Deserves Rules

		pollen ♂	
		B	b
pistil ♀	B	BB	Bb
	b	Bb	bb

$V_1 = 37$
 $g = 37 \frac{3}{4}$
 $gV_1 = 75 \frac{3}{4}$
 $V_1 W = 150$
 $gW = 150$
 $W = 150$

$V_1 + gV_1 = 112 \frac{1}{4}$
 $V_1 W + gW = 300$
 $W = 150$
 $gV_1 = 75 \frac{3}{4}$
 $g = 37 \frac{3}{4}$
 $V = 37$

343 BV dV
 92 B
 86 W

351
 100
 150

$7 \frac{1}{2}$
 $16 \frac{3}{4}$
 $4 \frac{1}{2}$

~~Wald~~
~~Lösche t~~
~~trans~~
~~cris~~

Lösche l
 von durch die Wild mill zu
 Der sich hinhalt bei

$30 = 39 \cdot 296$
 340
 $15 \frac{1}{2}$
 $17 \frac{1}{2}$

$W 150$
 $67 \frac{1}{2}$
 $113 \frac{1}{2}$
 $8V 300$
 $V 37$

$\frac{1}{4}$
 $\frac{1}{2}$
 $\frac{1}{16}$
 $\frac{1}{2}$
 $\frac{1}{16}$


W
 gV_1
 g
 $gW + V_1 W$
 V

75
 150
 $\frac{1}{2}$

Courtesy of the Mendelianum, Moravian Museum, Brno.
Noncommercial, educational use only

	A	a
A	AA	Aa
a	Aa	aa

World's Greatest
1000



Creation Scientists
2000

GREGOR MENDEL

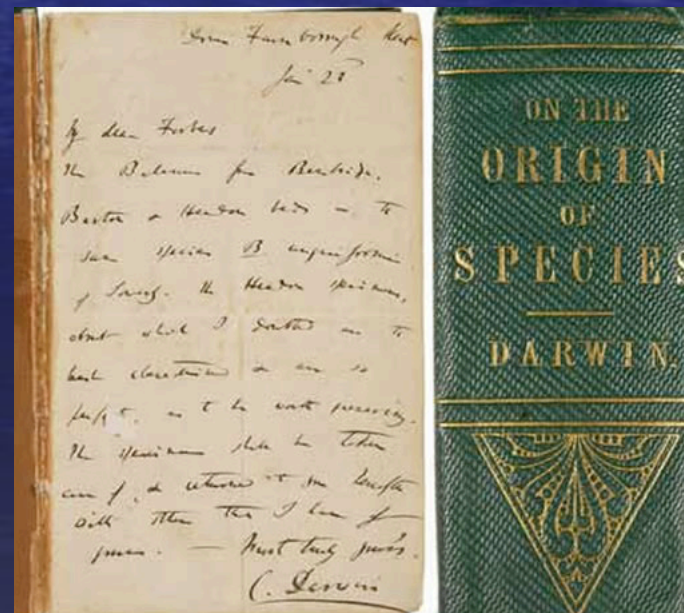
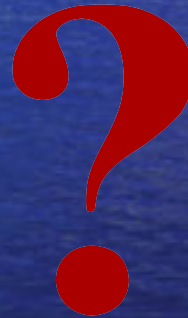
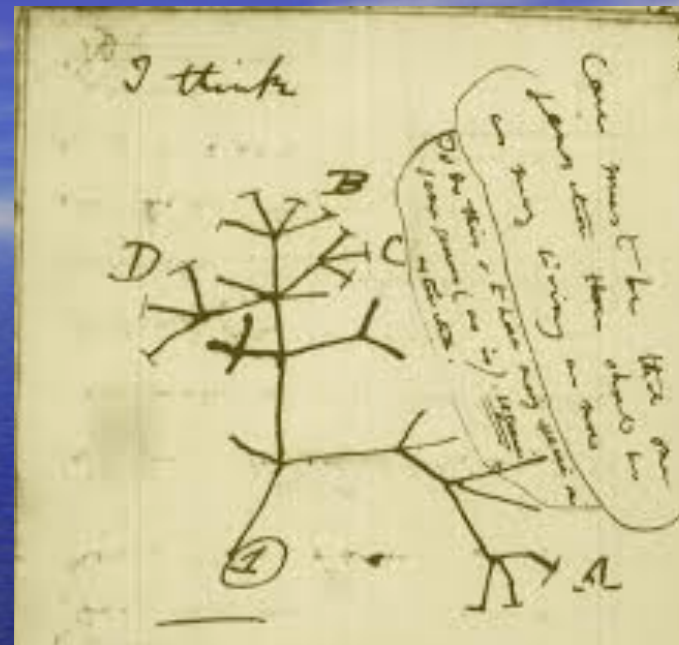
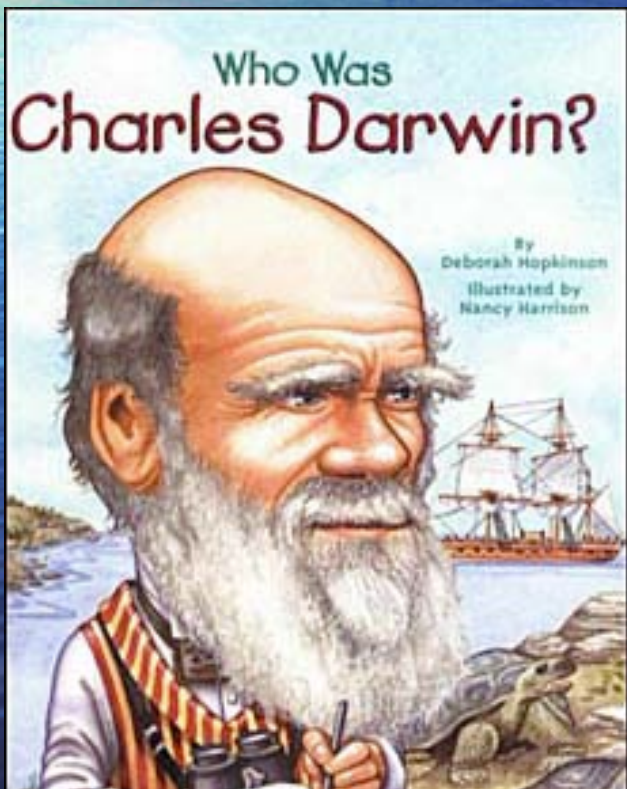
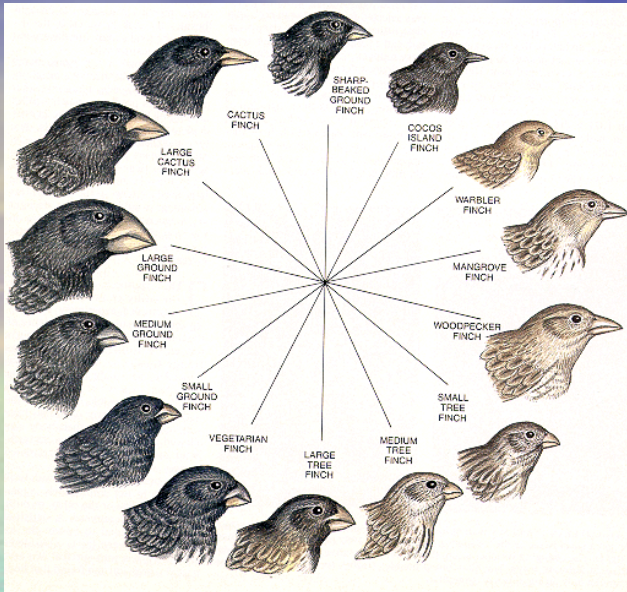
1822 - 1884

Genetics • Botany

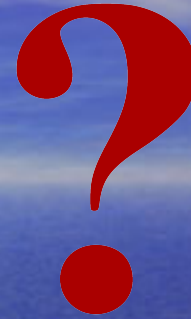
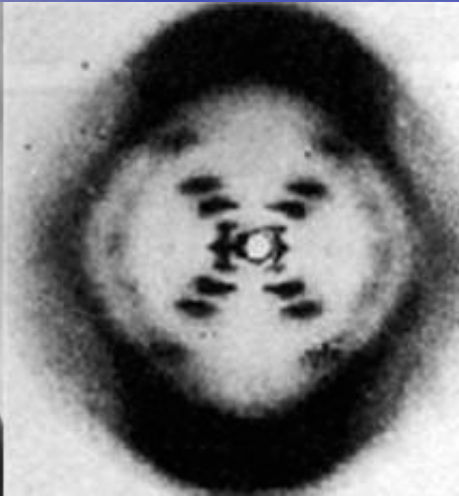
- **“The Father of genetics”**
- **Performed 28,000 tedious cross-breeding experiments with peas**
- **Discovered dominant and recessive genes**
- **Published his work in 1866, seven years after Darwin’s, but ignored for 35 years**



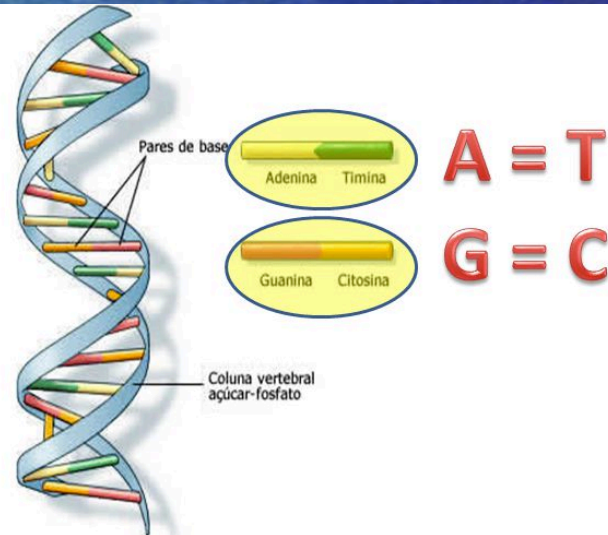
Of Beaks & Finches



Playing by the Rules



Erwin Chargaff (1905-1992)



U.S. National Library of Medicine





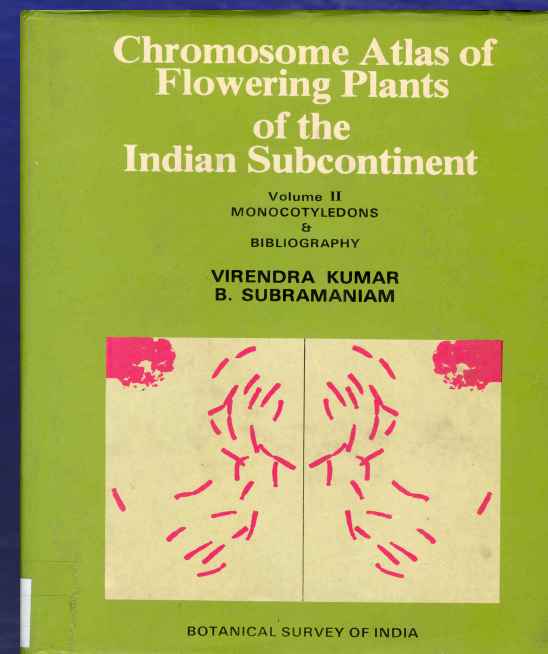
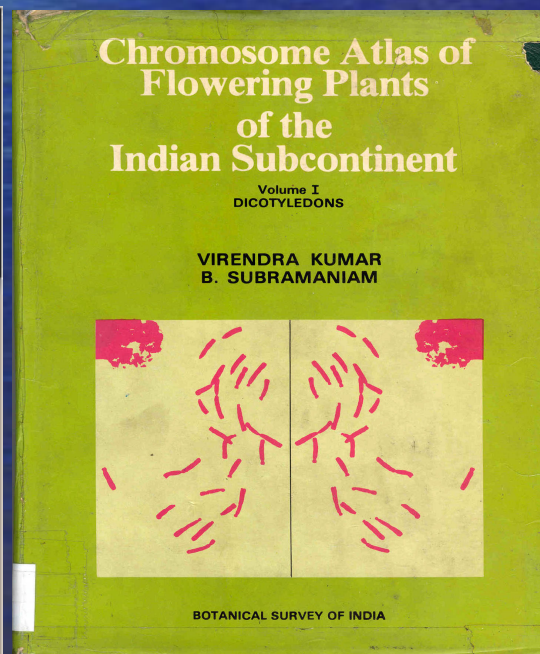
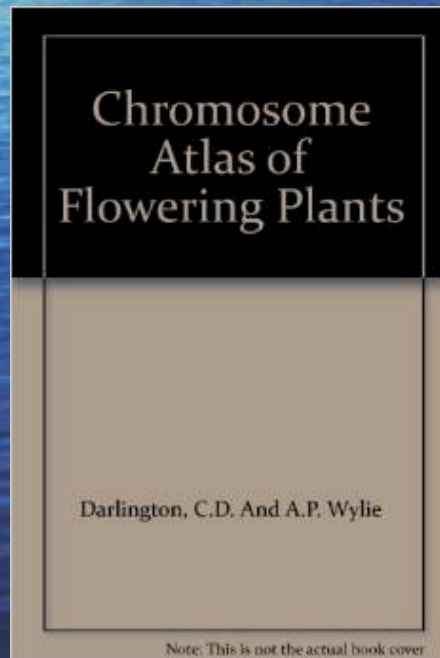
Why are some species rare, while others are invasive ?

- The Phylogenetic Approach
- Ecological Approach [Invasiveness]
 - Allelopathy
 - Soil-microbe interactions
 - Enemy release
 - ECA
- A Different Approach
 - Intuitive - Genetical

Database 1: First Searches

- Begin with home
- Indian endangered/invasives

Fedorov, A. A. (ed.) (1969) Chromosome Numbers of Flowering Plants



Database 2: Rare & Invasives

AGAVACEAE 465

AGAVACEAE Endl.

20/670 ; tropics and subtropics. 9/43 ; hotter parts of India, and Bangla Desh and Sri Lanka - many cultivated.

<p><i>Agave</i> Linn.</p> <p>300 ; Southern United States to tropical South America. 6 ; cultivated and naturalized.</p> <p><i>americana</i> Linn.</p> <p>20 Müller, C. 1912 60 MacKelvey, S.D. & Sax, K. 1933 ; Matsura, H. & Satō, T. 1935</p> <p>60, 120, 180 (118, 119) Granick, E.B. 1944 120 Inariyama, S. 1937 ; Sharma, A.K. & Bhattacharyya, U.C. 1961c</p> <p>120 (44, 96, 104, 110, 115, 125, 135) Sharma, A.K. & Bhattacharyya, U.C. 1962 120, 240 Satō, D. 1935b, 1938, 1942</p> <p><i>cantala</i> Roxb.</p> <p>90 Doughty, L.R. 1936</p> <p><i>sisalana</i> Perr.</p> <p>c. 138 Doughty, L.R. 1936 149 Granick, E.B. 1944 150 Inariyama, S. 1937 ; Vignoli, L. 1937 ; Satō, D. 1938, 1942</p> <p><i>vivipara</i> Linn.</p> <p>60 Satō, D. 1935b, 1938, 1942 ; Mahabale, T.S. & Bhat, F.D. 1941 ; Sharma, A.K. & Bhattacharyya, U.C. 1962</p> <p><i>wightii</i> Drumm. & Prain</p> <p>180 Sharma, A.K. & Bhattacharyya, U.C. 1961c 180 (52) Sharma, A.K. & Bhattacharyya, U.C. 1962</p> <p><i>Cordylone</i> Comm. ex Juss.</p> <p>15 ; tropics and warm temperate. 2 ; cultivated or occur as escapes in the Eastern Himalaya.</p>	<p><i>australis</i> Hook. f.</p> <p>38 Bowden, W.M. 1940a, 1945a ; Rattenbury, J.A. 1957 120 Matsura, H. & Satō, T. 1935</p> <p><i>terminalis</i> (Linn.) Kunth</p> <p>c. 152 Rattenbury, J.A. 1957</p> <p><i>Dracaena</i> Vand. ex Linn.</p> <p>150 ; warm Old World. 9 ; chiefly distributed in Khasi Hills and Andaman Islands, and Bangla Desh - a few cultivated.</p> <p><i>angustifolia</i> Roxb.</p> <p>40 Sarkar, A. K., Mallick, R. et al. 1977</p> <p><i>draco</i> Linn.</p> <p>38 Bowden, W.M. 1940a, 1945a 40 Borgen, L. 1969 ; Bramwell, D. et al. 1972</p> <p><i>metallica</i> Hort.</p> <p>14, 16, 21, 24, 28, 30, 32, 34, 35, 36, 38, 40, 42, 44, 46, 49, 50, 52, 56, 62, 63, 70, 77, 84 Dutta, P.C. 1971a</p> <p><i>tenellifera</i> Roxb.</p> <p>80 Sheriff, A. & Singh, B.K.S. 1973</p> <p><i>Furcraea</i> Vent.</p> <p>20 ; tropical America. 6 ; cultivated, a few naturalized.</p> <p><i>bedinghausii</i> C. Koch</p> <p>60 MacKelvey, S.D. & Sax, K. 1933 ; Whitaker, T.W. 1934</p> <p><i>foetida</i> (Linn.) Haw.</p> <p><i>gigantea</i> Vent.</p> <p>18 Catalano, G. 1930</p>
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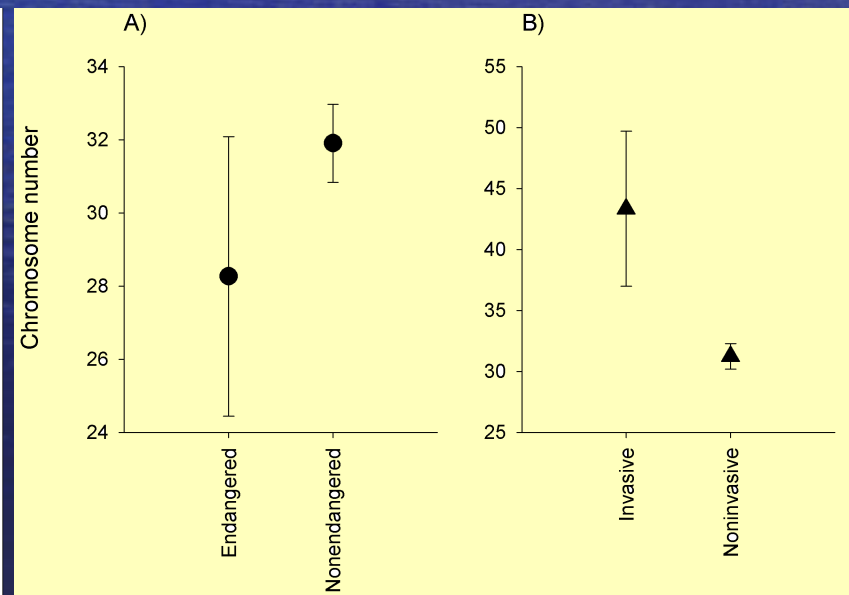
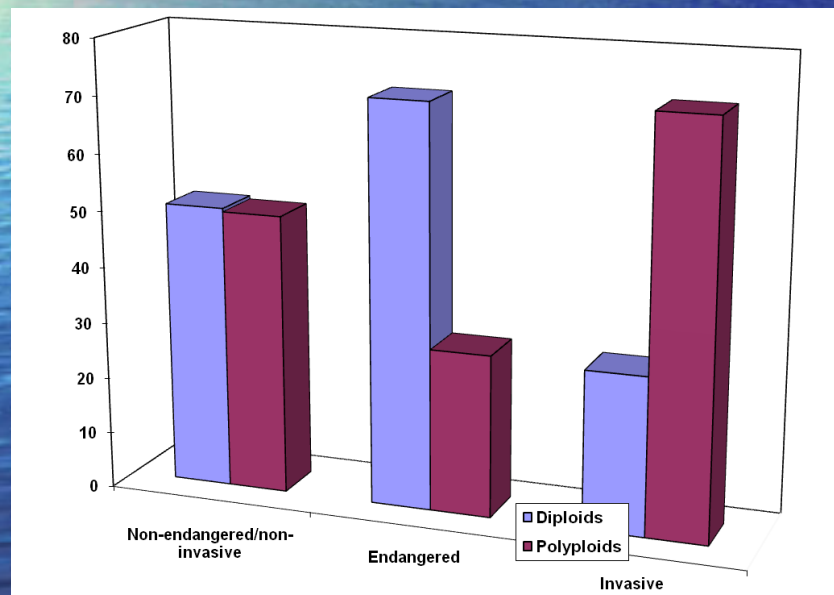
- Compared the preponderance of diploids and polyploids among the endangered species with those of the non-endangered species.
- Performed simple logistic regressions (logit model) of the probability of species endangerment and of species invasiveness as a function of chromosome number.
- Plant family was included to control for the effects of phylogenetic autocorrelation.

First Results

Evolutionary Ecology Research, 2006, 8: 543–552

Continuing the search for pattern among rare plants: are diploid species more likely to be rare?

M.K. Pandit*



Mean chromosome number with error (95% confidence interval) bars (y-axis) for (A) endangered and non-endangered species (x-axis) and (B) invasive and non-invasive species.

How Robust Were the Numbers?

Table 2. Summary of results of the test statistics carried out in this study

Type of test	<i>Z</i>	<i>P</i> -value
Representation of diploids and polyploids in non-endangered species	0.896	0.370
Representation of diploids and polyploids in endangered versus non-endangered/non-invasive species	2.269	0.023*
Representation of diploids and polyploids in invasive versus non-endangered/non-invasive species	3.131	0.001**

* $P < 0.05$; ** $P < 0.01$.

Pandit, 2006

Sure it was Not Phylogenetic?

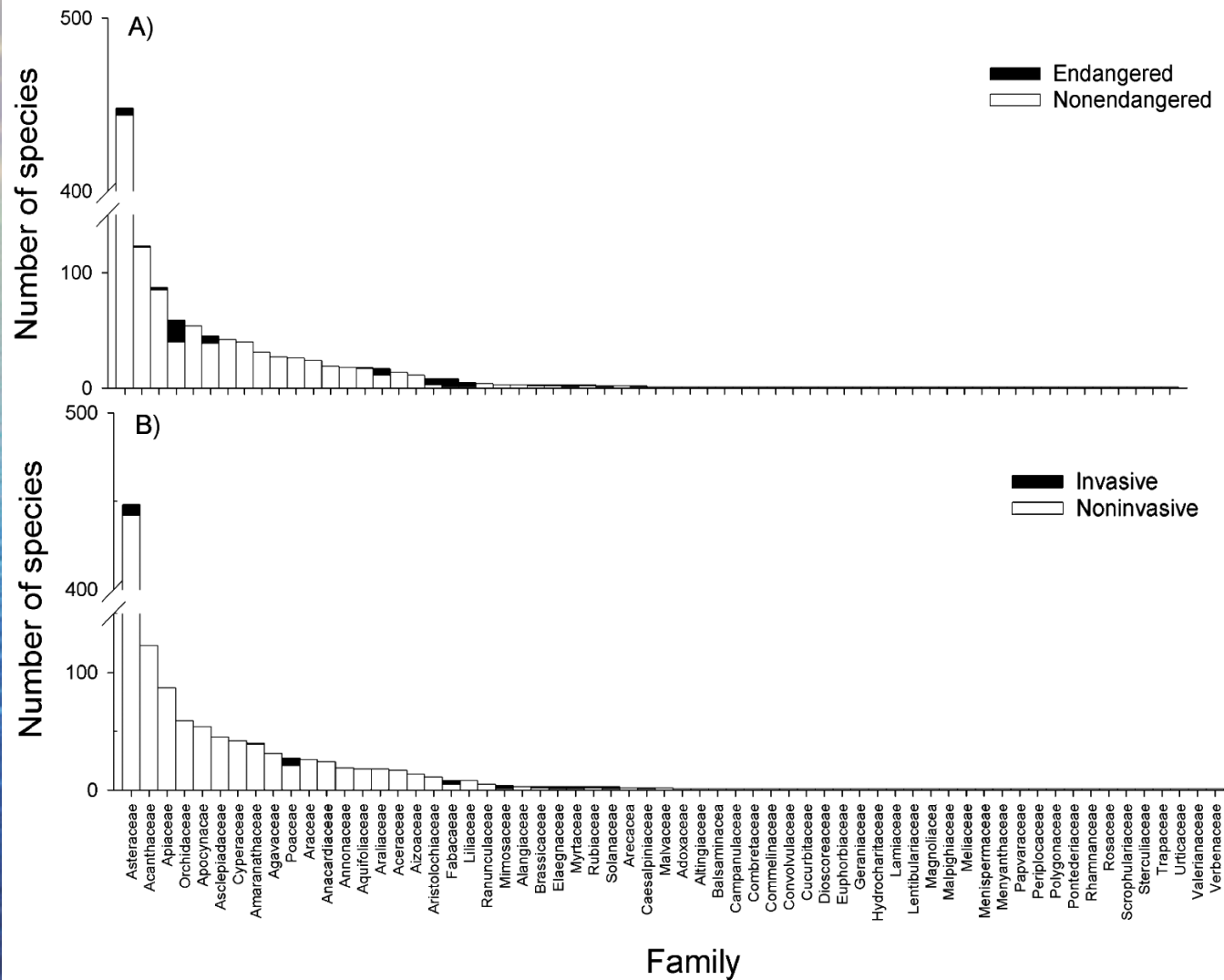
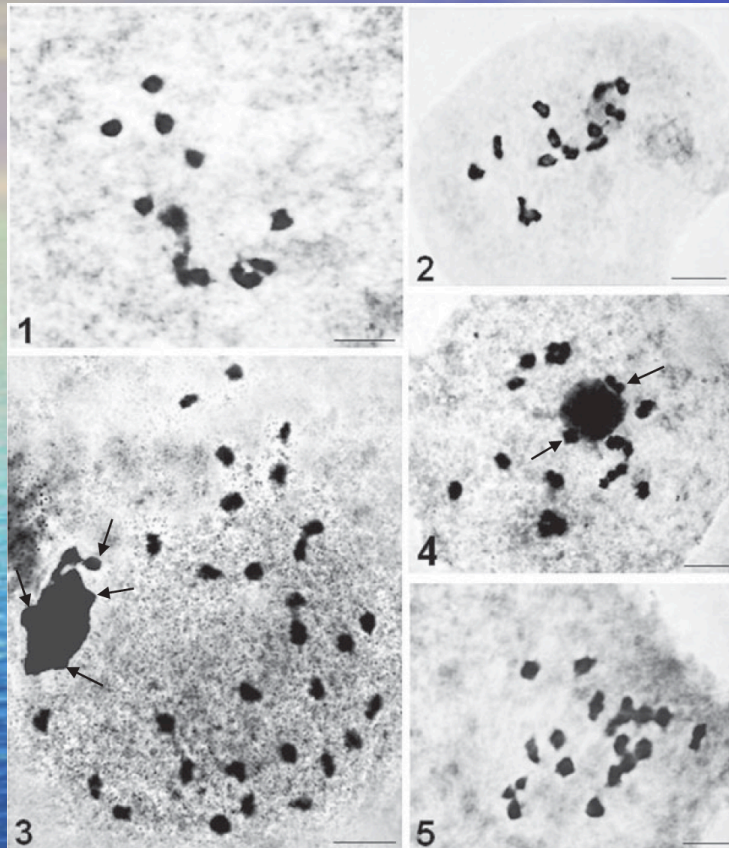


Fig. 1. The proportions of (A) endangered and non-endangered species (y-axis) and (B) invasive and non-invasive species (y-axis) for each family (x-axis).

Pandit, 2006

Where is the Empirical Evidence?



Male meiosis in some invasive species of Singapore. Fig. 1. *Asystasia gangetica* ssp. *micrantha*; 2. *Mimosa pigra*; 3. *Neptunia plena* ; 4. *Panicum maximum*; 5. *Urochloa mutica*

Scale bar = 4 μ m.

All the investigated species were polyploids
- allopolyploids

Botanical Journal of the Linnean Society, 2006, 151, 395–403. With 5 figures

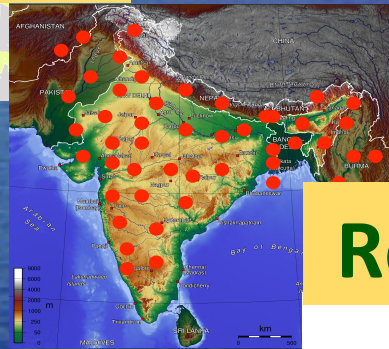
Polyploidy in invasive plant species of Singapore

M. K. PANDIT FLS^{1*}, H. T. W. TAN² and M. S. BISHT¹

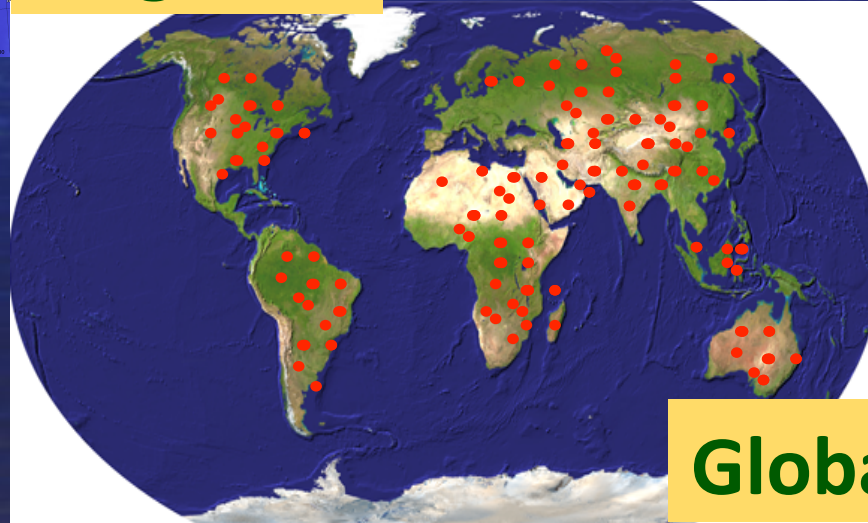
Scales Matter



Area



Regional



Global

Databases & Present Investigations

- **Endangered Species**
 - IUCN (IUCN 2007) www.iucnredlist.org
 - Germplasm Resource Information Network, USDA [GRIN]
 - Species listed by the Center for Plant Conservation, classed as Endangered /Threatened by the U.S. Fish and Wildlife Service or in Appendices I and II of the CITES.
- **Invasive species**
 - Species listed in the Global Invasive Species Database (<http://www.issg.org/database>).
- **Chromosome numbers & DNA C-values**
 - Fedorov (1969); Kumar & Subramaniam (1985)
 - Online sources such as:
 - IPCN (<http://mobot.mobot.org/W3T/Search/ipcn.html>)
 - Royal Botanic Gardens Kew Database - <http://data.kew.org/cvalues/CvalServlet>).

GBIF & Present Research

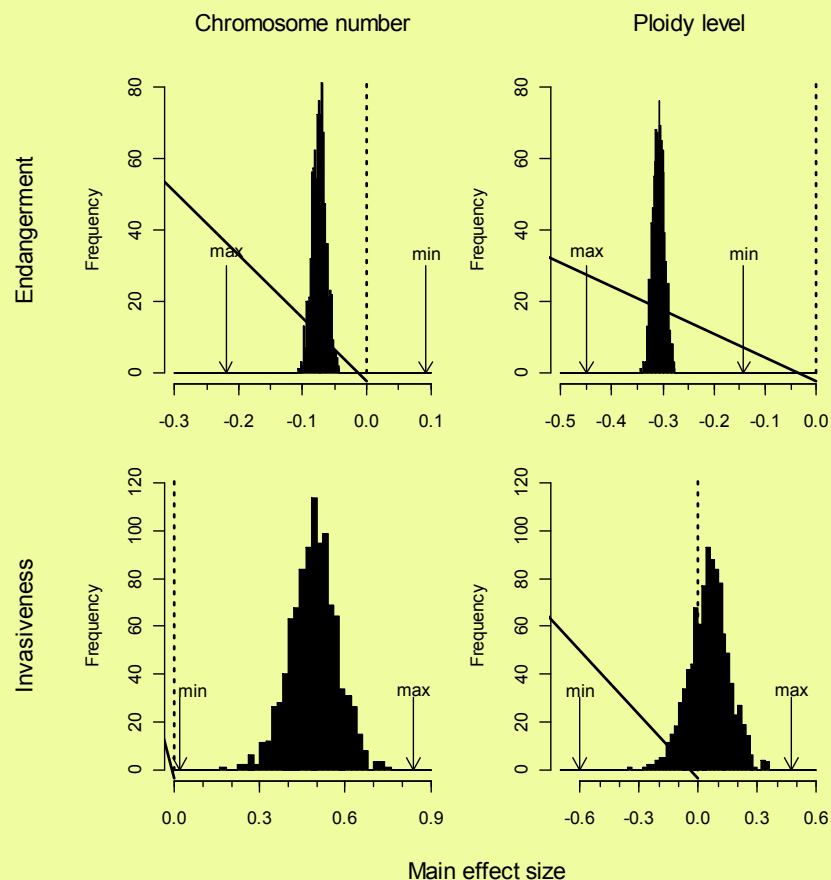
- Genome size and cytogenetic traits vary according to latitude, with a peak at temperate latitudes (Bennett, 1987; Knight et al., 2005).
- We, therefore, extracted information on the distribution of each species from the Global Biodiversity Information Facility (accessed through GBIF Data Portal, data.gbif.org, 2013-02-04).
- We calculated the average latitude of the centres of one-degree latitude/longitude grid cells in which the species had been recorded.
- The extraction of these data from GBIF was automated with the Rgbif package (Chamberlain et al., 2012) in R 2.15.2 (R Development Core Team, 2012), with additional code written by us to gather data on all the synonyms of each taxon under consideration (as listed by GBIF).

Thank You GBIF!!



Ploidy influences rarity and invasiveness in plants

Maharaj K. Pandit^{1*}, Michael J. O. Pocock² and William E. Kunin³



- Chromosome # = 640 endangd. spp. (worldwide) + 9005 congeners, and 81 invasives + their 2356 congeners.
- We related ploidy to endangerment & invasiveness. We also related chromosome # (absolute number and relative to the minimum recorded for the genus) to endangerment and invasiveness with randomization test, taking the variation of reported chromosome # into account.
- Our findings - new hypotheses on plant rarity and invasiveness - influenced by genomic attributes; further our understanding of the role of ploidy in rarity and invasiveness in plants. Understanding the mechanistic basis of traits could aid conservation programs seeking to identify potentially endangered or invasive species.

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Published online 6 April 2011 | Nature | doi:10.1038/news.2011.213

News

Ecologists find genomic clues to invasive and endangered plants

Findings could be used in conservation and control efforts.

Natasha Gilbert

Ecologists have discovered strong links between how many sets of chromosomes a plant species has and whether it is in danger of becoming rare, or conversely, becoming invasive. The findings¹ could help conservation scientists to predict whether species will need protecting or



Genomic data could help control invasive plants like this kudzu in the south-

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References

1. Pandit, M. K., Pocock, M. J. O. and Kunin, W. E. advance online publication doi:10.1111/j.1365-2745.2011.01838.x (2011).

Genome Size : General Results

We tested the ability of genome size (DNA 1C-values) to explain invasiveness and compared it with cytogenetic traits (chromosome number and ploidy). We considered 890 species from 62 genera, from across the angiosperm phylogeny and distributed from tropical to boreal latitudes

We showed - invasiveness was negatively related to genome size & positively related to chromosome number (and ploidy level), yet there was a positive relationship between genome size and chromosome number; that is, our result was not caused by collinearity between the traits. Including both traits in explanatory models greatly increased the explanatory power of each.

This demonstrates the potential unifying role that genome size, chromosome number and ploidy have as species' traits, despite the diverse impacts they have on plant physiology. It provides support for the continued cataloguing of cytogenetic traits and genome size of the world's flora

The Next Step : Genome Size

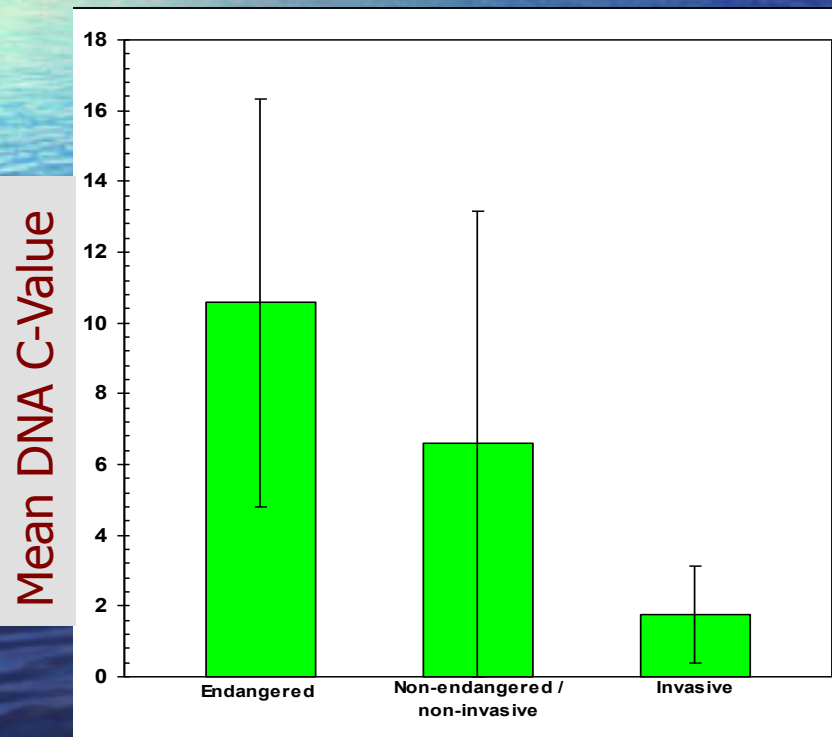


New Phytologist (2014) 203: 697–703

Research

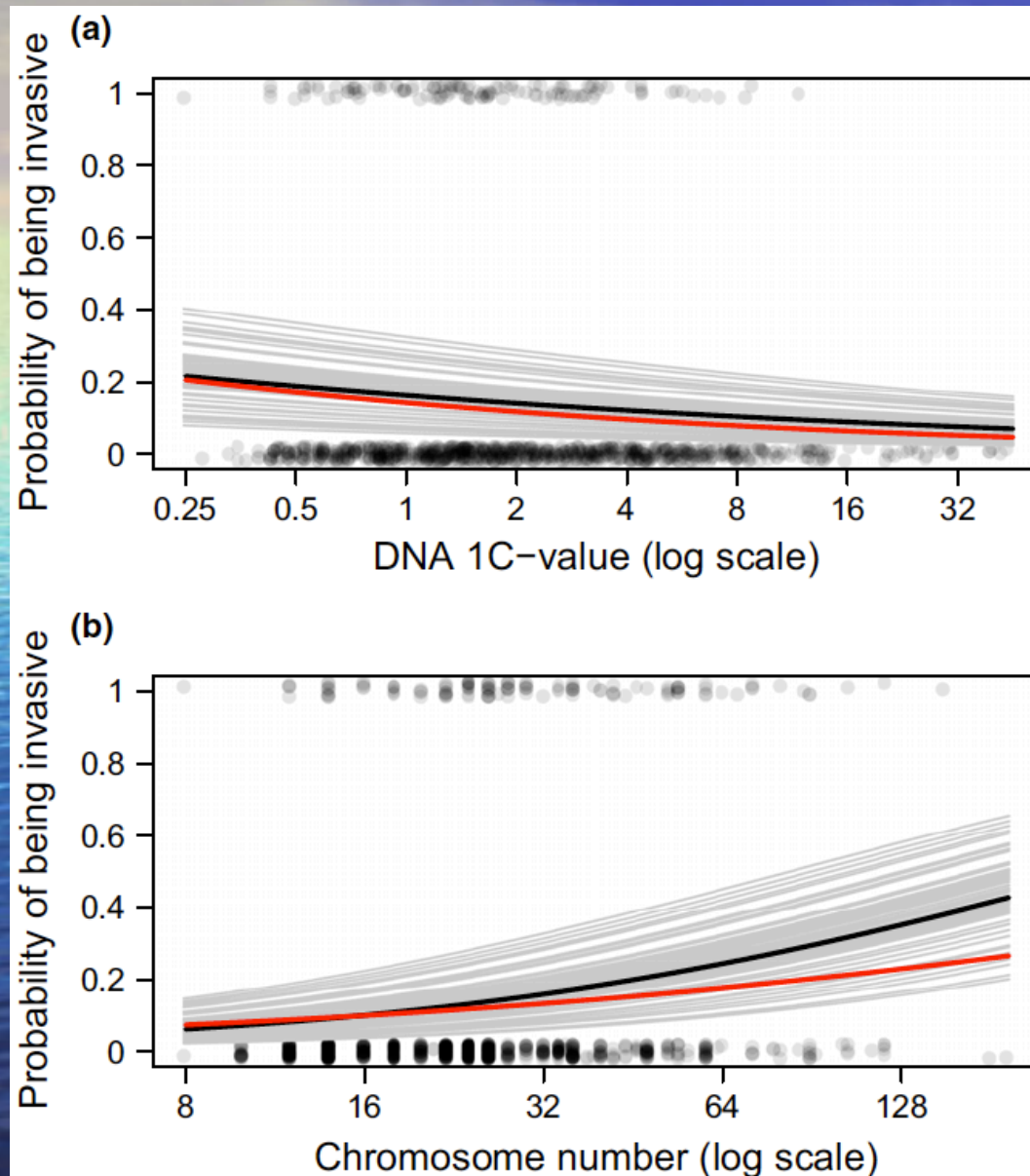
The contrasting effects of genome size, chromosome number and ploidy level on plant invasiveness: a global analysis

Maharaj K. Pandit¹, Steven M. White^{2,3} and Michael J. O. Pocock²



Comparison between the mean CDNA values of endangered, invasive and non-endangered/non-invasive plants (means \pm standard deviation). Endangered plants had a significantly higher mean DNA C-values compared to non-endangered/non-invasive plants ($t = 11.67$, $p < 0.0001$). In contrast, invasive plants had a significantly lower mean DNA C-value when compared to non-endangered/non-invasive controls ($t = -22.71$, $p < 0.0001$).

Genome Size : Plant Invasion



The relationship of probability that a species in our dataset is invasive with: (a) genome size (DNA 1C-value);(b)chromosome number; In (a) and (b) the results of fully phylogenetically informed analyses (phylogenetic logistic regression; PLR) are shown in red, while, from the generalized linear mixed model, the overall average effect is shown in black and effects for individual genera are shown in grey.

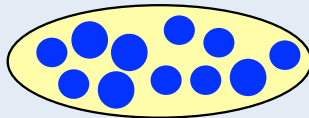
Application Science - Ecogenomics

Native range

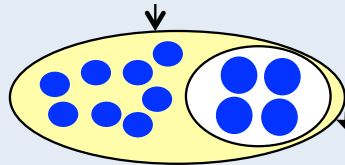
Ecological Variables

- Soil biota
- Specialist and generalist enemies
- Coevolved communities
- Adapted neighbors

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Niche discrimination



Pre-adapted traits

- Superior reproductive potential
- Genome downsizing,
- Rapid carbon capture

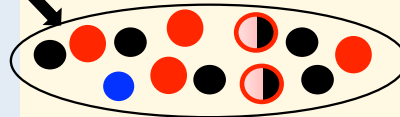
- Native diploid (small blue circle)
- Native polyploid (large blue circle)

Introduced range

Disturbance

- Empty niche
- Resource availability

Invasibility

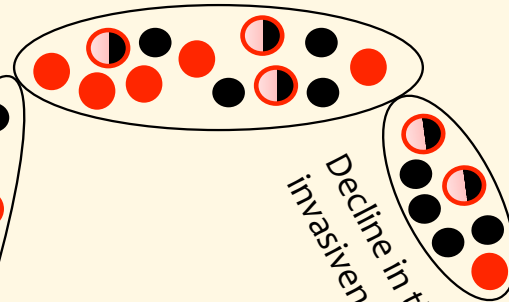


Introduction

- Native congener (black circle)
- Exotic polyploid (red circle)
- Hybrids (exotic polyploid x native congener) (half-red, half-black circle)

Colonization

Naturalization



Decline in the invasiveness?

Invasion success +

Ecological Variables


- Soil biota
- Enemy release
- Naïve communities
- Sensitive neighbors

Databases & Invasion Research

- Enable us to make general predictions on macro-ecological theory.
- Assist us in quick screening of problematic taxa – both in conservation & invasion biology : **Management & Control**.
- Ascertain invasion history – herbarium record
- Help our decision-making process & allow us to make more informed policy choices?

Databases, Invasion Research & Policy

- One such important political framework covers Convention on Biological Diversity (CBD) and the Article 8h specifies: "*Each contracting party shall, as far as possible and as appropriate, prevent the introduction of, control or eradicate those alien species which threaten ecosystems, habitats or species*".
- COP 5 Decision V/8 of CBD concerning "Alien species that threaten ecosystems, habitats or species" in its Guiding Principle 2 provides for "*a three-stage hierarchical approach: (i) Prevention, (ii) Eradication, and (iii) Long-term control measures should be considered*".



“If at one time or another I have brushed a few colleagues the wrong way, I must apologize: I had not realized that they were covered with fur.”

— Erwin Chargaff,

A full-page background image of a calm ocean under a vast blue sky. A faint rainbow is visible on the horizon to the left. The water is a deep blue with gentle ripples. The sky is a lighter blue with wispy white clouds.

Thank You