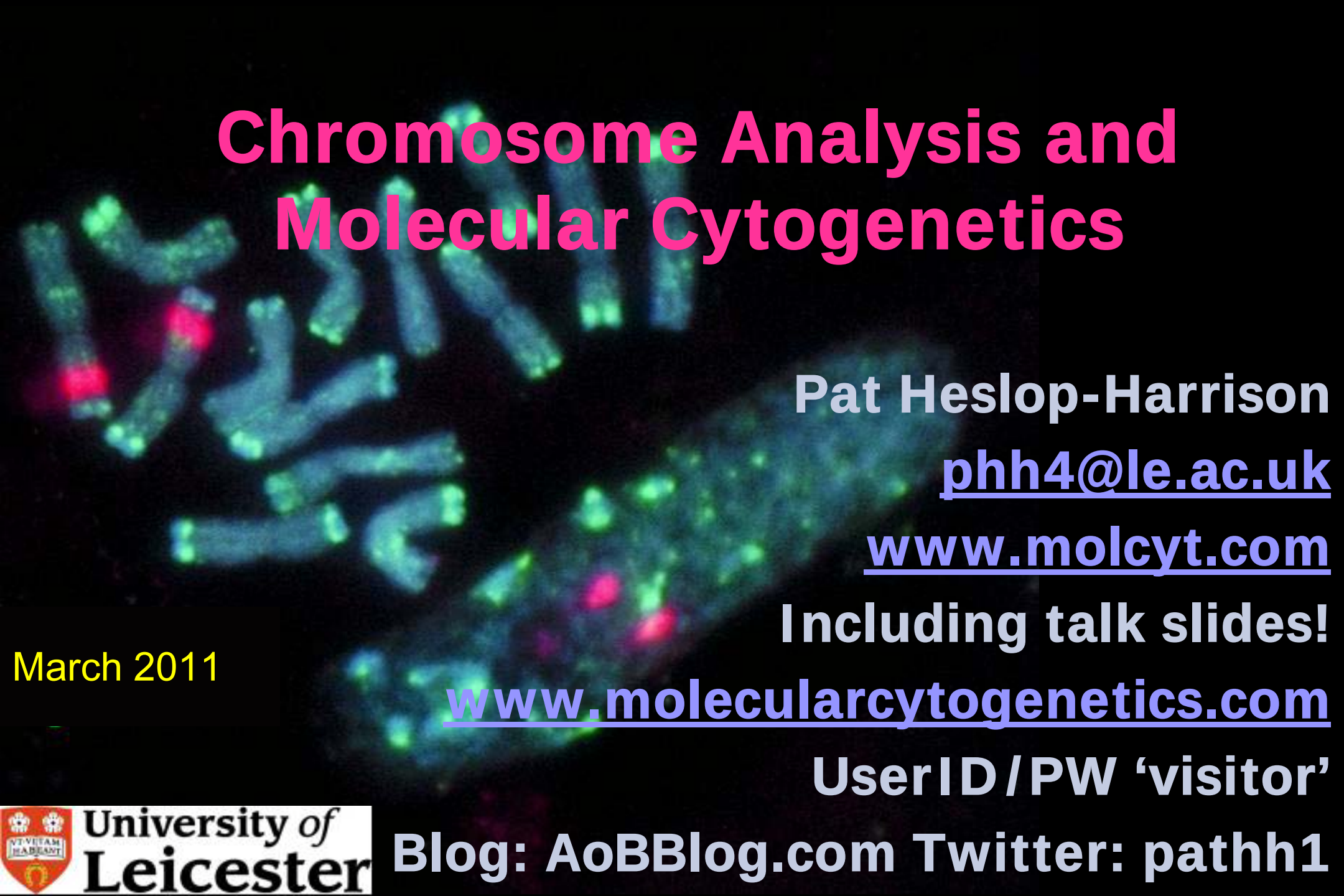

Chromosome Analysis and Molecular Cytogenetics

Pat Heslop-Harrison

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www.molcyt.com

Including talk slides!

March 2011

www.molecularcytogenetics.com

User ID / PW 'visitor'

University of Leicester

Blog: AoBBlog.com Twitter: pathh1

Crocus species and hybrids

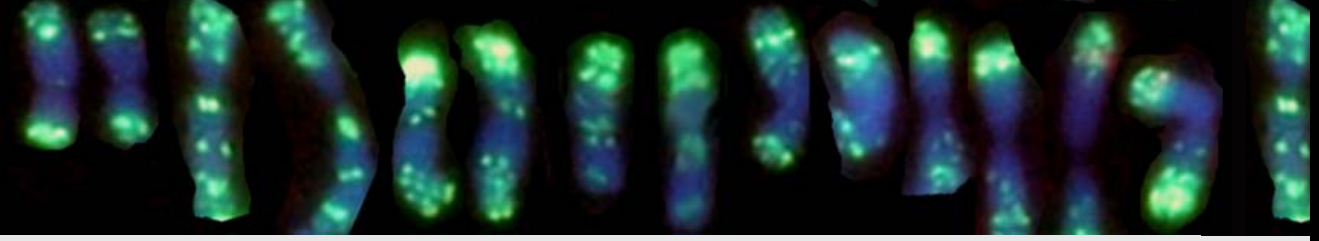
C. flavus
2n=8

C. 'Stellaris'
2n=2x=10

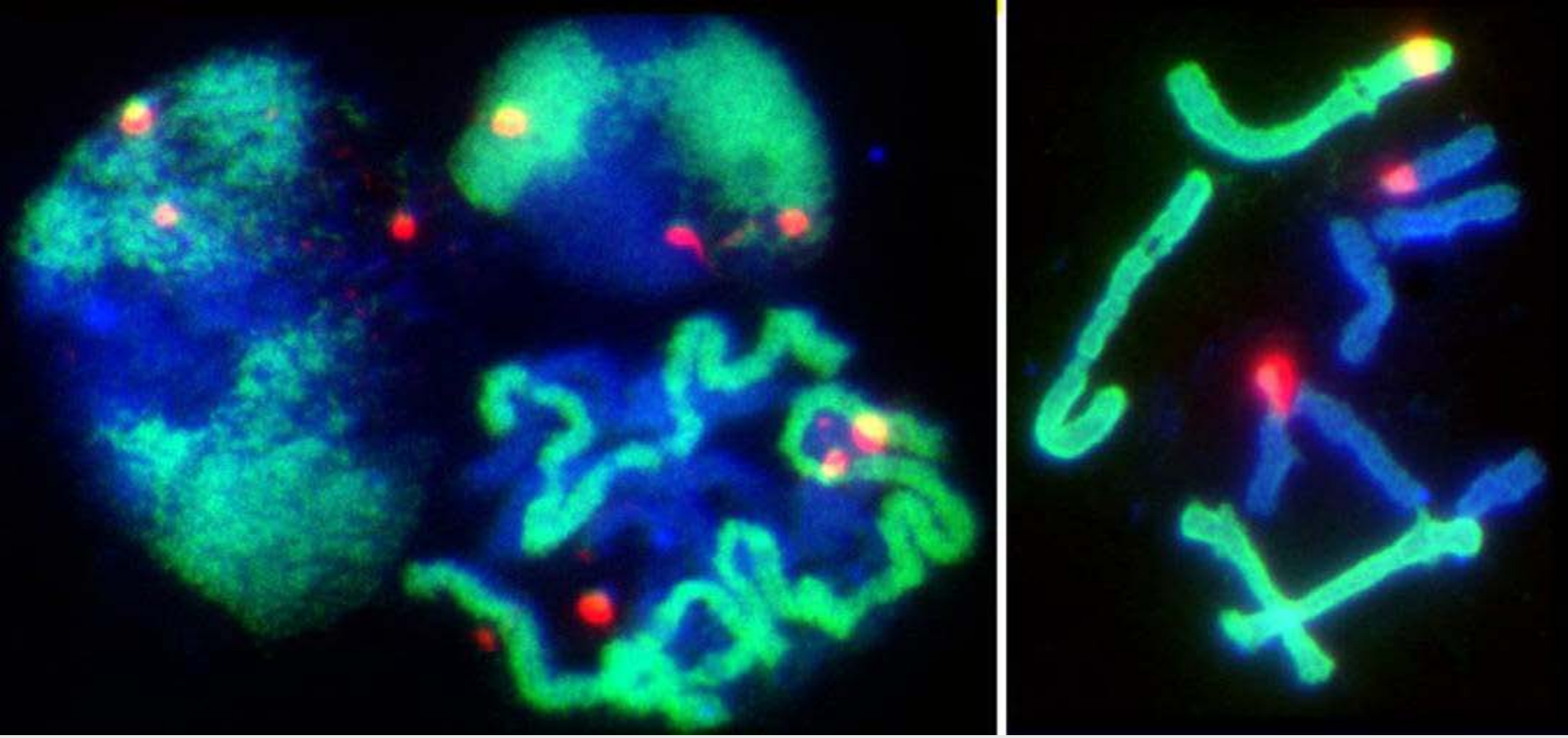
C. angustifolius
2n=12

C. 'Golden Yellow'
2n=3x=14

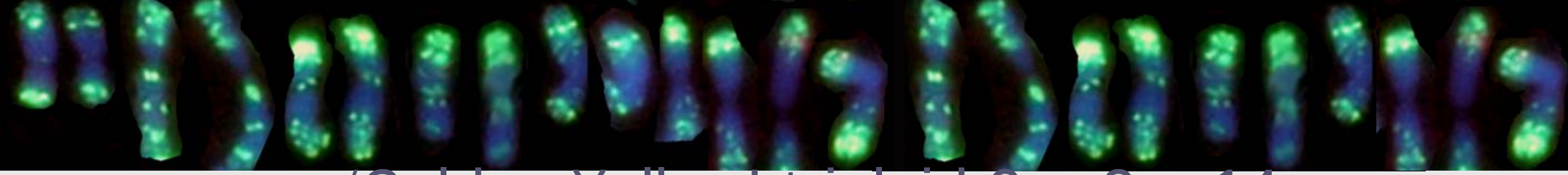
B.J.94



- The parents look similar, sharing many genes
- Total genomic DNA as a probe labels the parental genomes differentially



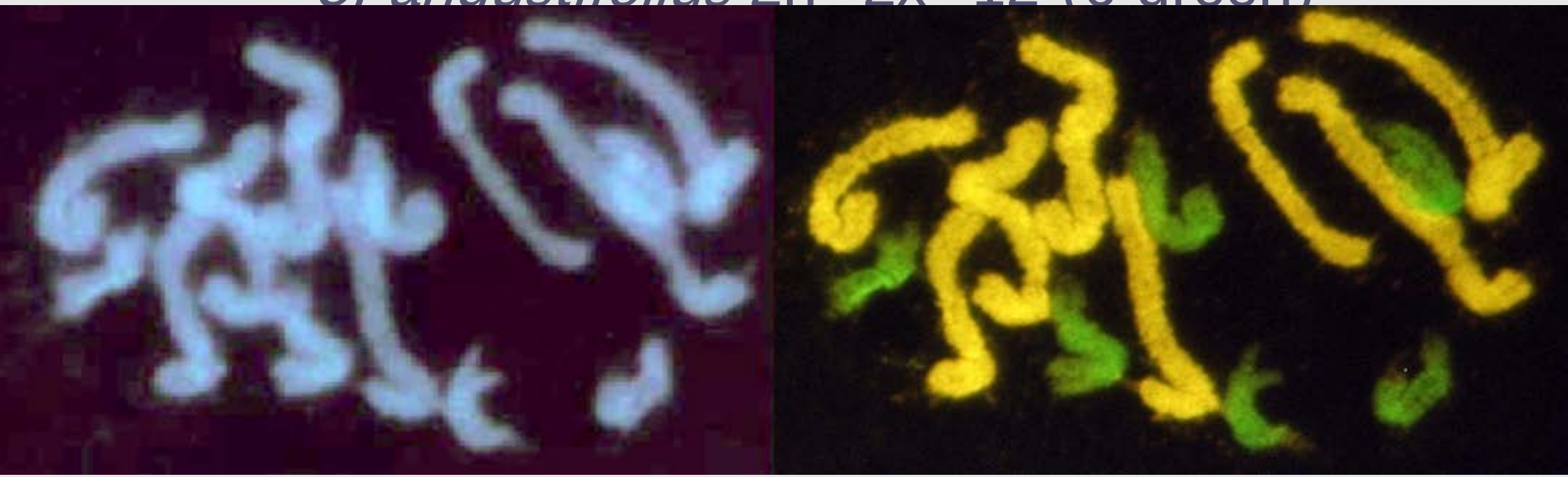
- The parents look similar, sharing many genes
- Total genomic DNA as a probe labels the parental genomes differentially
- Farah Badakshi, John Bailey, Trude Schwarzacher, Marian Orgaard



‘Golden Yellow’ triploid 2n=3x=14

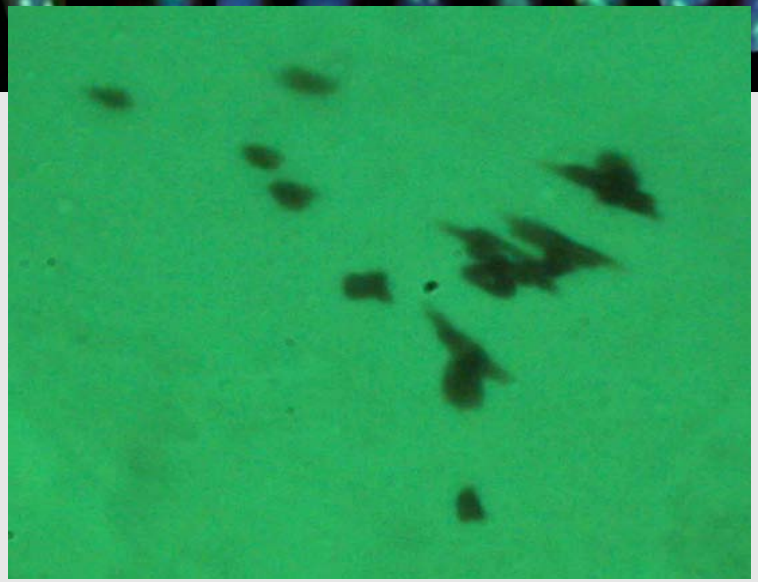
C. flavus 2n=2x=8 (8 yellow)

C. angustifolius 2n=2x=12 (6 green)



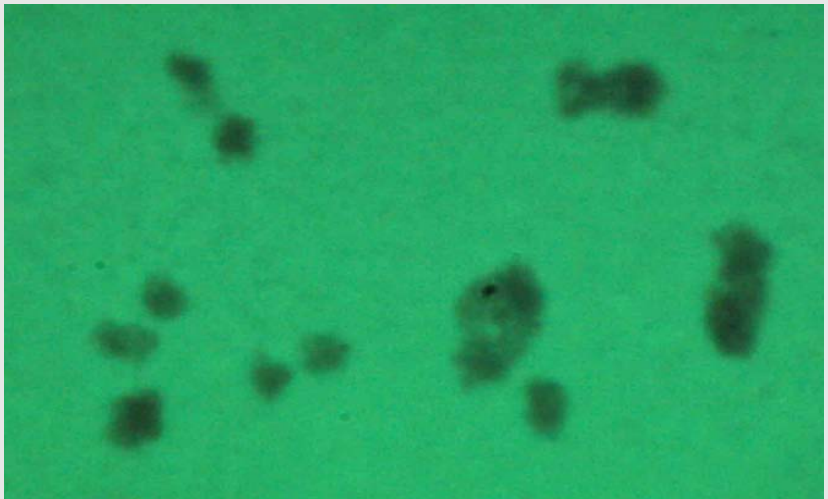
Orgaard, Jacobsen & HH

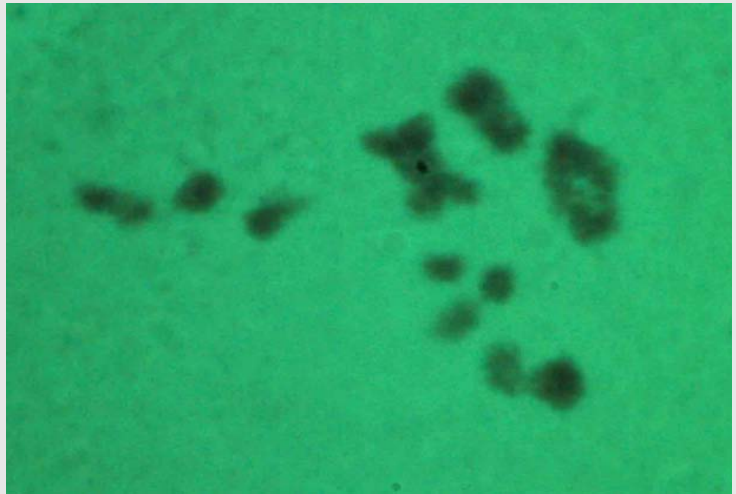
Metaphase I in triploid Golden Yellow Crocus



In many metaphase I cells of this triploid, we see four bivalents from pairing of the four pairs of *C. flavus* (2n=2x=8)-origin chromosomes, with the six chromosomes from *C. angustifolius* (2n=2x=12) present as univalents.

Alternative meiotic configurations were also identified: eg 3 bivalents and 8 univalents.

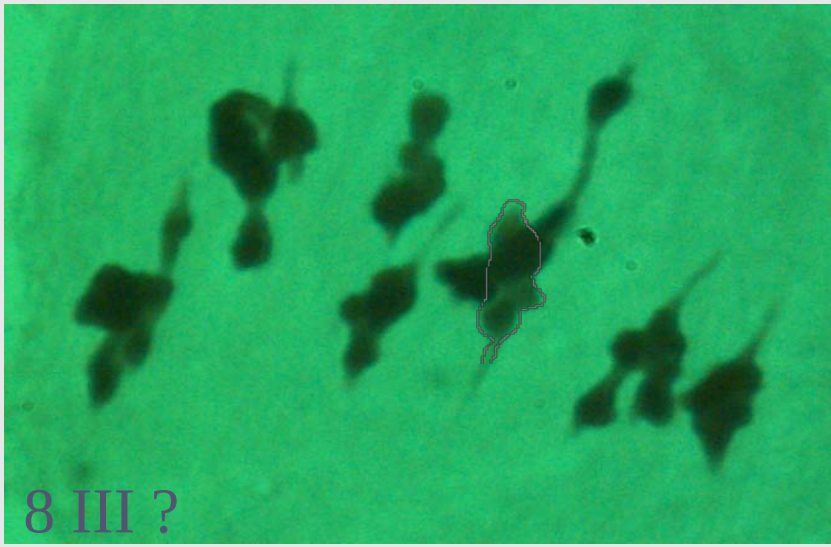




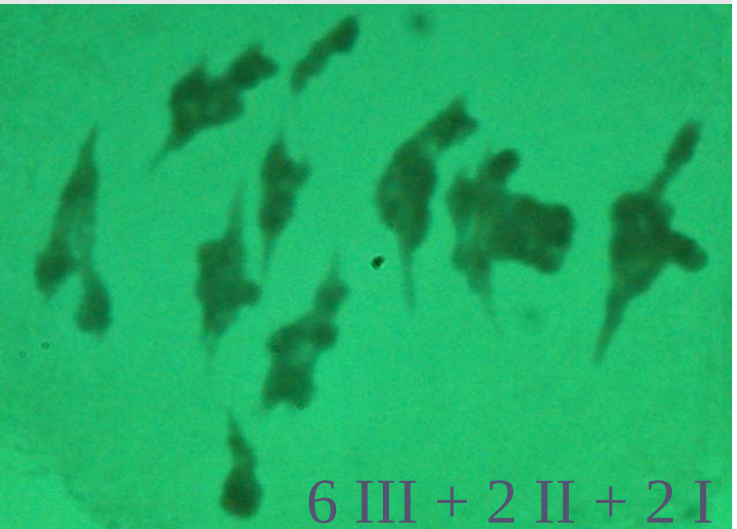
Metaphase I in triploid Saffron (*C. sativus*)

Saffron, the world's most expensive spice, consists of the stigmas of *Crocus sativus*, a sterile triploid (2n=3x=24). One wild ancestor is *C. cartwrightianus* (2n=2x=16), but the other is unknown.

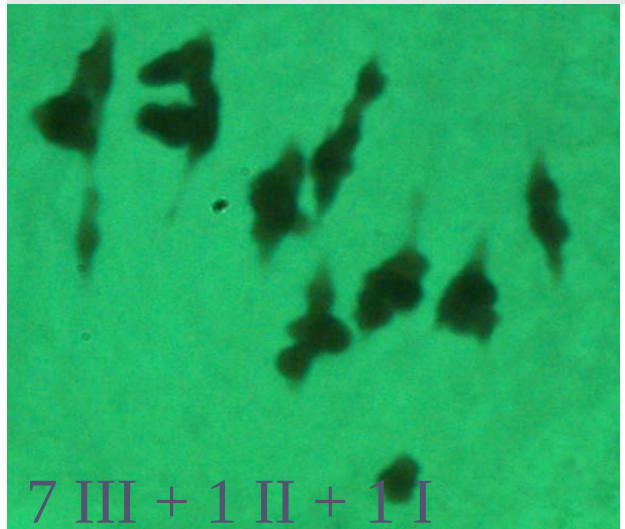
Metaphase I cells of this triploid (2n=3x=24) showed as few as 8 structures, a mixture of trivalents, quadrivalents and univalents.



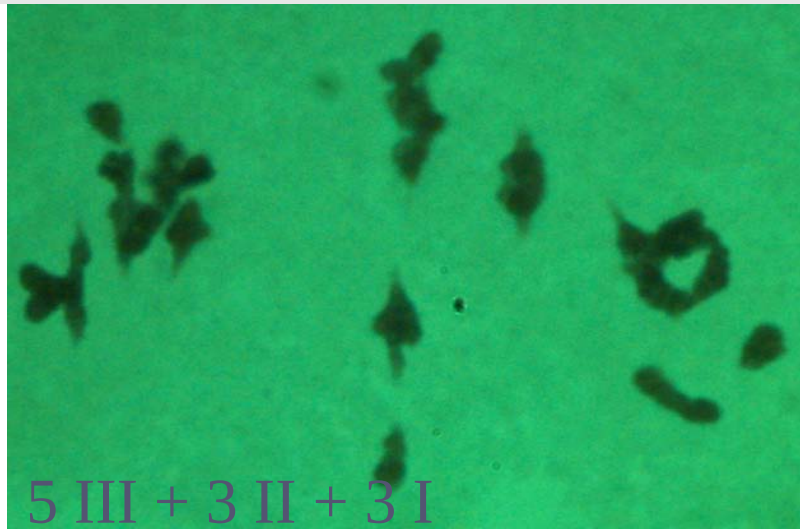
8 III ?



6 III + 2 II + 2 I



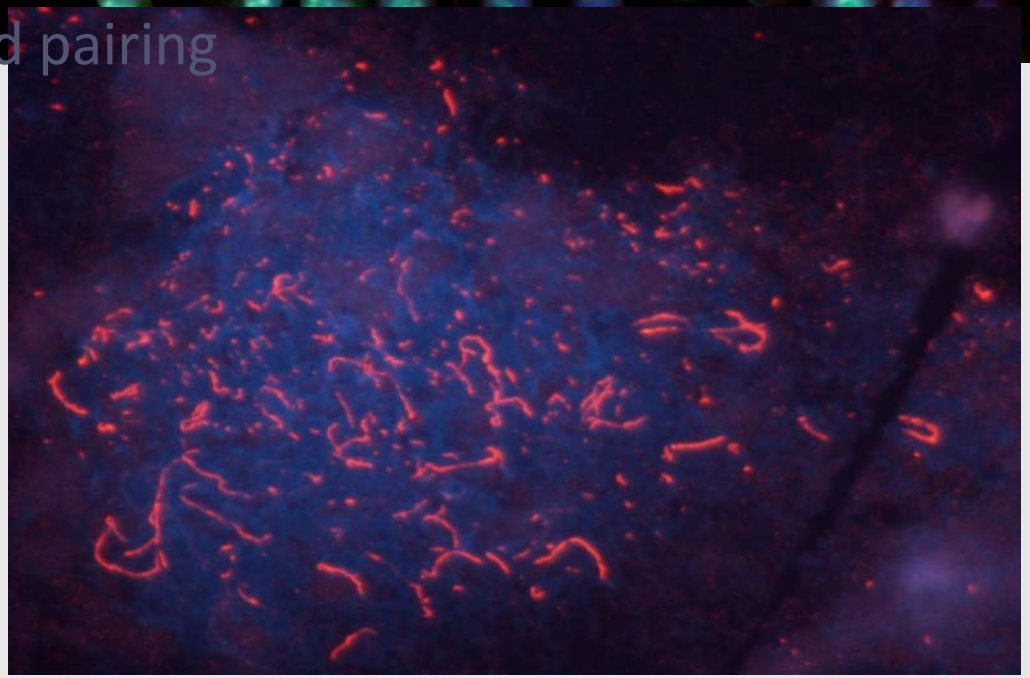
7 III + 1 II + 1 I

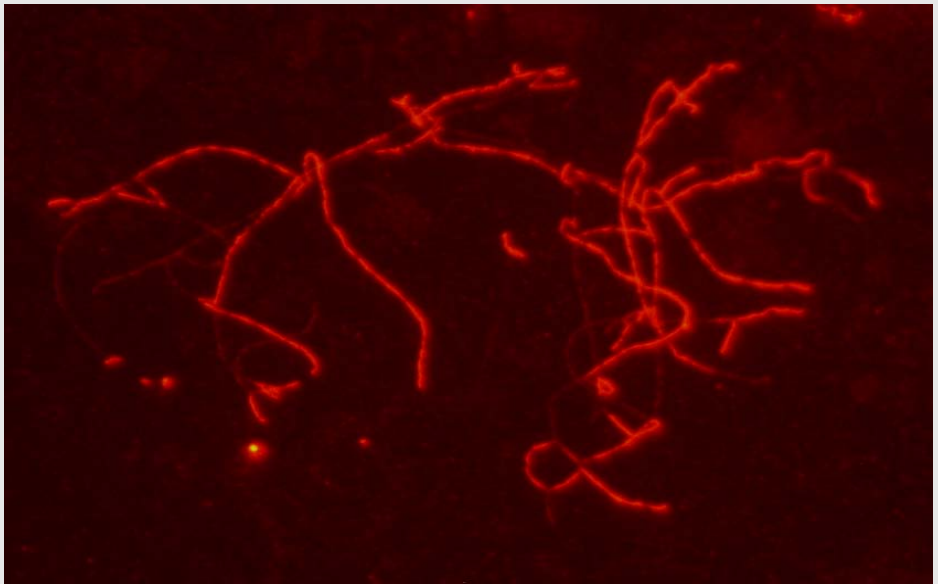


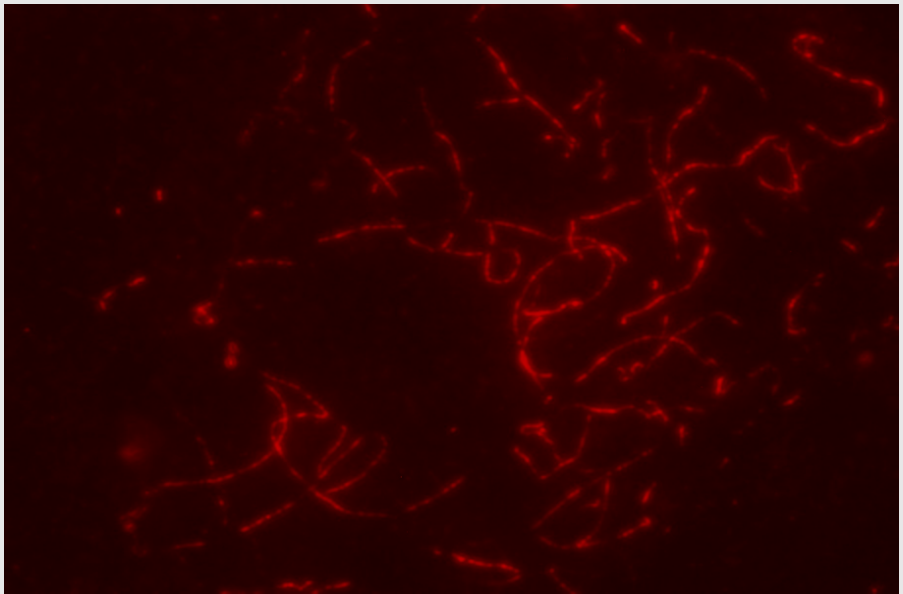
5 III + 3 II + 3 I

Meiotic prophase in triploid Saffron (*C. sativus*)

ASY1 antibodies (Franklin and Armstrong) show the progression of lateral element formation and pairing







Plant Genome Sizes

ANNALS OF BOTANY

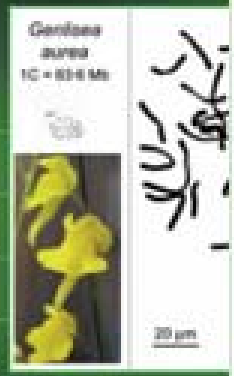
Fo

EDITORIAL OFFICES IN UK, AUSTRALIA, CANADA, CHINA, JAPAN AND

Volume 107

Number 3

March 2011



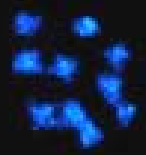
Genlisea aurea

1C = 63·6 Mb

Paris japonica

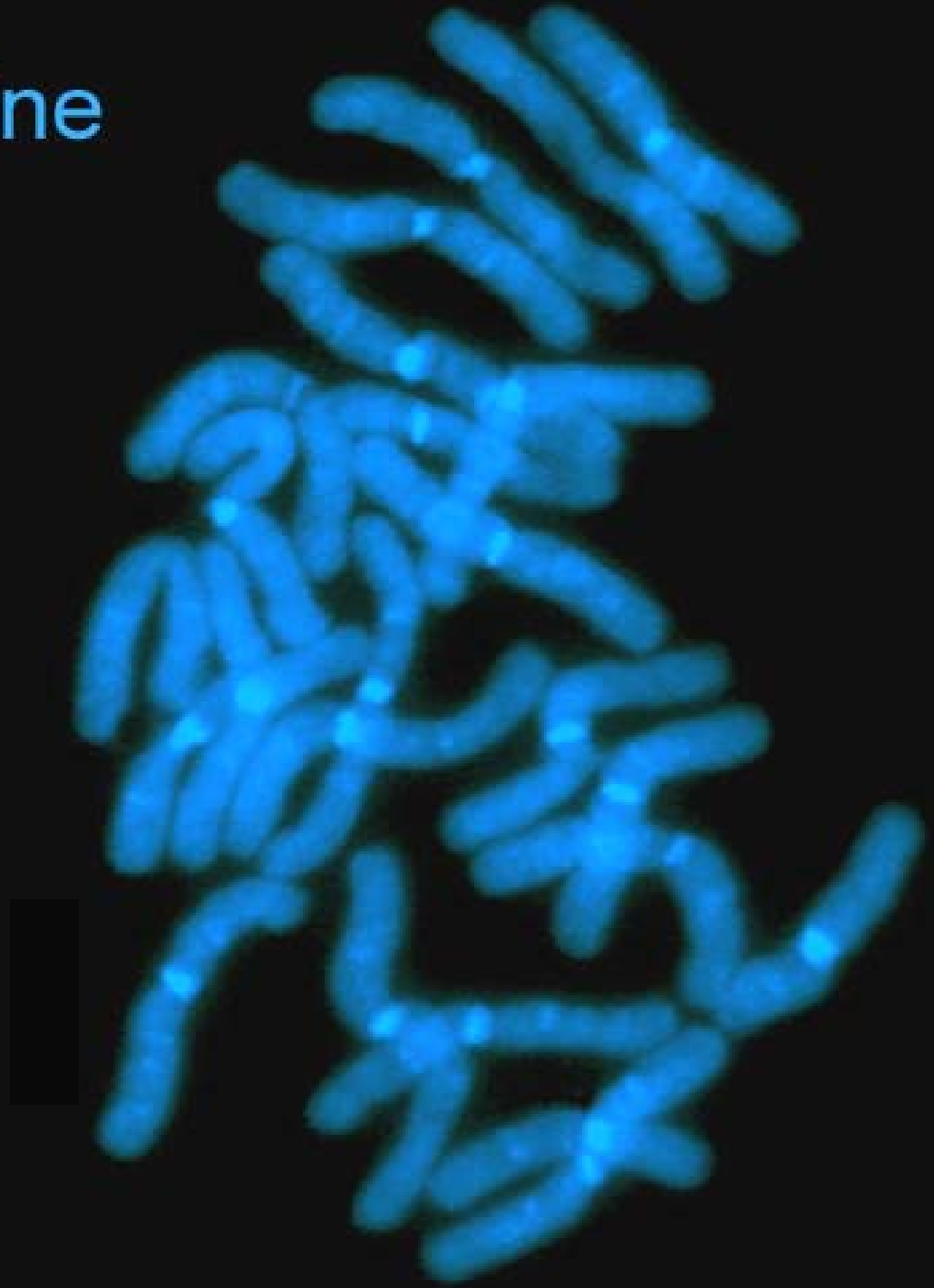
1C = 148,852 Mb

Arabidopsis



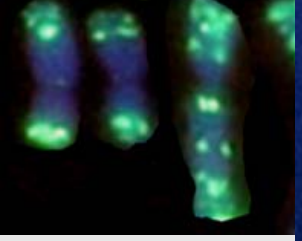
Human

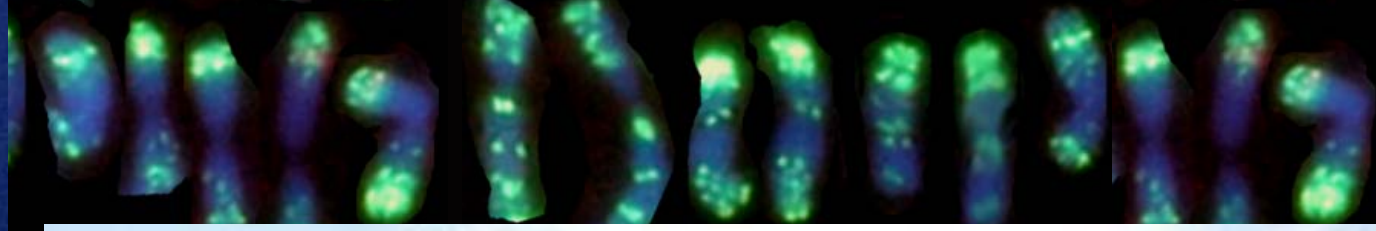
Pine



Genome sizes: reading them out base-by-base

HIV type 1 Virus	2hr 40 min
Bacteria *(E. coli)*	53 days
Yeast	138 days
Genlisea	2 years
Arabidopsis	5 years
Man	100 years
Wheat	5 centuries
Paris	4 millennia



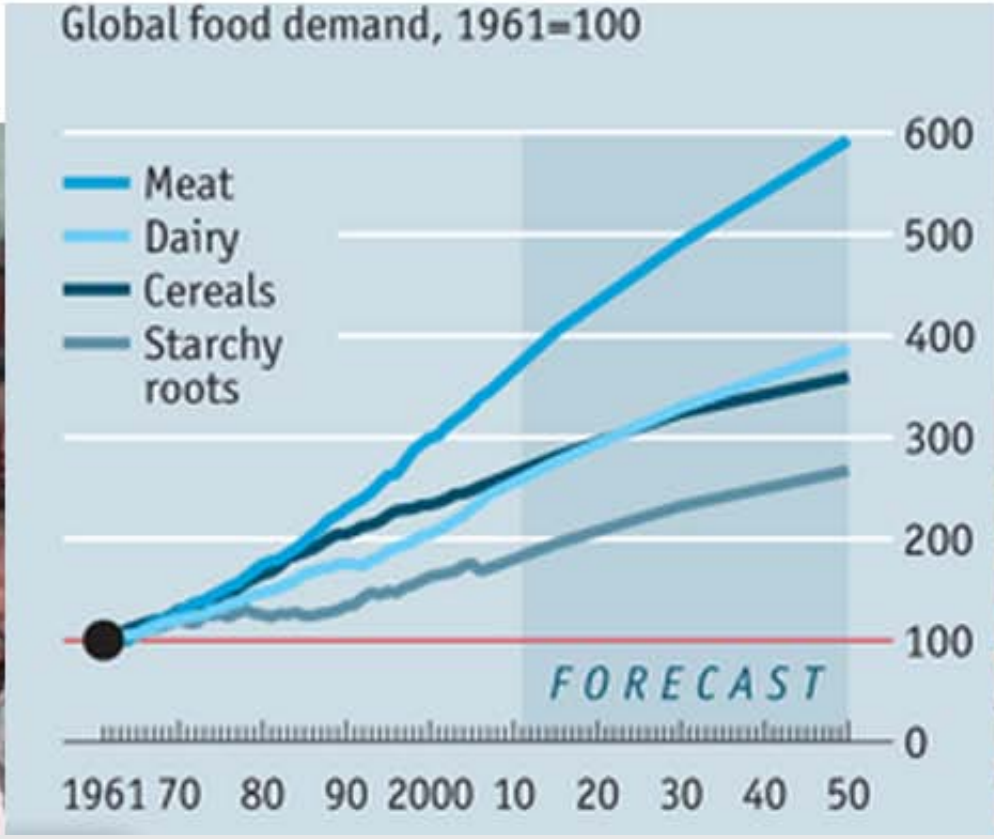


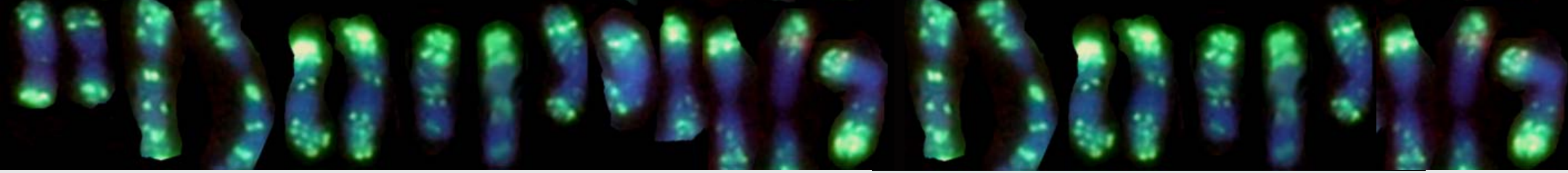
A special report on feeding the world

The 9 billion-people question

The world's population will grow from almost 7 billion now to over 9 billion in 2050. John Parker asks if there will be enough food to go round

Feb 24th 2011 | from the print edition





Molecular Cytogenetics

Part I:

- Chromosomes
- Genomes and their sizes
- DNA components of a chromosome
- Retroelements
- Chromosomes and sources of genetic markers

Part II:

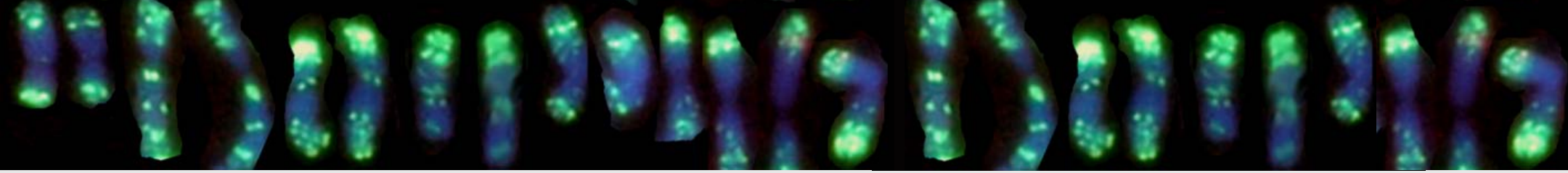
- Chromosome and genome painting
- Polyploids and cereal chromosome evolution
- Plant breeding and aliens

OBJECTIVES
Fundamental and Practical

- Explain major structures and features of the DNA in genomes
- Understand the structure of chromosomes and genomes
- Explain the nature and origin of molecular markers
- Understand key events in evolution and generation of diversity including induced mutations

OBJECTIVES
Fundamental and Practical

- Understand how genomes and diversity can be manipulated and exploited
- Relate genome information and models to the applications in the genome of particular species
- Decide which molecular markers are appropriate for various applications
- Introduce the concept of superdomestication into breeding programmes and consider solutions to major problems facing breeders and farmers
- Use the literature relating to genomics, genetics and plant breeding and communicate it in writing

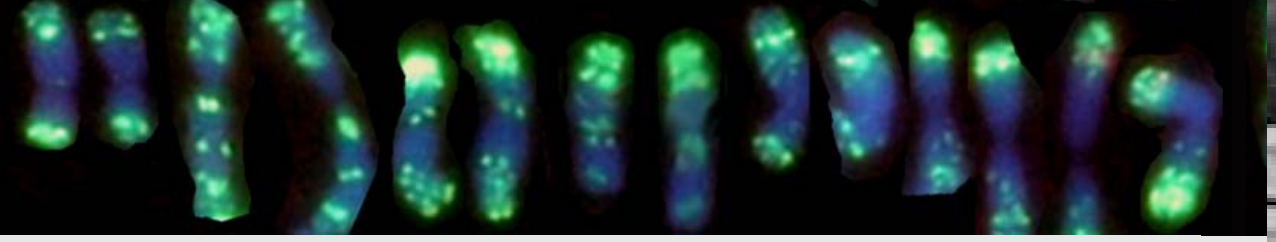


Molecular Cytogenetics

- Lecture
  - 10.05-11.00
  - 11.10-12.00

- Microscopy (Adrian 264 near computer room)
- Three slots: 3.00 - 3.30 - 4.00


EVOLUTION



- **Nothing in Biology Makes Sense Except in the Light of Evolution**

Theodosius Dobzhansky (1900-1975)

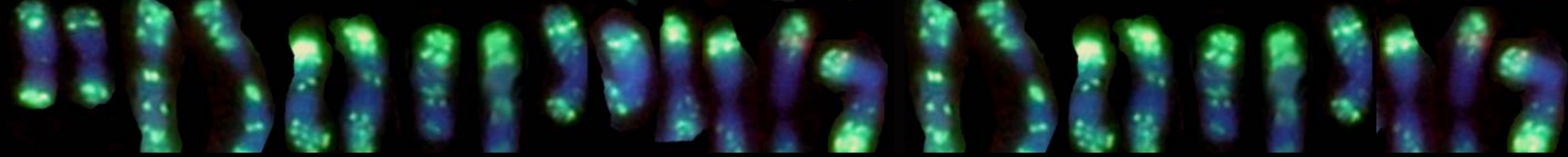
***The American Biology Teacher*, March 1973 (35:125-129).**

Darwin: The final paragraph of “The Origin”

- It is interesting to contemplate ... many plants of many kinds ... and to reflect that these elaborately constructed forms, so different from each other ...

Darwin: The final paragraph of “The Origin”

- It is interesting to contemplate ... many plants of many kinds ... and to reflect that these elaborately constructed forms, so different from each other ... have all been produced by laws acting around us ... from so simple a beginning endless forms most beautiful and most wonderful have been, and are being evolved.



Components of a Chromosome

Arm: 10-500 Mb

Arm: 0-1000 Mb

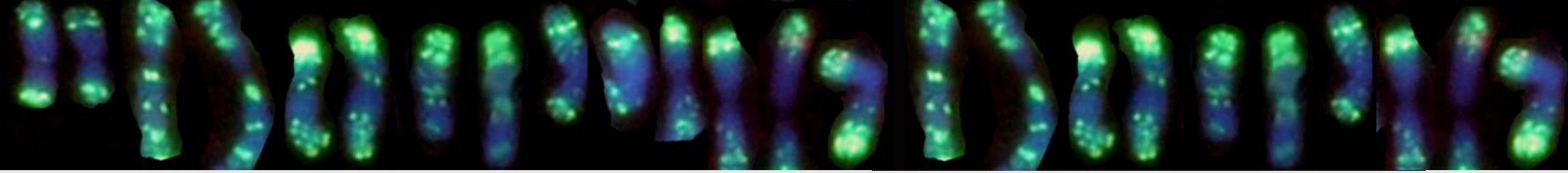
Centromere

Telomeres

Genes!

Packaging
- Division
- Organization

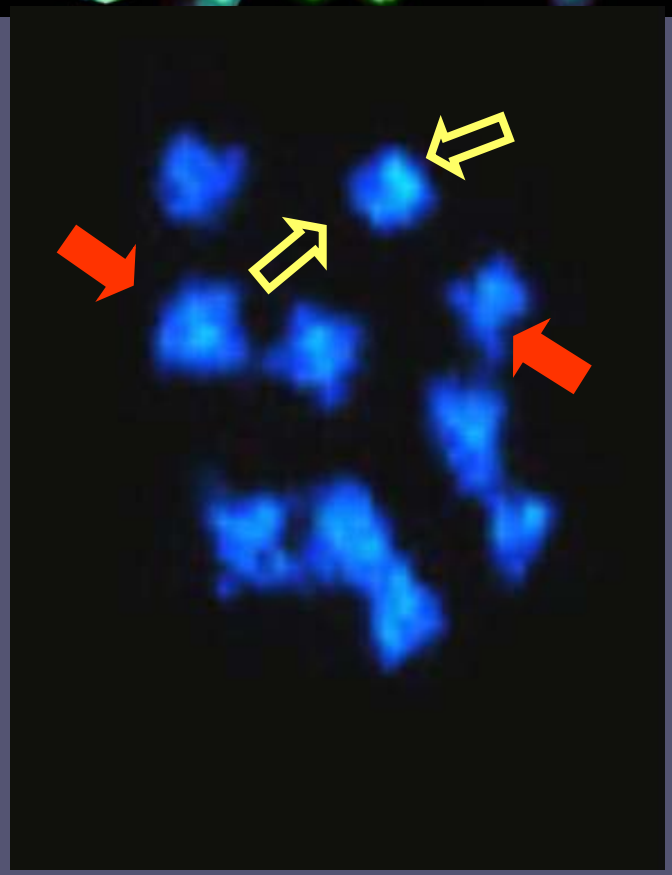
Replication and Transcription
- Enzyme access
- Regulation



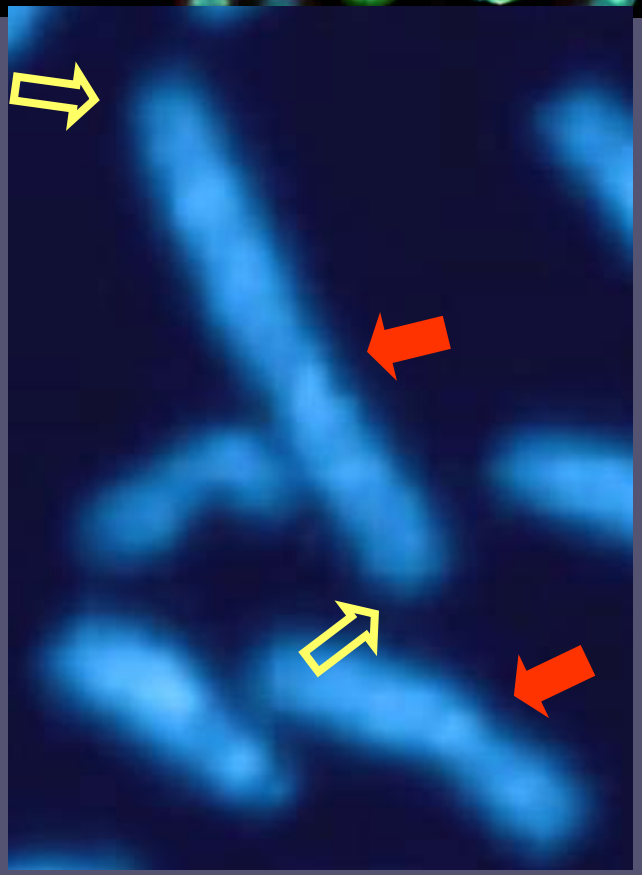
Chromosome

- Basic 'unit' of DNA in a cell
- Basic unit of heredity – Thomas Hunt Morgan 1911
- Macromolecule of DNA
  - very long, continuous
  - Contains genes, regulatory elements, other sequences
  - Structural components
- A broader definition of "chromosome“
  - includes the DNA-bound proteins which serve to package and manage the DNA.
- The word *chromosome* comes from the Greek *χρώμα* (*chroma*, colour) and *σώμα* (*soma*, body) due to its capacity to be stained very strongly

Somatic metaphase chromosomes



Arabidopsis



Human

Pine

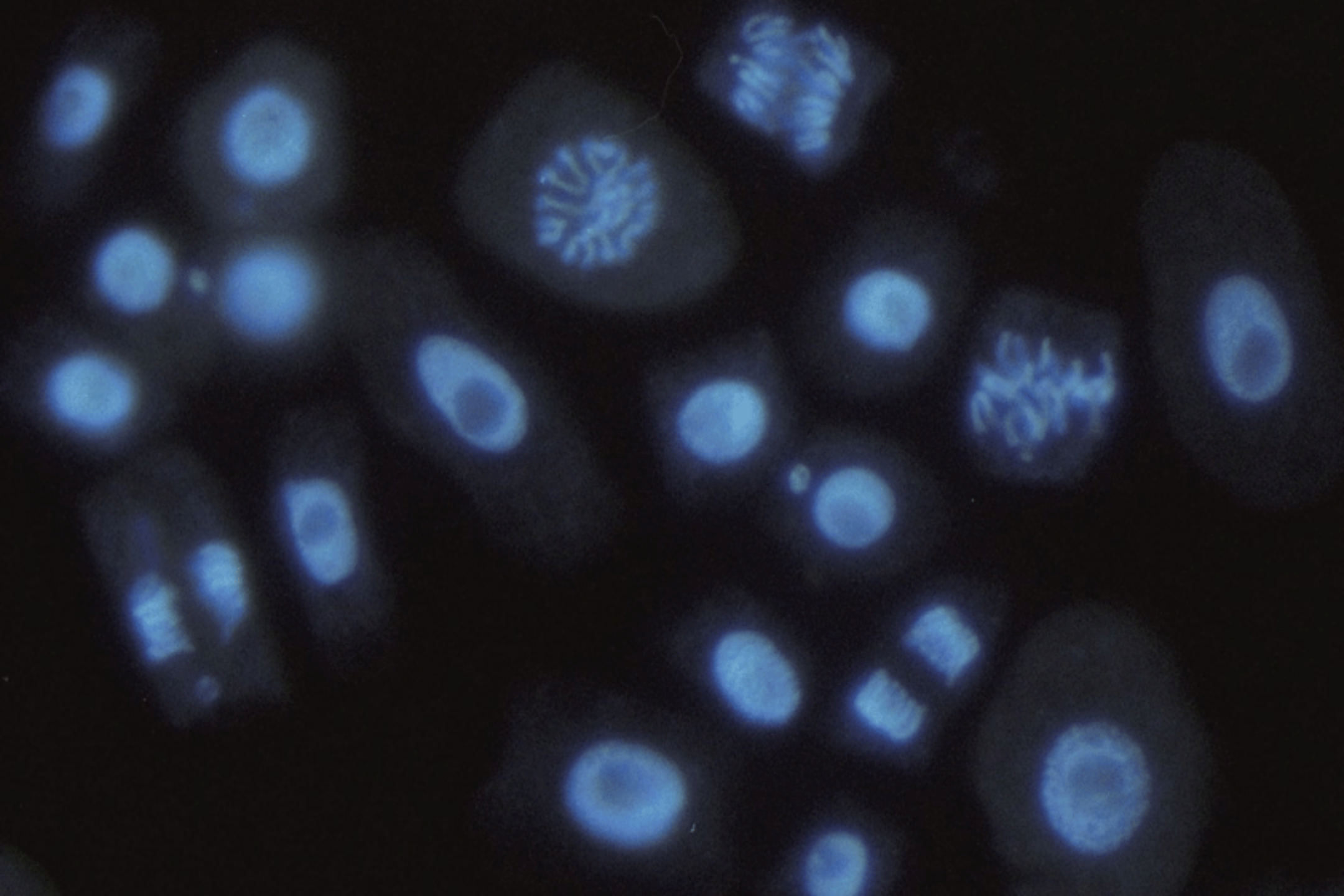
Centromere

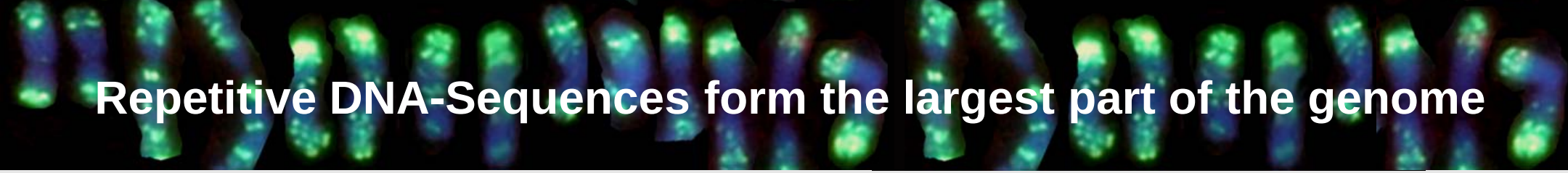
Telomere

The Genome and Chromosomes

- The DNA is organized in multiple chromosomes
- Each is a single, linear DNA molecule
- The DNA is packaged around proteins (histones)
- The nuclear chromosome has special sequences at its ends

- There are separate genomes in the plastids and mitochondria
- There can be viral and bacteria-like genomes in the nucleus and cytoplasm



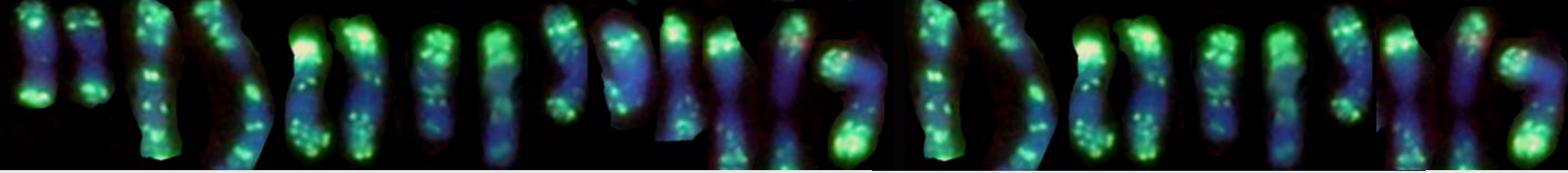


Repetitive DNA-Sequences form the largest part of the genome

Species	Repetitive DNA	Genome size
Arabidopsis thaliana	>25%	145 Mbp
Sugar beet *Beta vulgaris*	63%	758 Mbp
Broad bean *Vicia faba*	85%	12000 Mbp
Rye *Secale cereale*	92%	8800 Mbp
Onion *Allium cepa*	95%	15100 Mbp

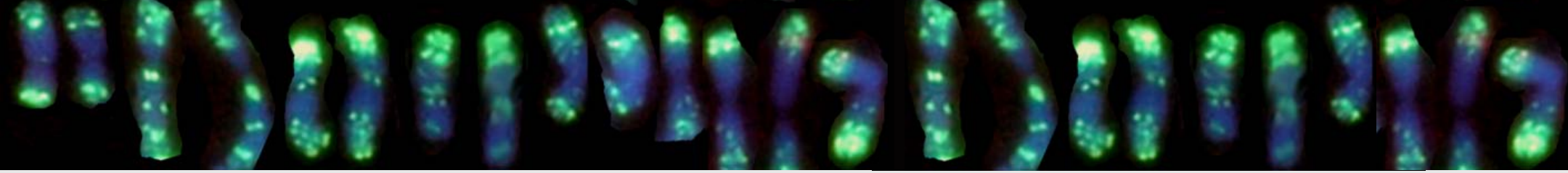
These species are all diploid – 2x

Human *Homo sapiens*	35%	3000 Mbp



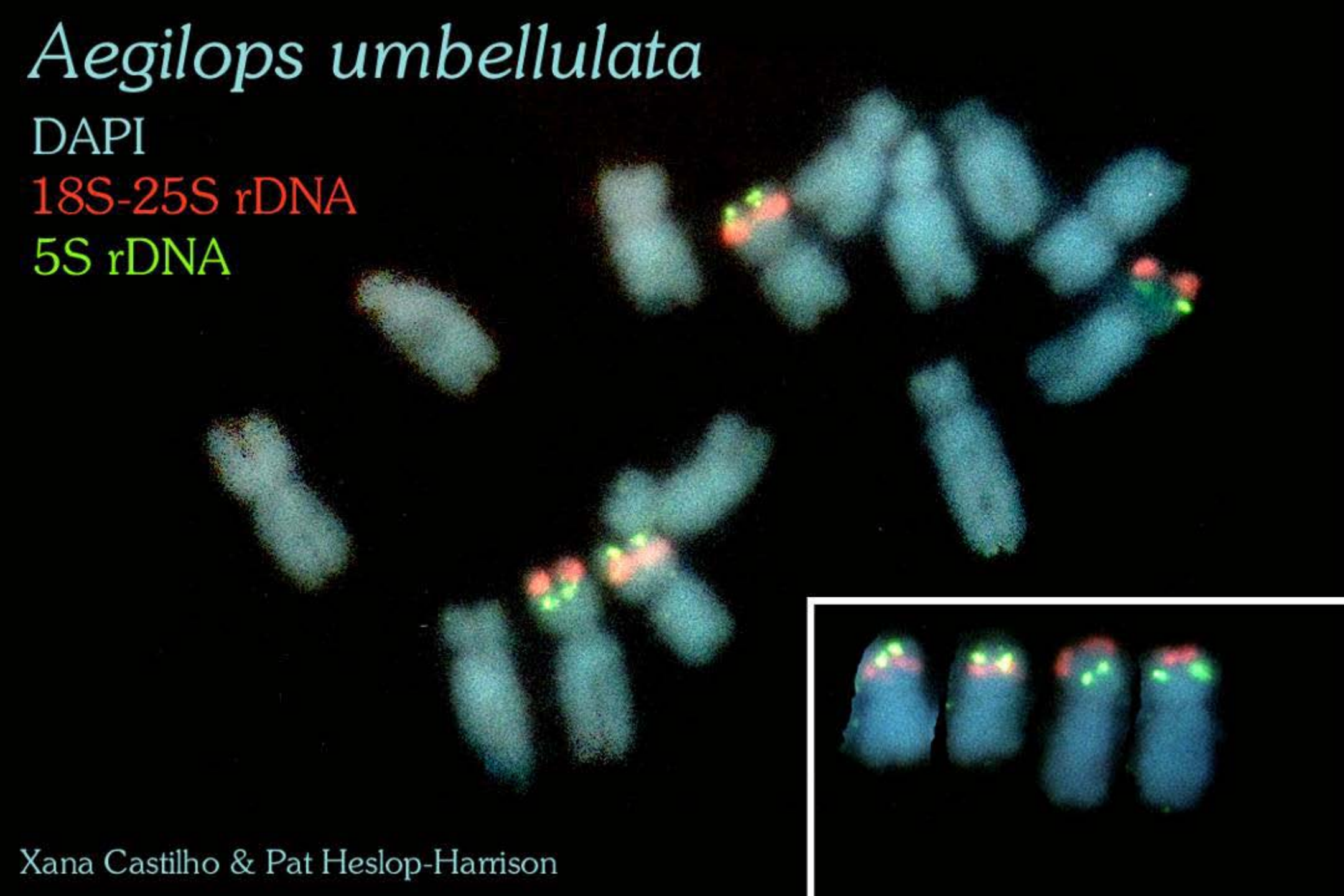
Genome

- Genes and regulatory sequences make up a small proportion of the genome
- The majority of DNA sequences in all higher eukaryotic genomes are repetitive sequences (50-90%)
- JUNK – no?; FUNCTION – largely unknown

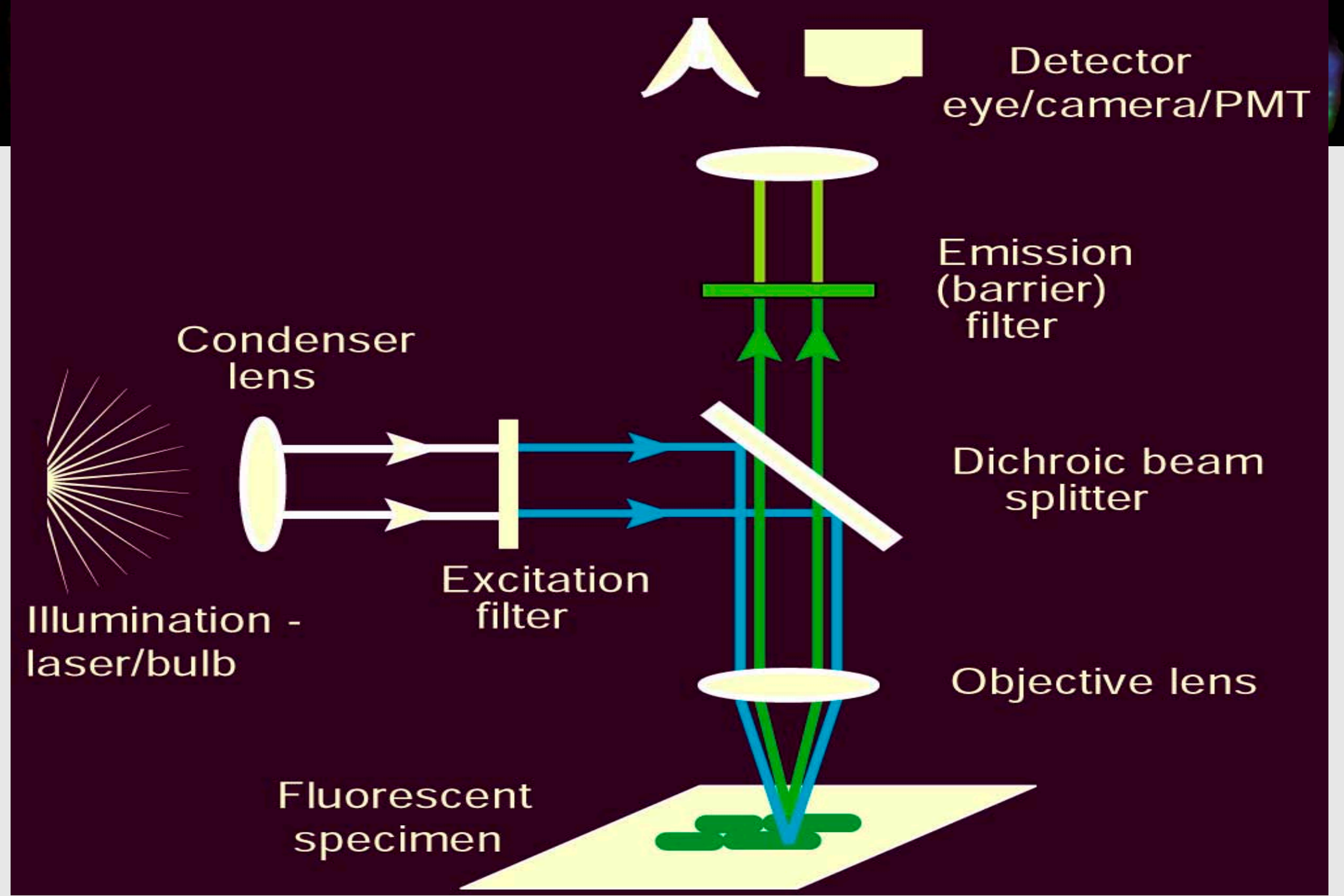


What is the rest of the genome?

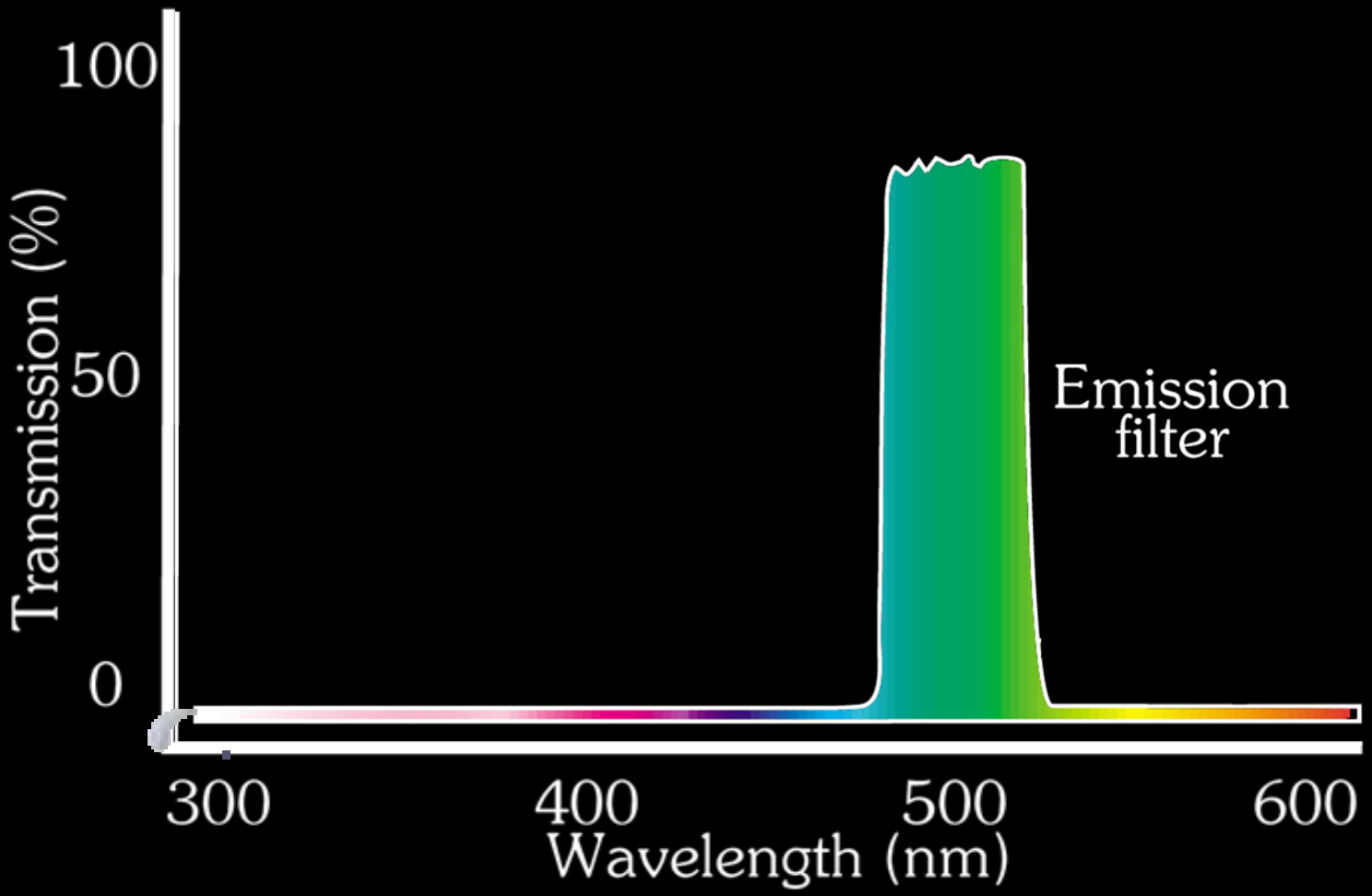
- Repetitive DNA
  - Repeated genes
    - rDNA (45S and 5S)
  - Sequence motifs from 2 to 20,000 bp long ...
    - Repeated thousands of times in the genome


Aegilops umbellulata
DAPI
18S-25S rDNA
5S rDNA
Xana Castilho & Pat Heslop-Harrison

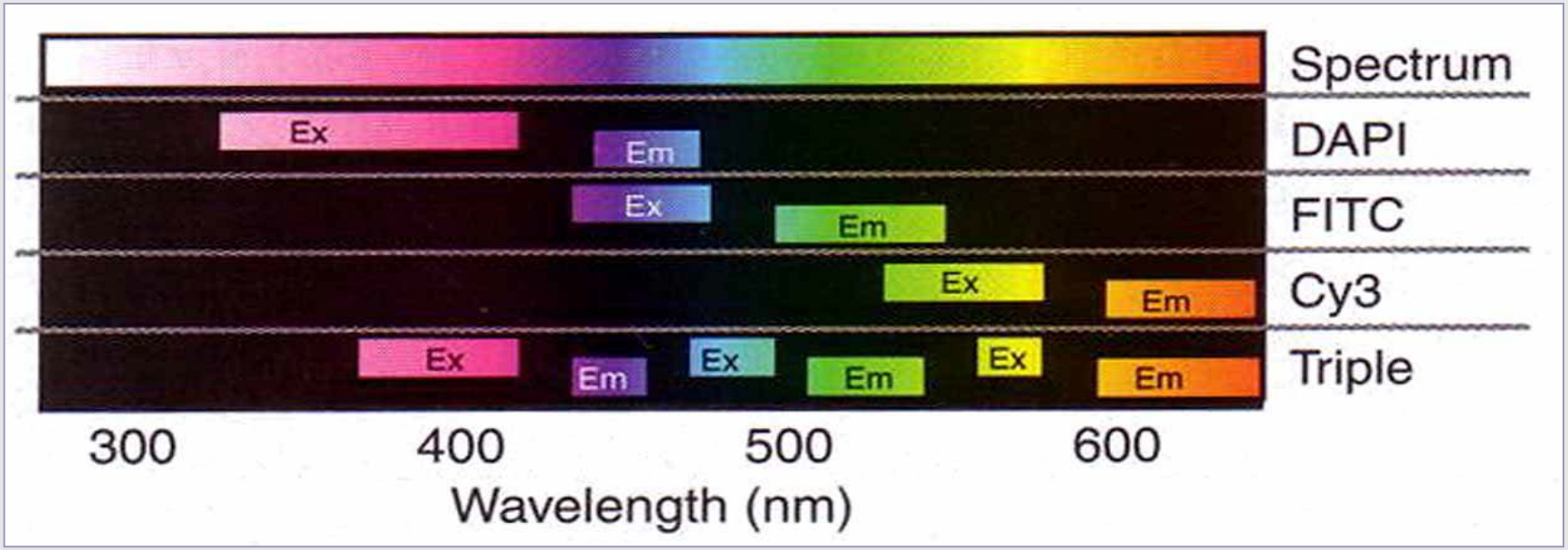
Fluorsecence microscopy


Detector
eye/camera/PMT
Emission
(barrier)
filter
Condenser
lens
Dichroic beam
splitter
Excitation
filter
Illumination -
laser/bulb
Objective lens
Fluorescent
specimen

Fluorescence microscope filter properties

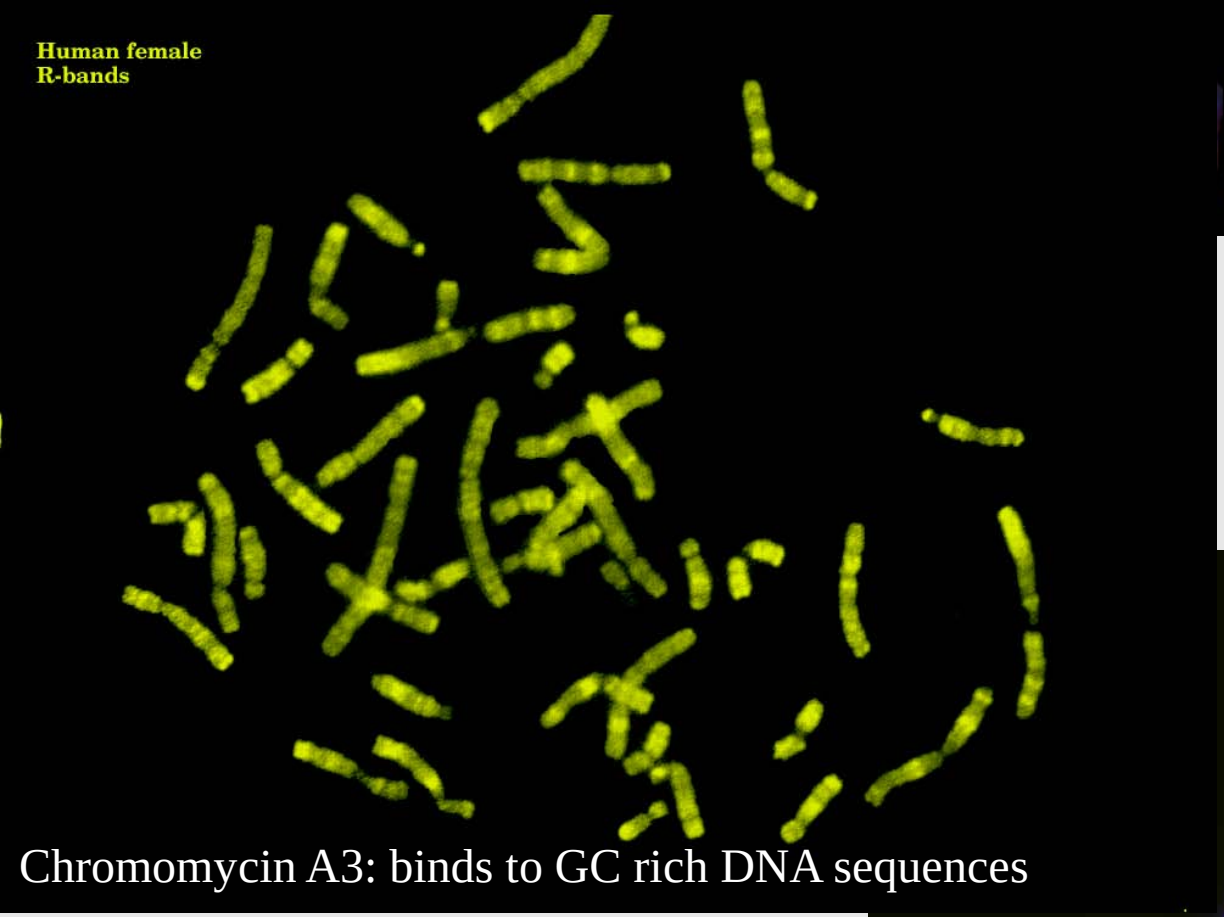


Fluorsecence microscopy

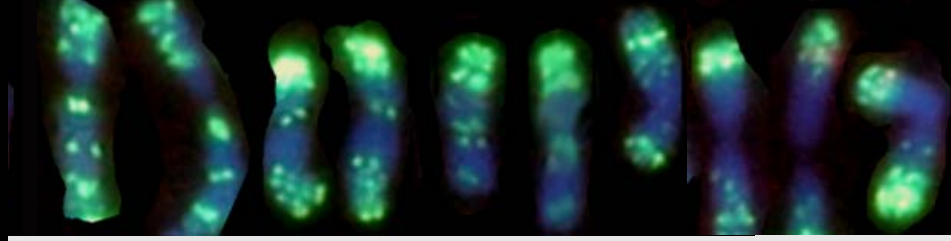


Multi-colour FISH:

- Hybridizing two or more DNA pobes simultaneous
- Multibandpass filters

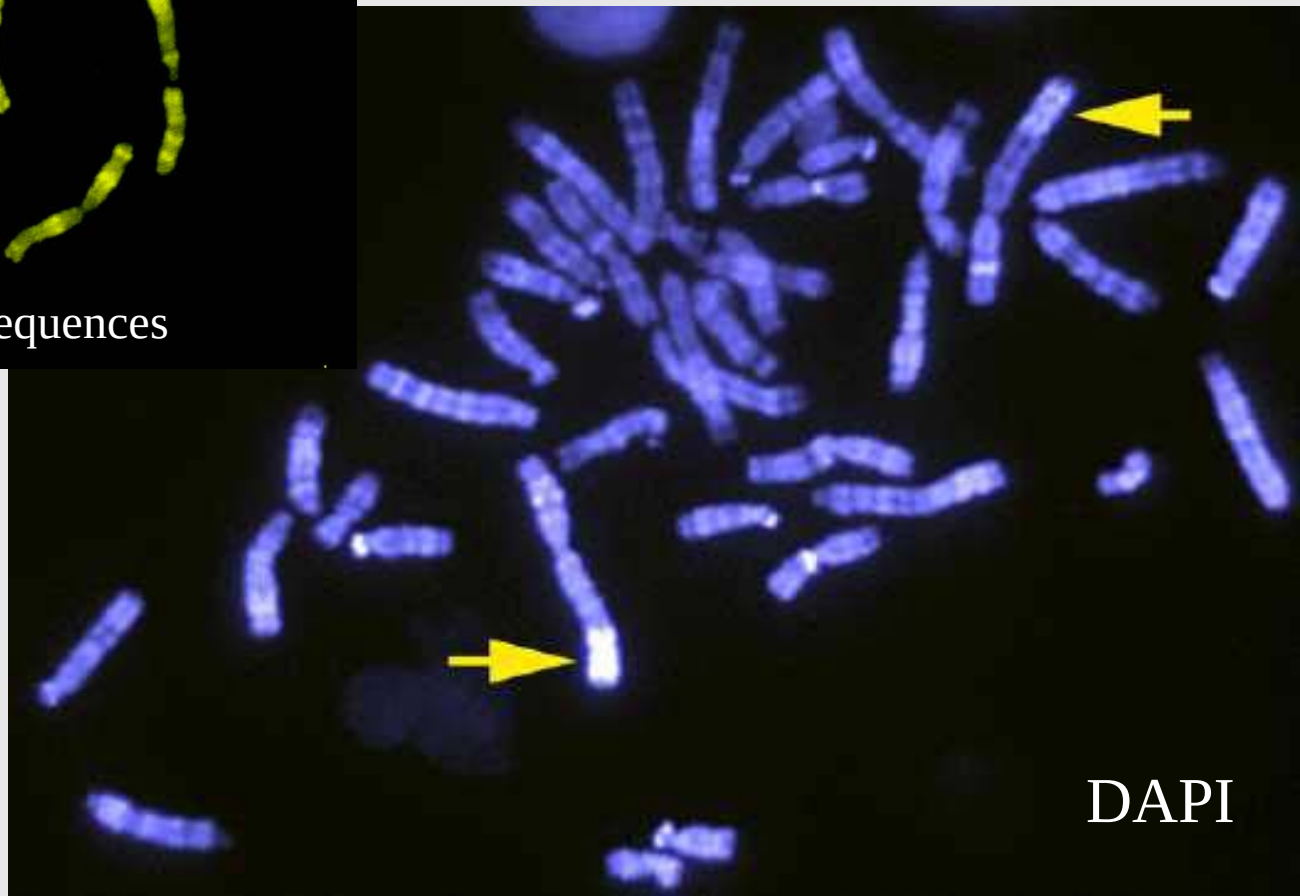


Chromomycin A3: binds to GC rich DNA sequences

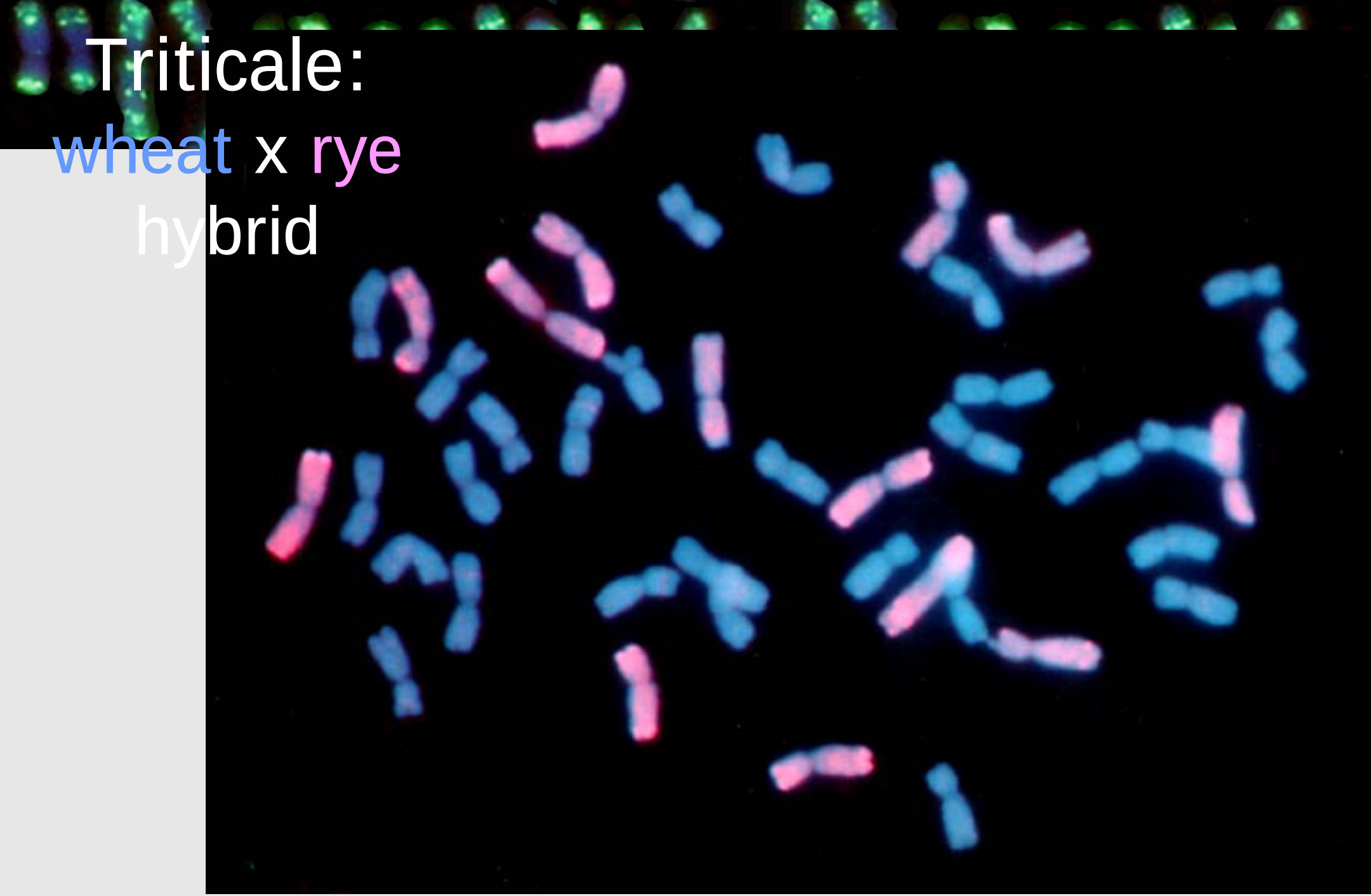


Fluorescent banding

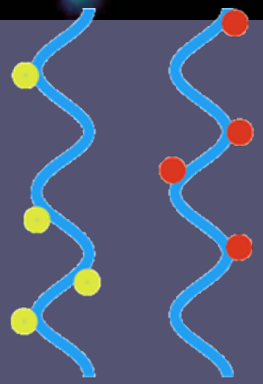
DAPI: AT-rich
ChromomycinA3: GC-rich



DAPI

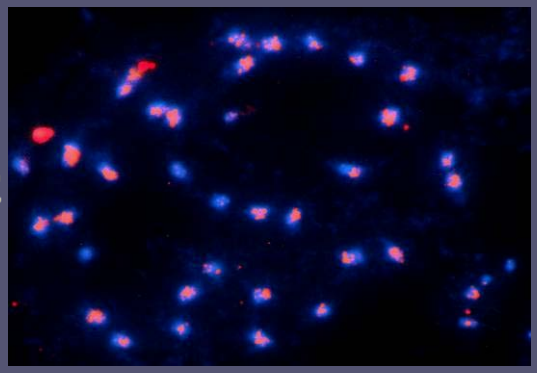

Triticale:
wheat x rye
hybrid

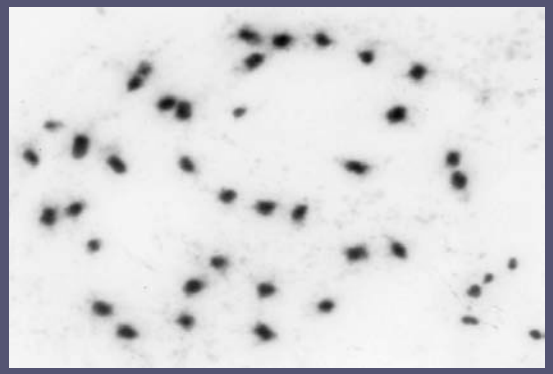
In situ (and array) hybridization technology



Probes

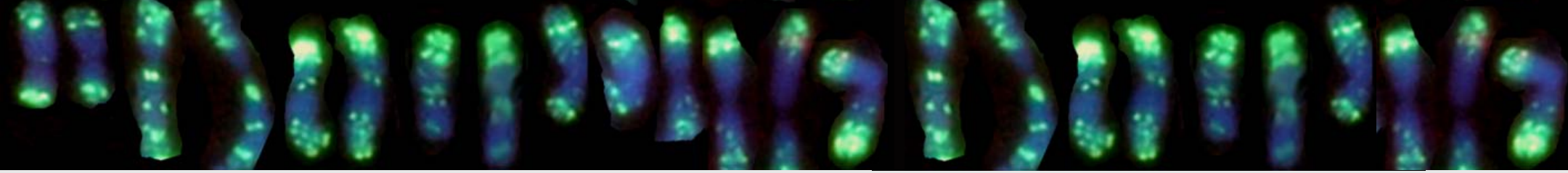
Hybridize



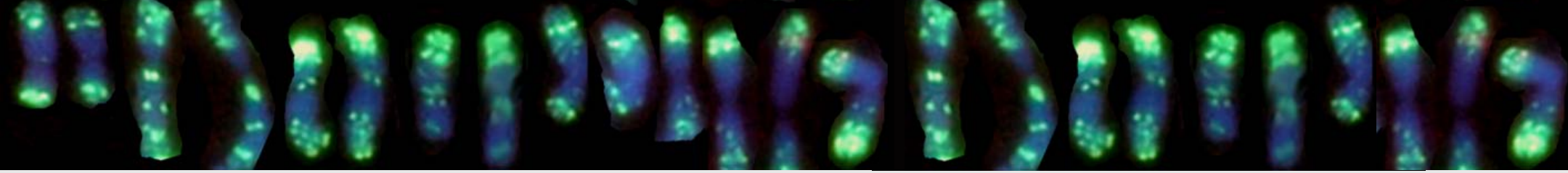


Chromosome preparation

Detection of Hybridization sites



What are the most important things you have learned so far?



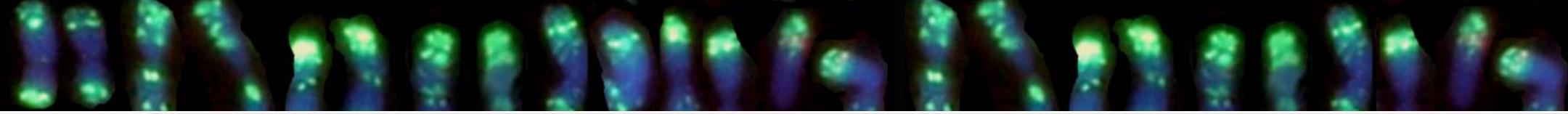
What are the most important things you have learned so far?

My answer: CONTACTS

… lecturers and other students.

SOURCES OF INFORMATION

... solving the overload



www.google.com/ig

BBC - Homepage | EJP AoB | AoB Blog « | Post to CiteULike | Times Higher Educatio... | Import to Mendeley | Blackboard | Share on FriendFeed | www.hpa.org.uk/ | Amazon.com: Custom...

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Pat H

iGoogle

Advanced search
Language tools

Google Search | I'm Feeling Lucky

Home

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Friends

Chat

Search contacts...

Pat Heslop-Harriso
available

David Ray

Options | Add Contact

AoB Blog

- Mechanical perturbation of Arabidopsis
- Darwin reviews reviewed
- Disproving a C4 reversion in Eragrostis

Google Reader: Starred items

Starred items | refresh | mark all as read

- annbot: Link: Feeding the World – who pays? from Twitter / annbot
- A fast-neutron induced chromosome fragment from Chromosome Research (Online First™)
- Comparing chromosomal and mitochondrial from Chromosome Research (Online First™)
- A Three-Dimensional RNA Motif in Potato from The Plant Cell current issue
- Improved reporting shows wider prevalence of from Health Protection Agency
- Pathh1: Plant Breeding: It's a Journey, Not a from Twitter / Pathh1

MicrobiologyBytes

- New Year resolution failure
- There's an awful lot of zombie ant fungi in Brazil
- Innate immune sensing of DNA viruses

Science of the Invisible

- Cracking the mysteries of R
  For the last two years I've been slowly working my way towards a new approach to teaching statistics. As my teaching load eases off I've finally...
- Face to face #scireadr
- A discussion breaks out #oerbital

Nature - Issue - nature.com science feeds

- The generation game
- Invest to diversify

Gatsby Plants | Plant News fe

- India needs more plant tax
- Agriculture: A bowl half full
- Alien plant invaders threat
  Parks

BBC News - Science & Enviro

- UK rocket test for 1,000m
  The first full test firing of the rocket that will power a Bri to over 1,000mph (1,670k will take place in the comi
- EU 'won't change carbon t
- Nasa Glory launch ends in

Weather

Nîmes, Languedoc-Roussi

14°C Current: C
Wind: SW

TweetDeck v0.37.5

Search: annbot

Link: Feeding the World – who pays? http://dlvr.it/JQG9d

annbot, [+]
Sun 06 Mar 12:52 via dlvr.it

Mechanical perturbation of Arabidopsis http://dlvr.it/JFF1m

annbot, [+]
Fri 04 Mar 13:27 via dlvr.it

Darwin reviews reviewed http://dlvr.it/J82zN

annbot, [+]
Thu 03 Mar 13:04 via dlvr.it

ANNbotRT

Search: pathh1

Feeding the World - who pays? Alun Cann's commentary on The Economist article on the 9 billion people question. http://t.co/VdB3e44

Pathh1, [+]
Sun 06 Mar 15:16 via FriendFeed

Lots of good points on informal learning, social networks and teaching from Steve Wheeler, Plymouth. tks @rusource http://slidesha.re/e4Go8H

Pathh1, [+]
Sun 06 Mar 10:50 via web

Plant Breeding: It's a Journey, Not a Destination. From US National Assn of Plant Breeders. http://bit.ly/iaoR79

Pathh1, [+]
Fri 04 Mar 15:42 via TweetDeck

Read The Annbot Daily -

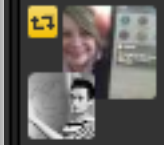
Search: chromosomes

Photosynthesis, Homologous Chromosomes, Cellular Respiration, Oxidative Phosphorylation, Meiosis, Deoxyribonucleic Acid. #FML

Anthony_WSUC, [+]
Mon 07 Mar 09:26 via txt

Réplication des chromosomes et lutte contre le #cancer http://goo.g/NS5W2 #biothérapies

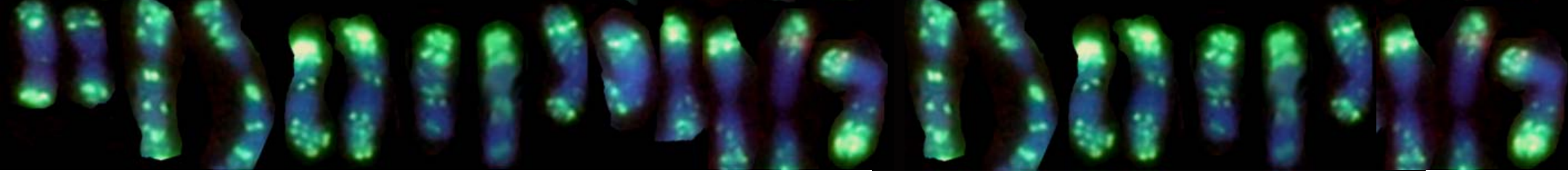
PierricChalois, [+]
Mon 07 Mar 09:11 via web



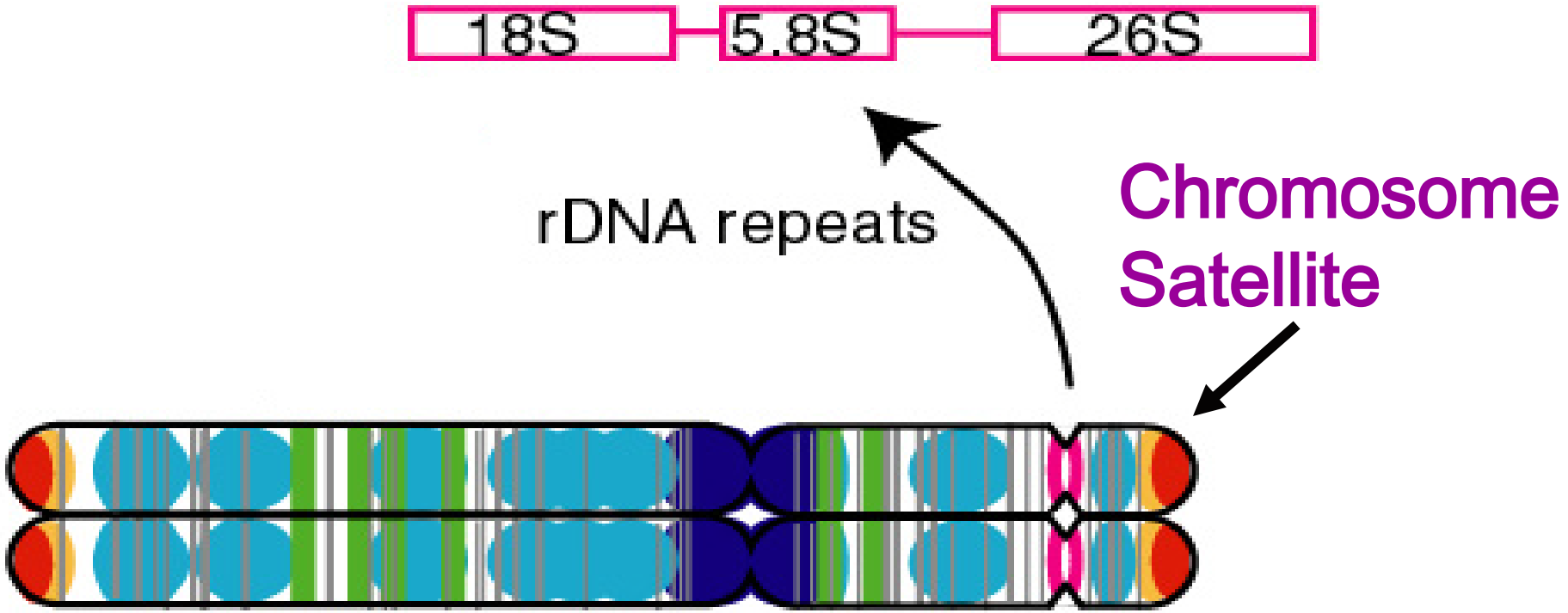
Holy cow - read a great paper, was looking up more by same author - she uses Mendeley - just asked to connect. Wow. Just wow.

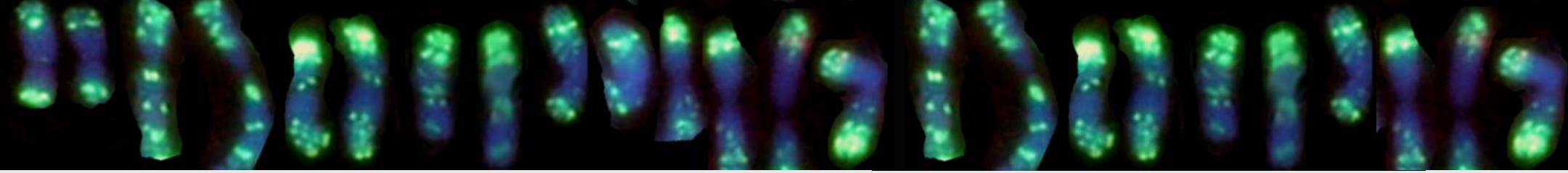
kerryjcom, (RT by mendeley_com), [+]
Mon 07 Mar 11:49

@Bronxbomber777 What comes

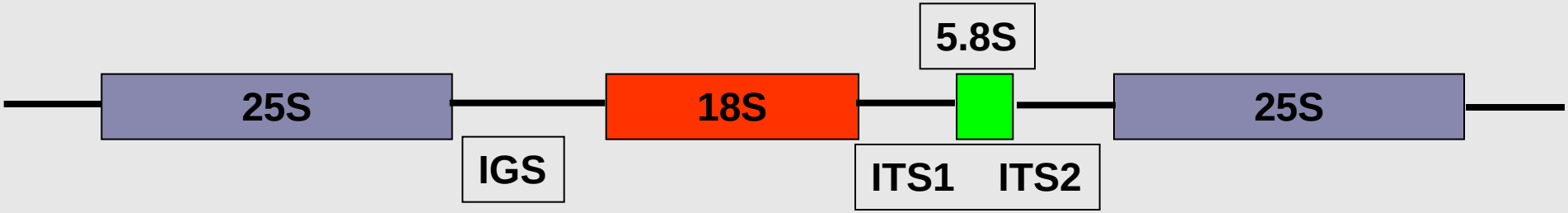


NOR: rDNA loci vary in number, position and size



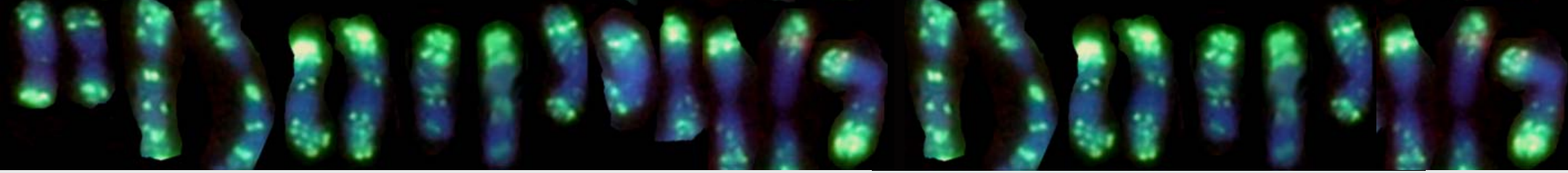


rDNA

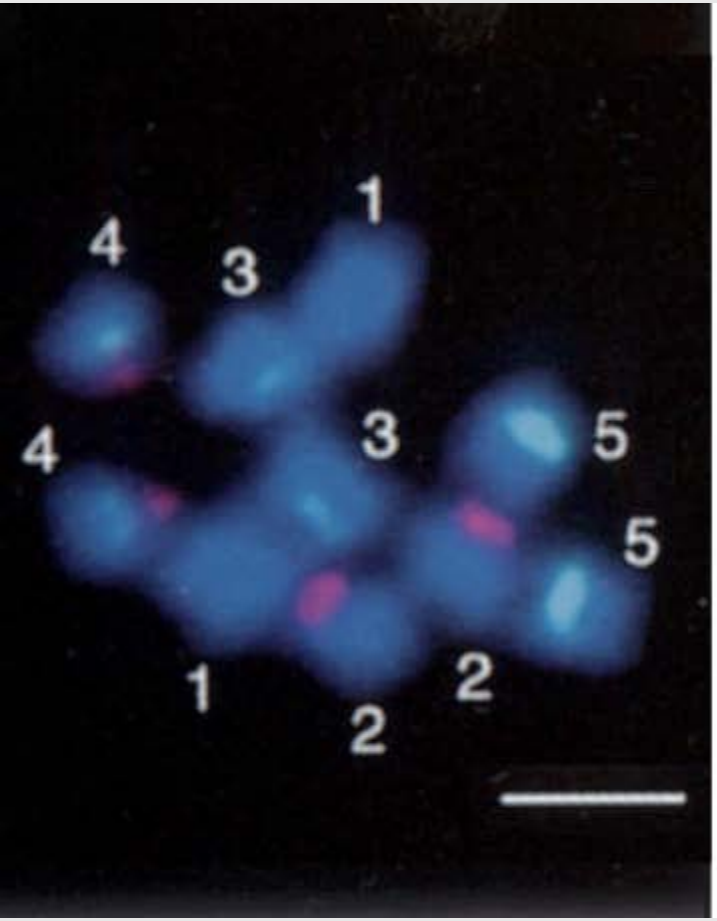


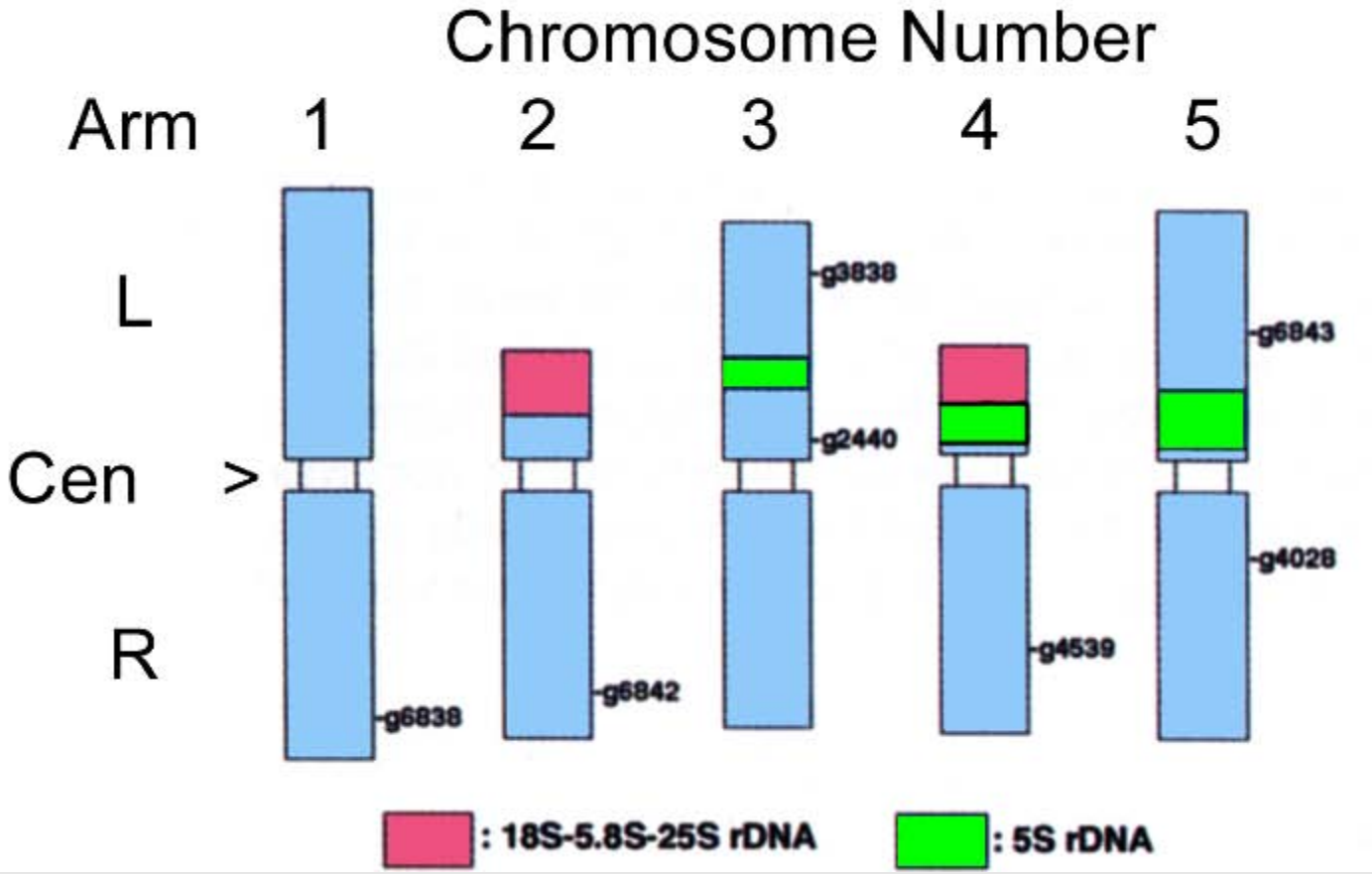
- Coding regions (nS) highly conserved, e.g. 18S gene of soybean shares 75% nucleotide homology with yeast.
  - Thus can compare over a long evolutionary distance
  - Can be used as anchors for PCR amplification
- Spacer regions highly variable
  - Species or below
  - Genus
  - Populations (sometimes)

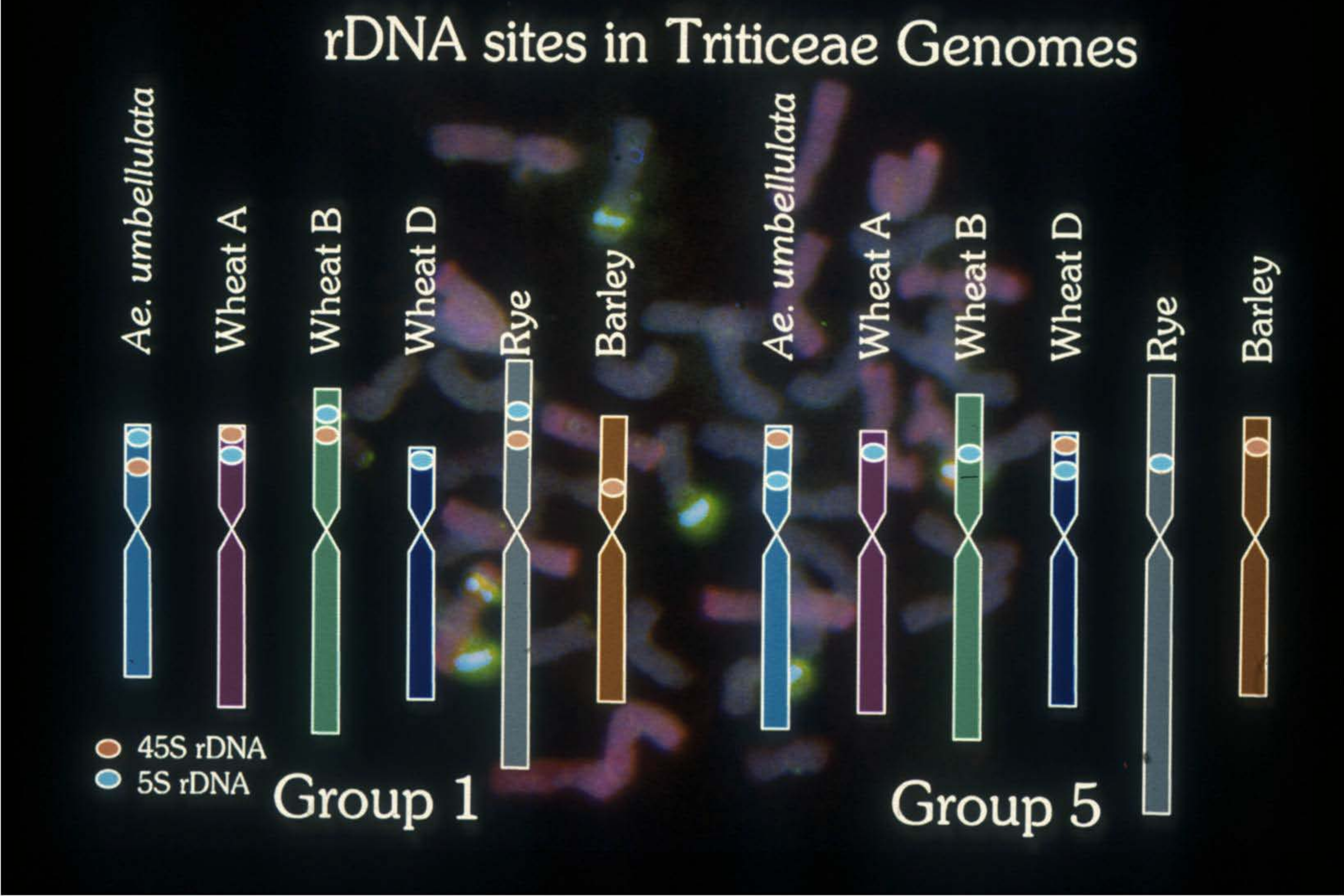
IGS…InterGenic Spacer or non-transcribed spacer
ITS…Internal Transcribed Spacer



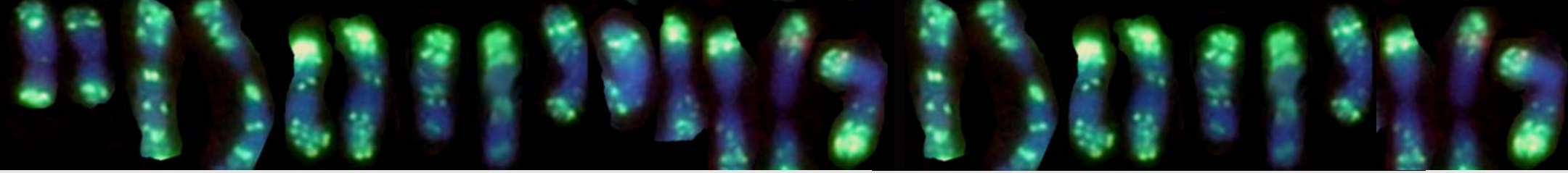
Arabidopsis thaliana 2n=10







rDNA sites in Triticeae Genomes
Ae. umbellulata
Wheat A
Wheat B
Wheat D
Rye
Barley
Ae. umbellulata
Wheat A
Wheat B
Wheat D
Rye
Barley
45S rDNA
5S rDNA
Group 1
Group 5

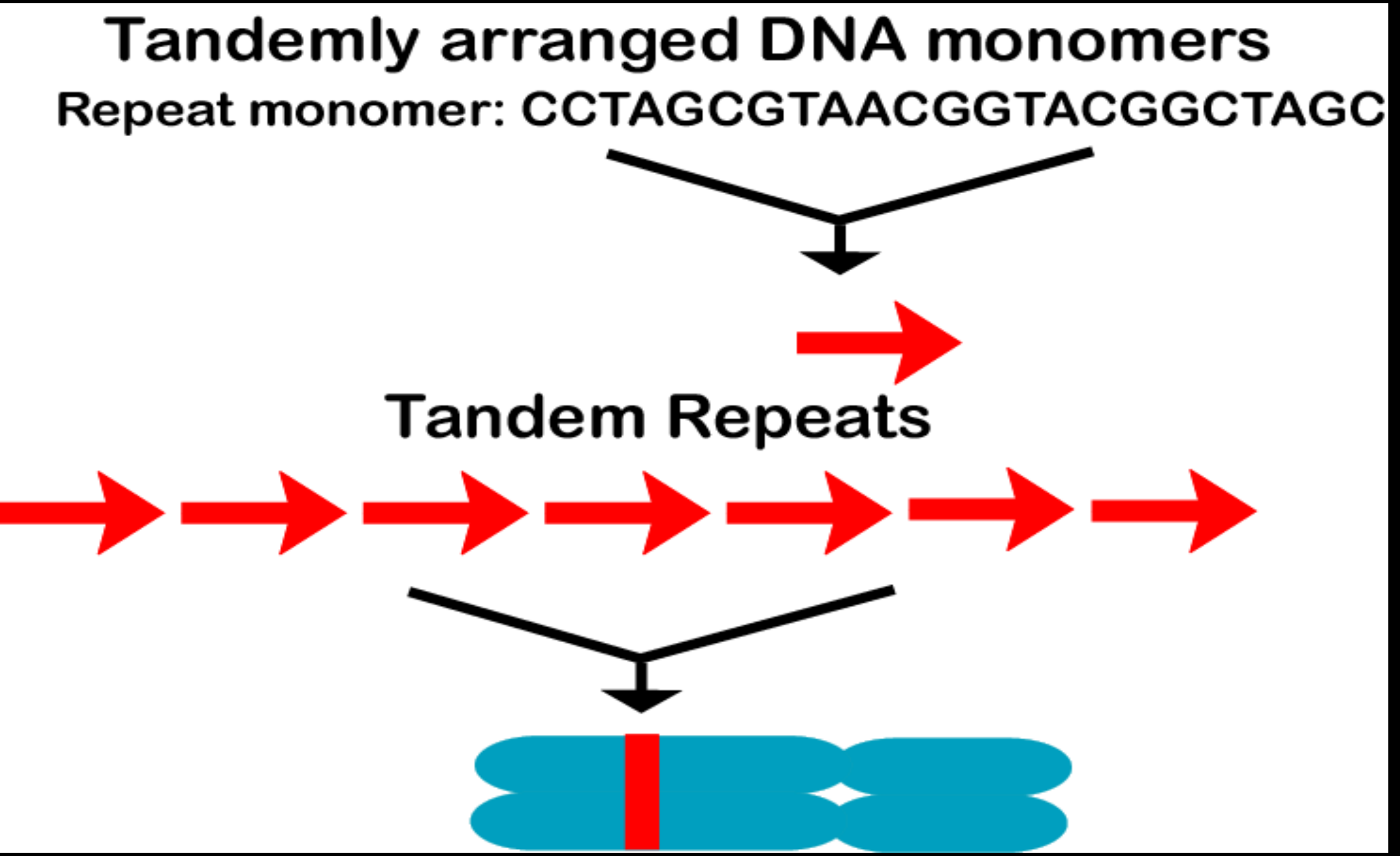


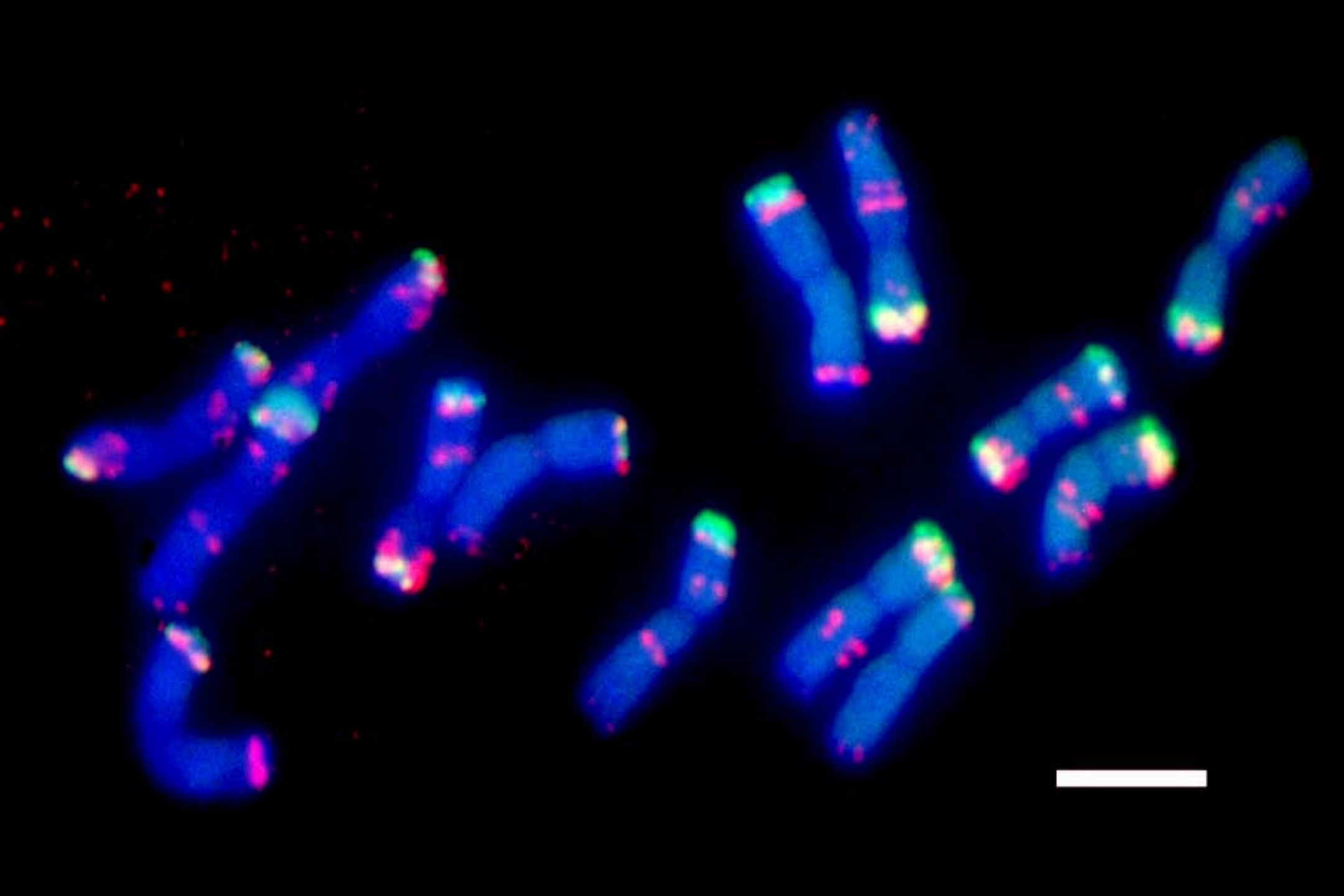
What is the rest of the genome?

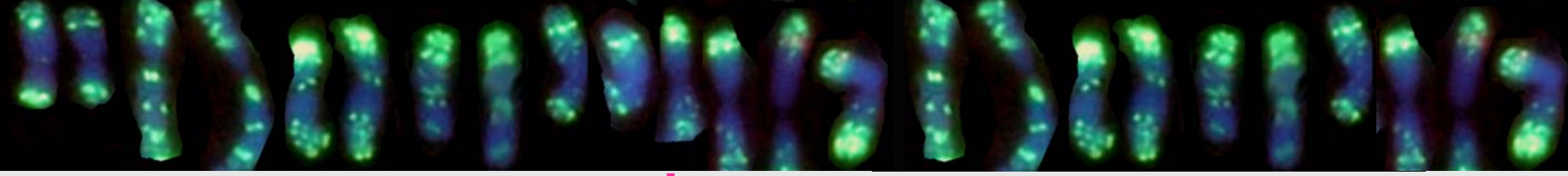
- Repetitive DNA
  - Repeated genes
    - rDNA (45S and 5S)
  - Sequence motifs from 2 to 20,000 bp long ...
    - Repeated thousands of times in the genome

Tandem Repeats

- Where each arrow is a single unit of a repeat –
- - often a multiple of 180 bp but up to 10kb long
-
- Head-to-tail organization
- GCGCTAG GCGCTAG GCGCTAG GCGCTAG GCGCTAG GCGCTAG


Tandemly arranged DNA monomers
Repeat monomer: CCTAGCGTAACGGTACGGCTAGC
Tandem Repeats



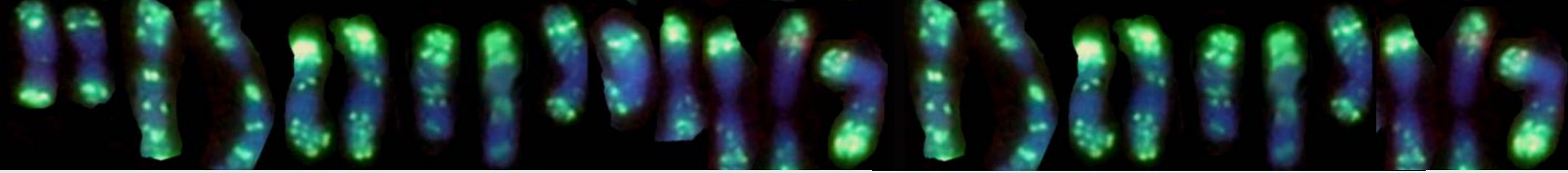


Repeated DNA sequences

motifs of 2-1000s of bp, repeated 10-10 000x

- Tandem repeats
  - genes: rDNA, histones
  - long tandem repeats or satellite sequences
  - simple sequence repeats
    - Microsatellites
    - Minisatellites

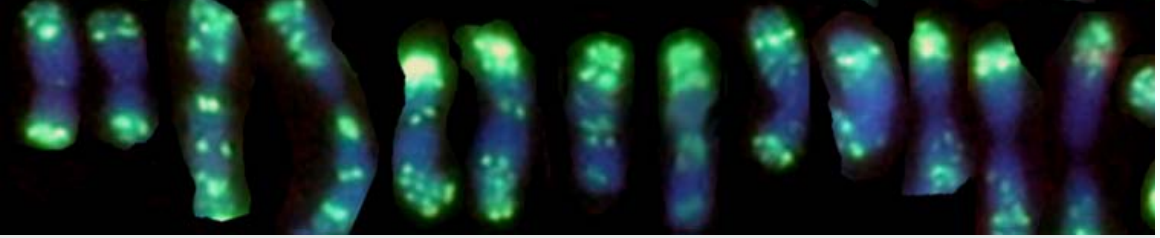
Satellite: shoulder on CsCl gradient centrifuge or Band in restriction digest

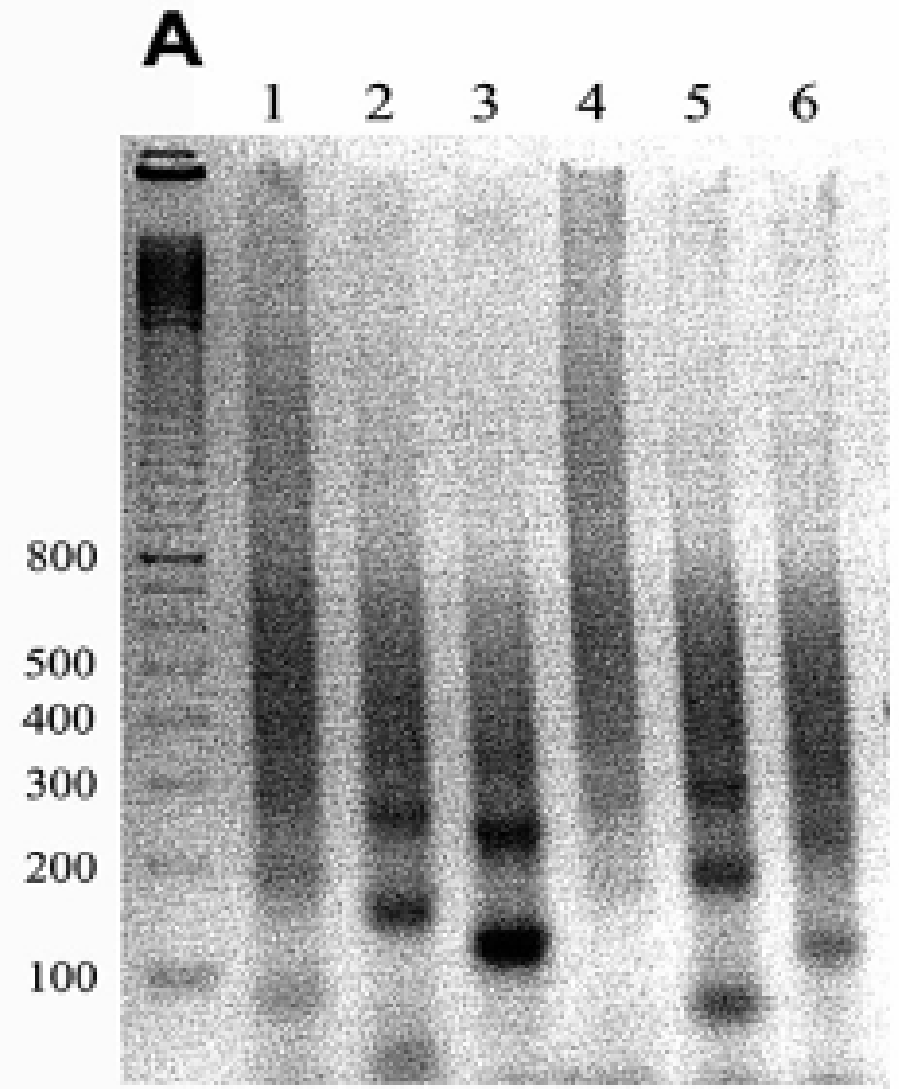


Tandem Repeats

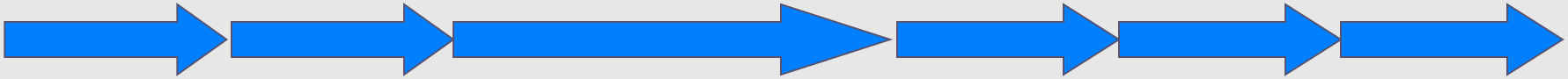
- Where each arrow is a single unit of a repeat – often a multiple of 180 bp but up to 10kb long

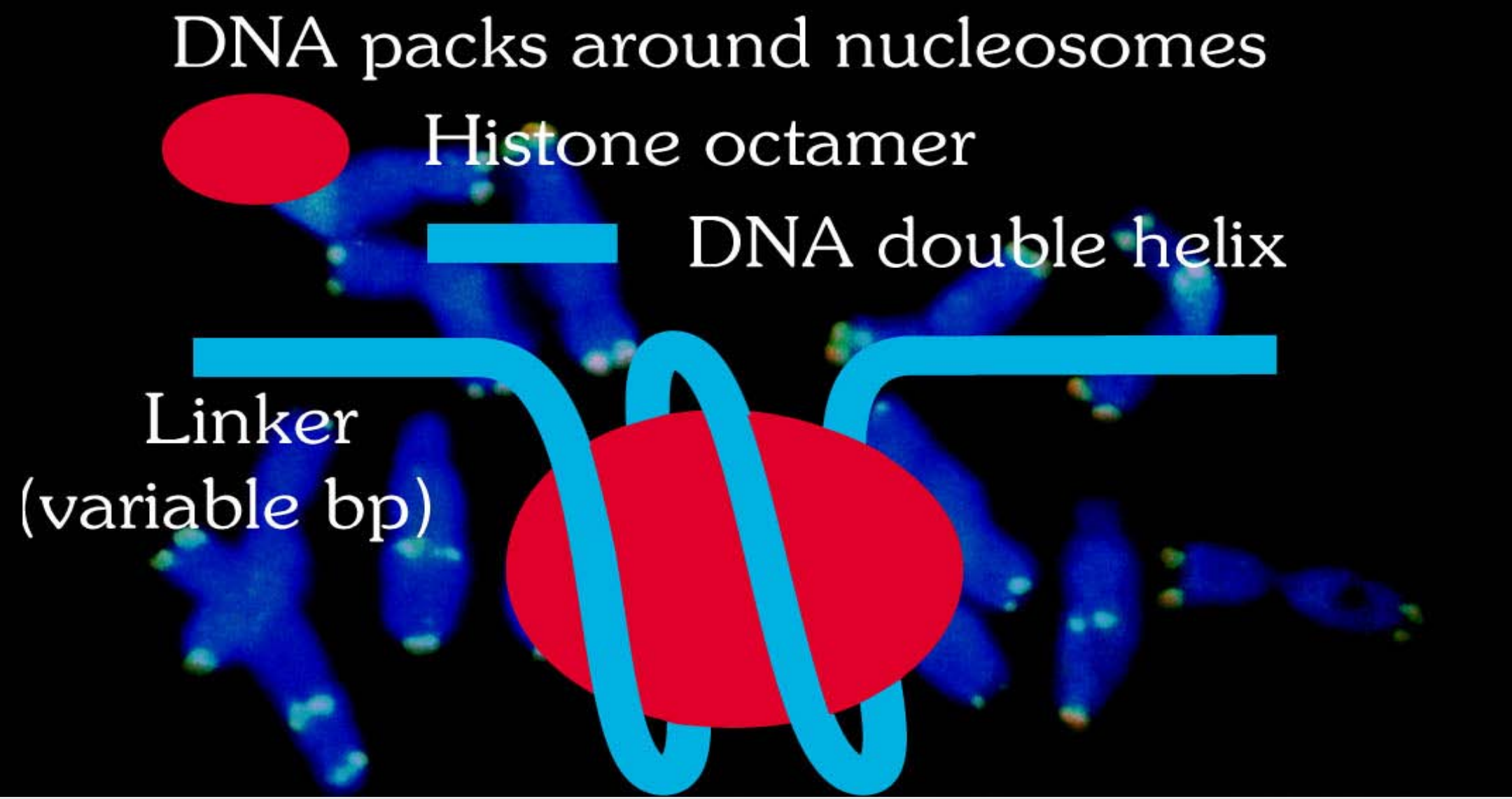
- GAGGCGTC GAGGCGTC GAGGCGTC GAGGCGTC GAGGCGTG GAGGCGTC GAGGCGTC GAGGCGTC GAGGCGTC GAGGCGTC GAGGCGTC GAGGCGTC



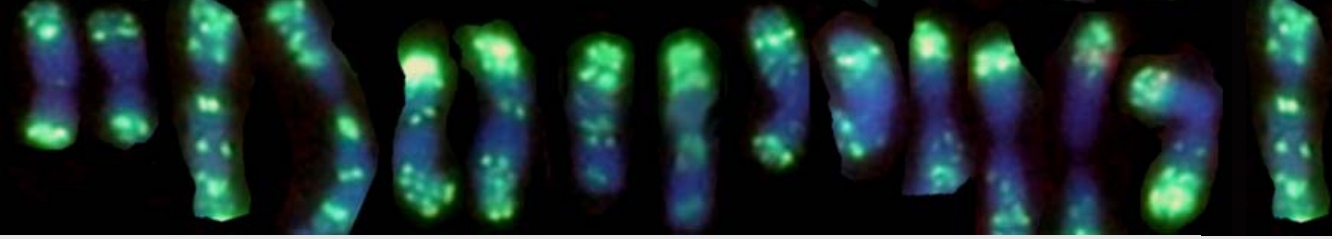


A complex sequence organization





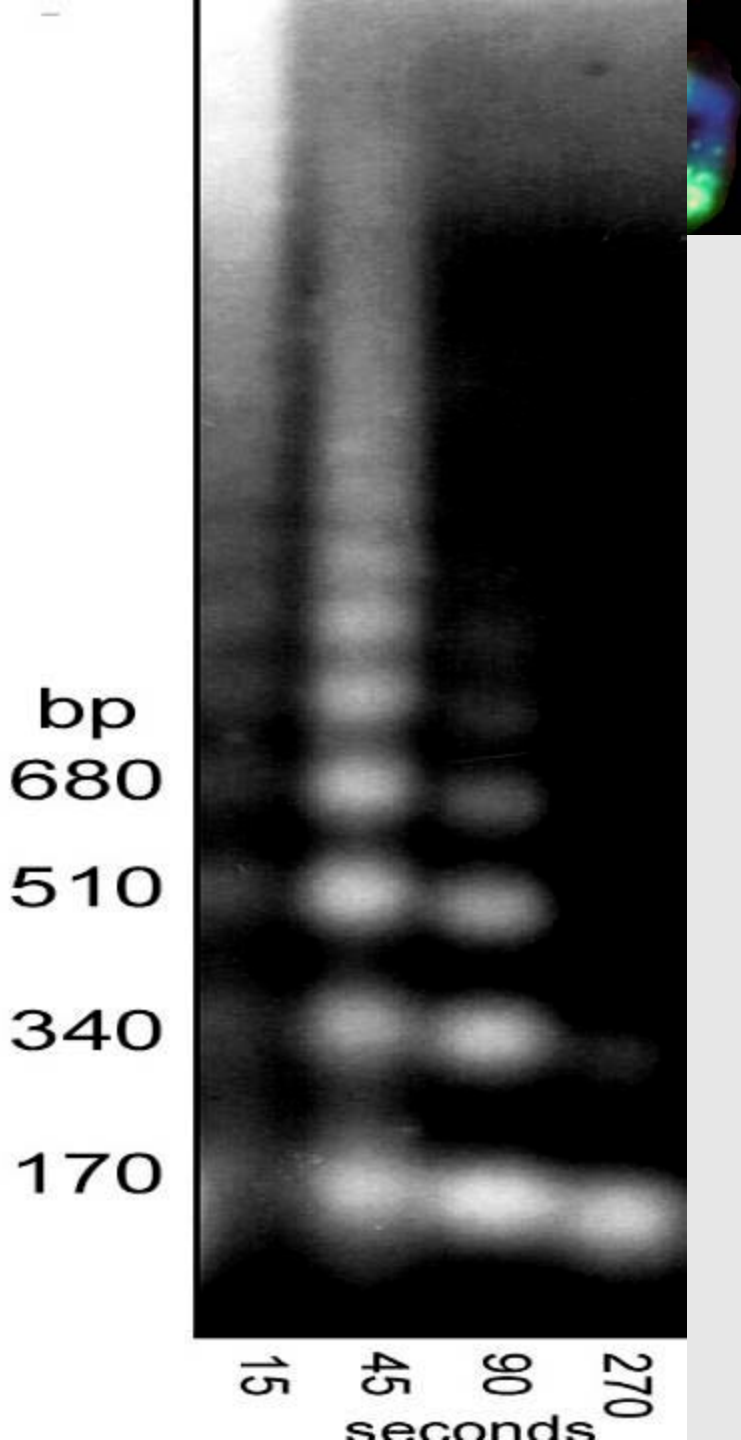
Two turns = 147 bp + linker to next nucleosome

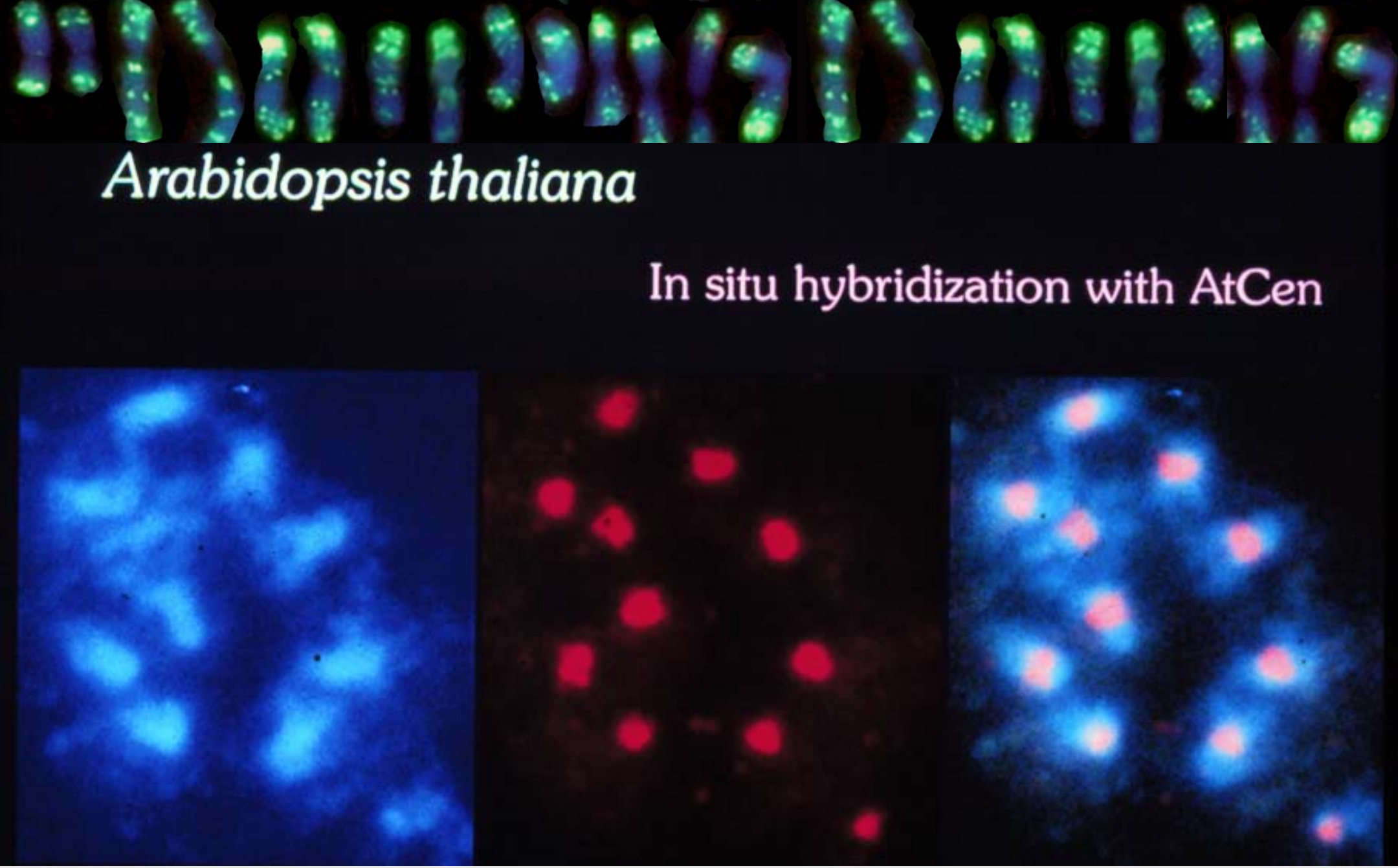


Nucleosomes in Rye

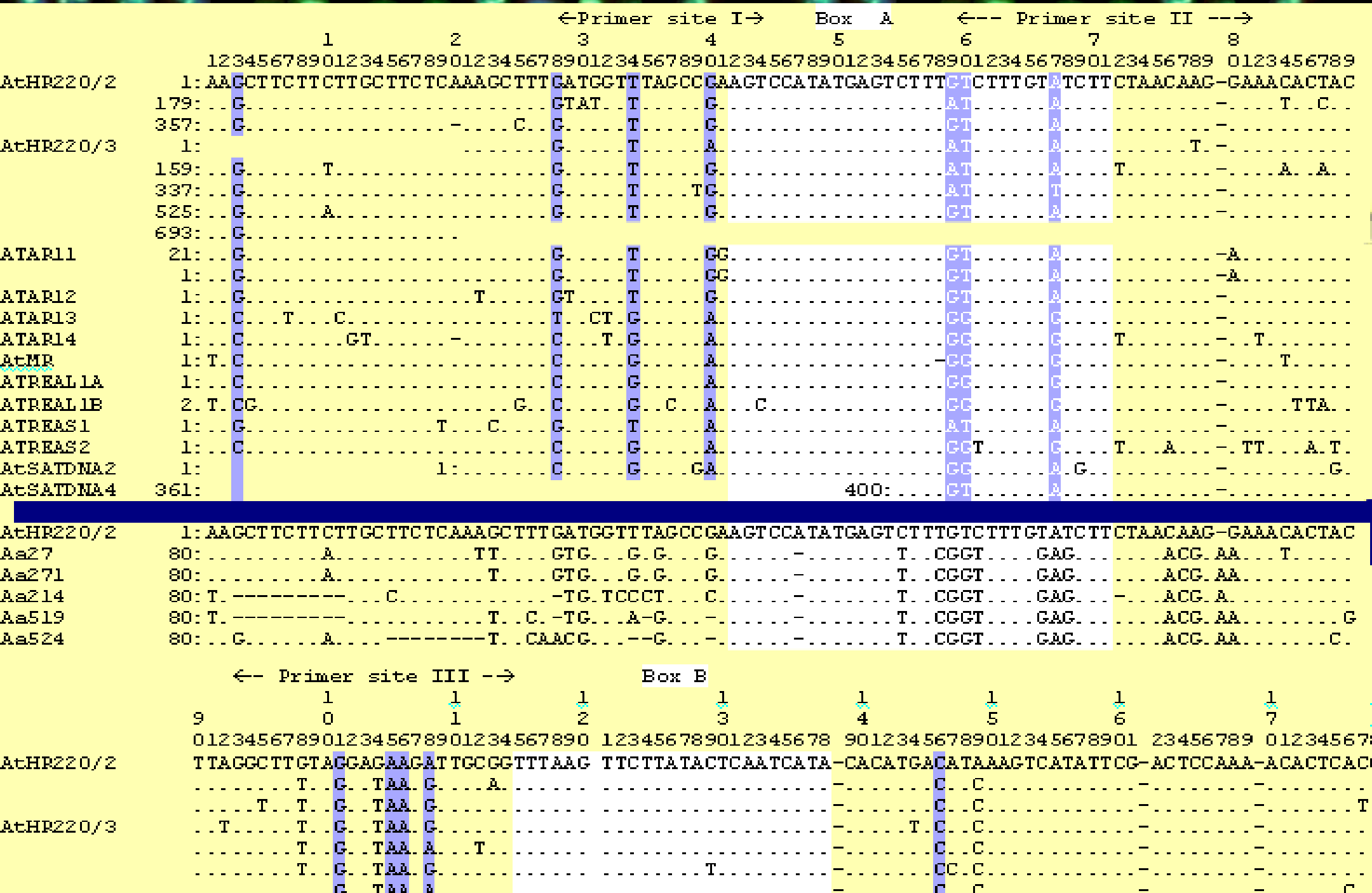
Digest intact chromatin (DNA + histone) with micrococcal nuclease for a few seconds, cutting between the nucleosomes. Then treat with protease and run on agarose gel.

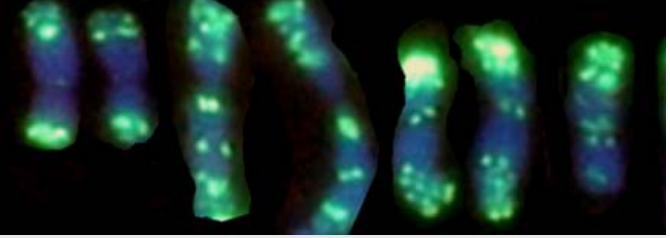
- Vershinin &
- Heslop-Harrison

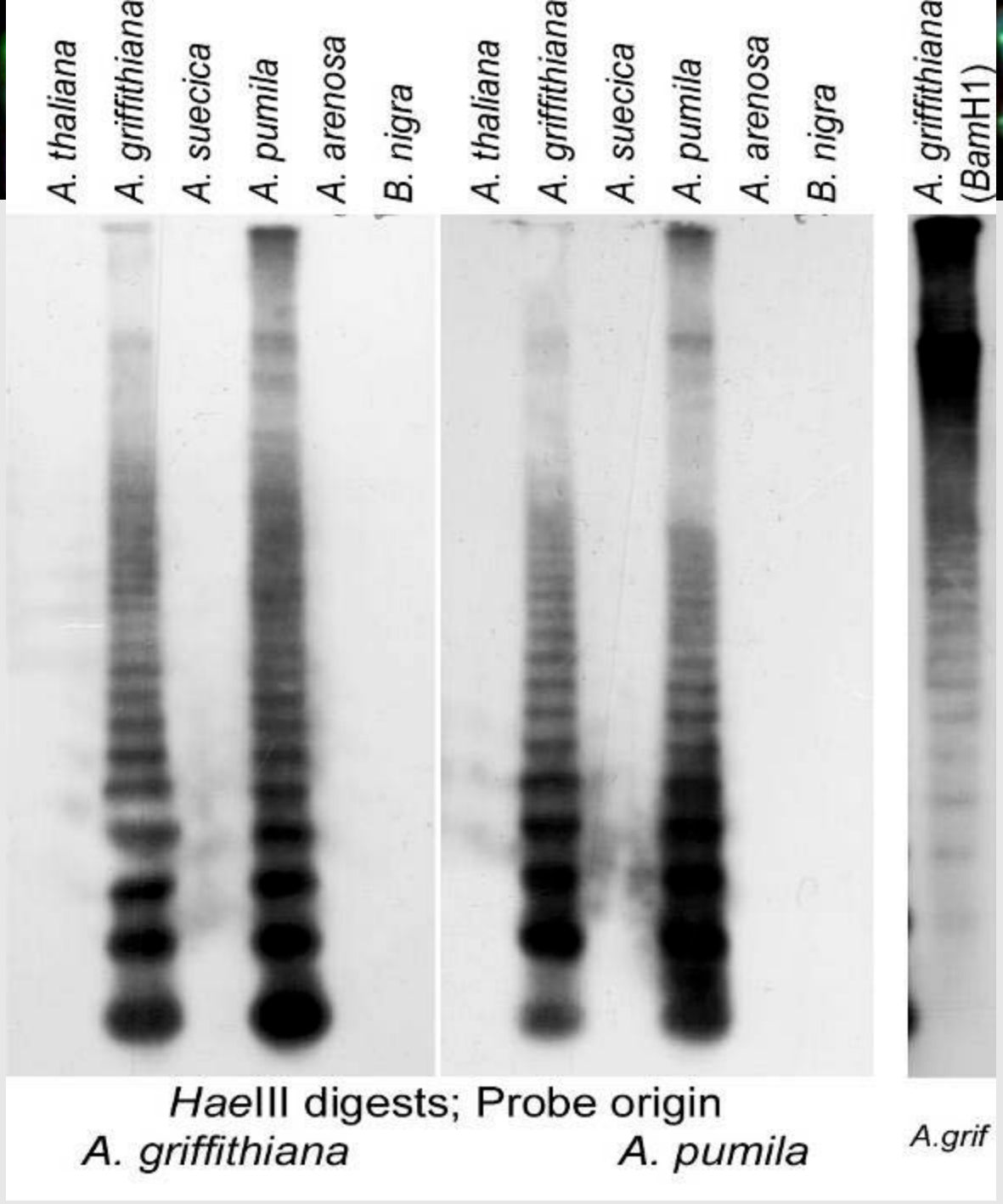


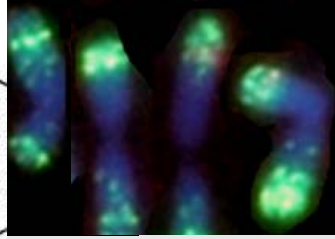


HH, Murata, Motoyoshi, Schwarzacher. Plant Cell


←Primer site I→ Box A ←-- Primer site II -->
AtHR220/2
AtHR220/3
ATAR11
ATAR12
ATAR13
ATAR14
AtMR
ATREAL1A
ATREAL1B
ATREAS1
ATREAS2
AtSATDNA2
AtSATDNA4
Aa27
Aa271
Aa214
Aa519
Aa524
← Primer site III →
Box B



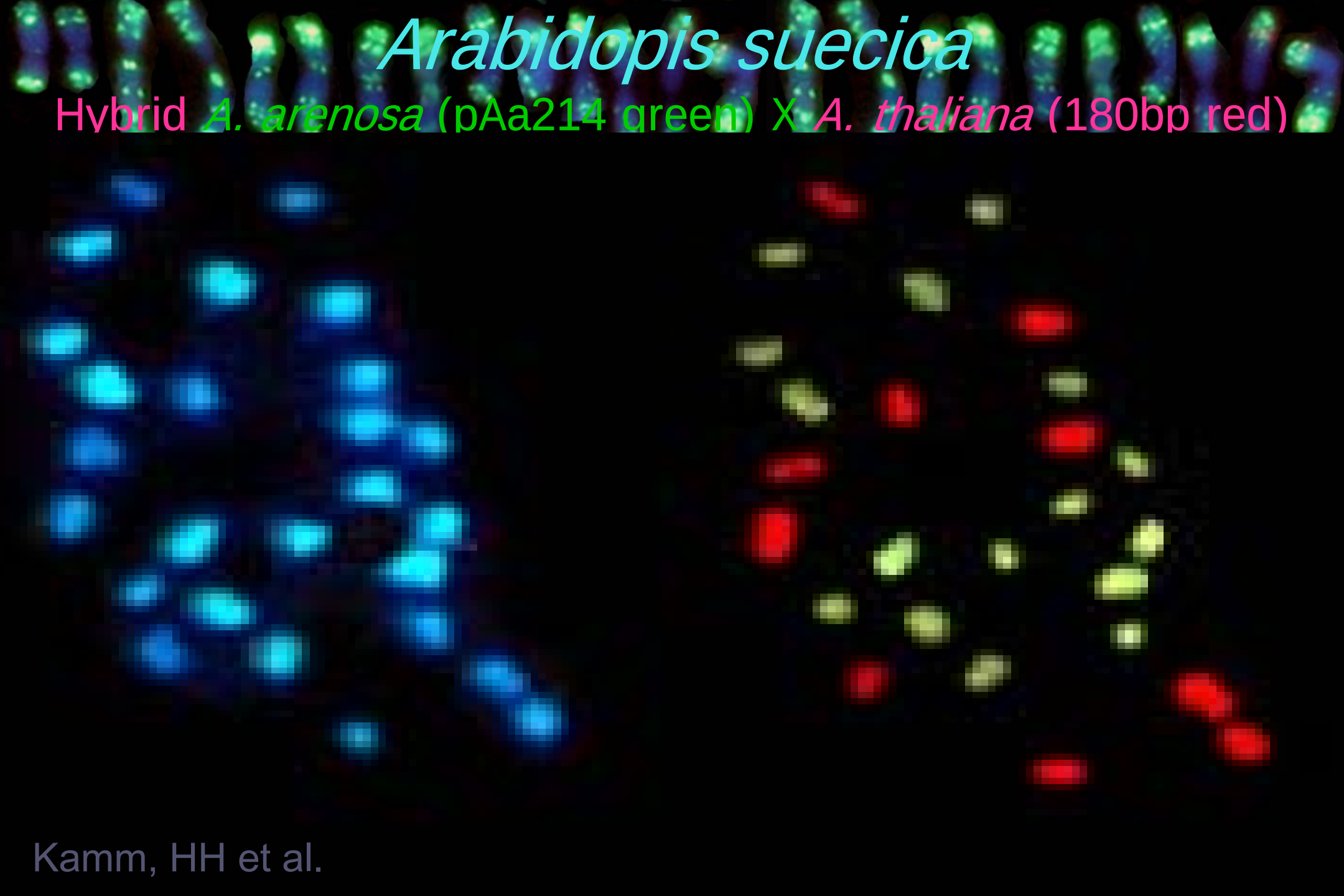




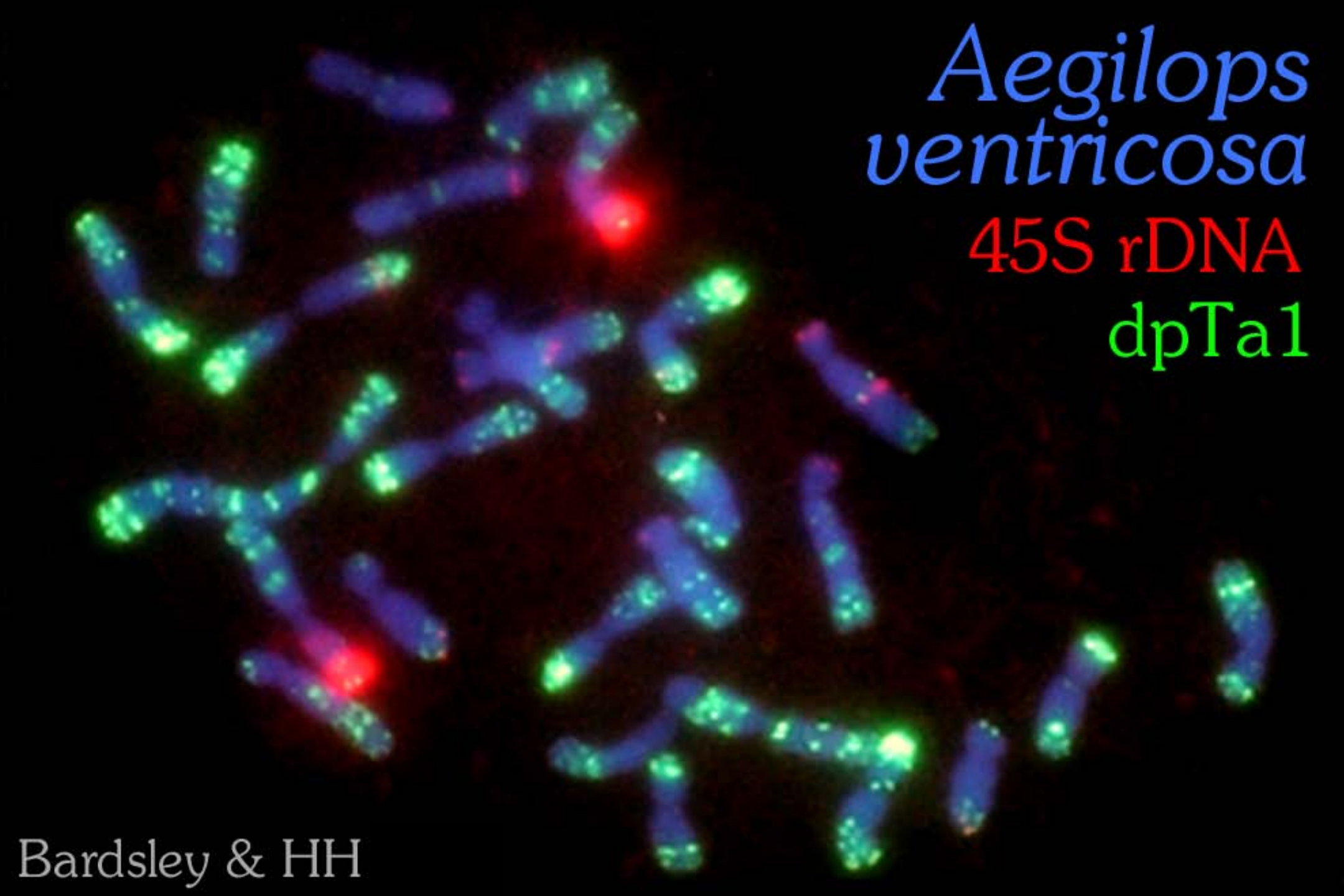
- HH, Brandes 2003

Arabidopis suecica

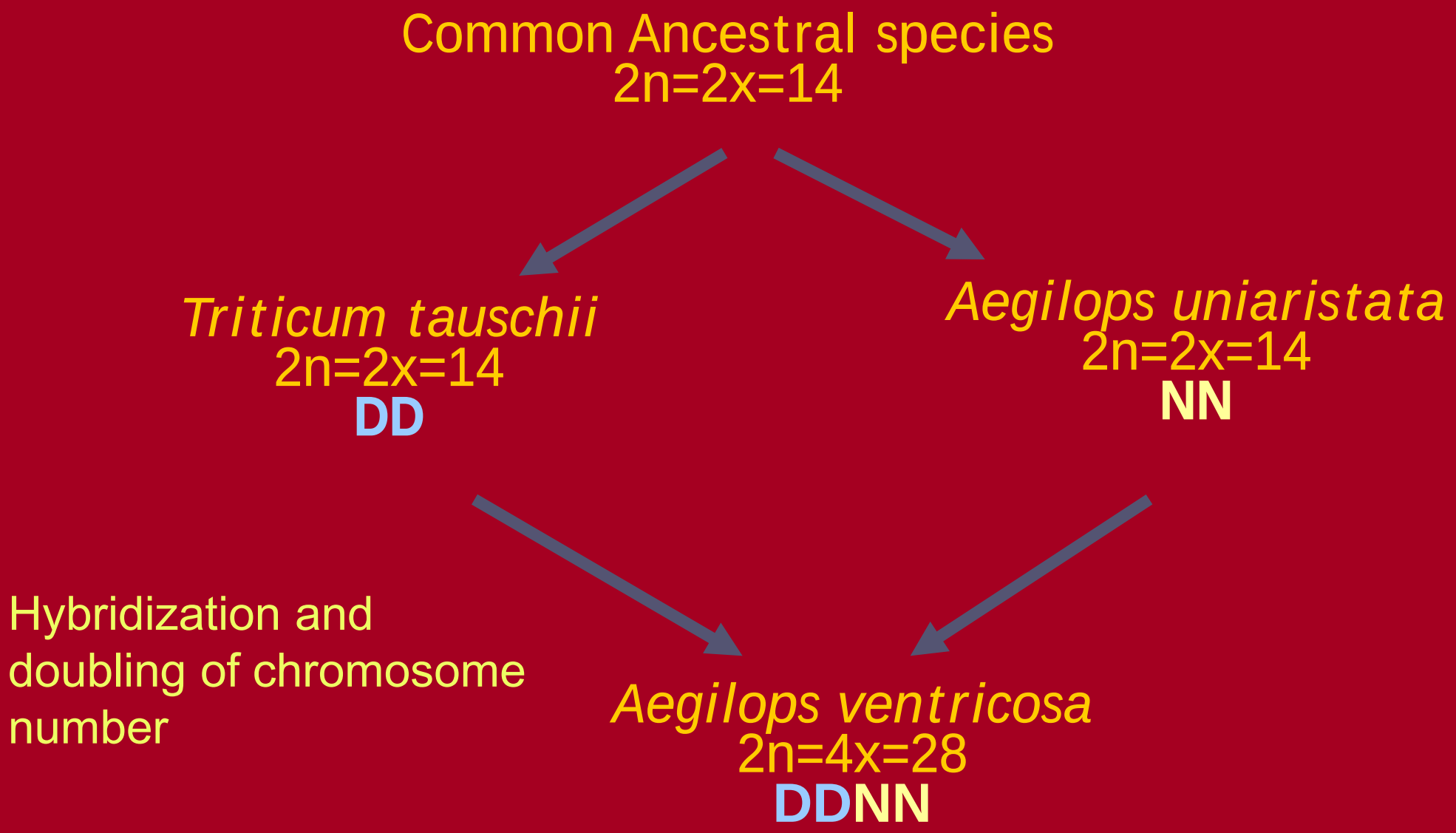
Hybrid *A. arenosa* (pAa214 green) X *A. thaliana* (180bp red)



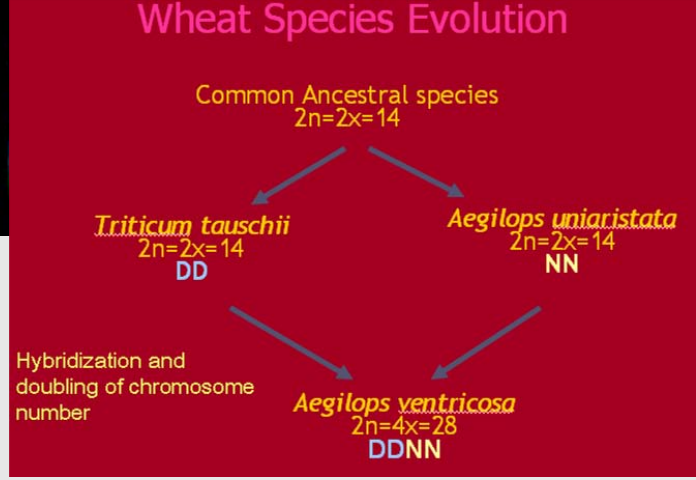
Kamm, HH et al.


Aegilops ventricosa
45S rDNA
dpTa1
Bardsley & HH

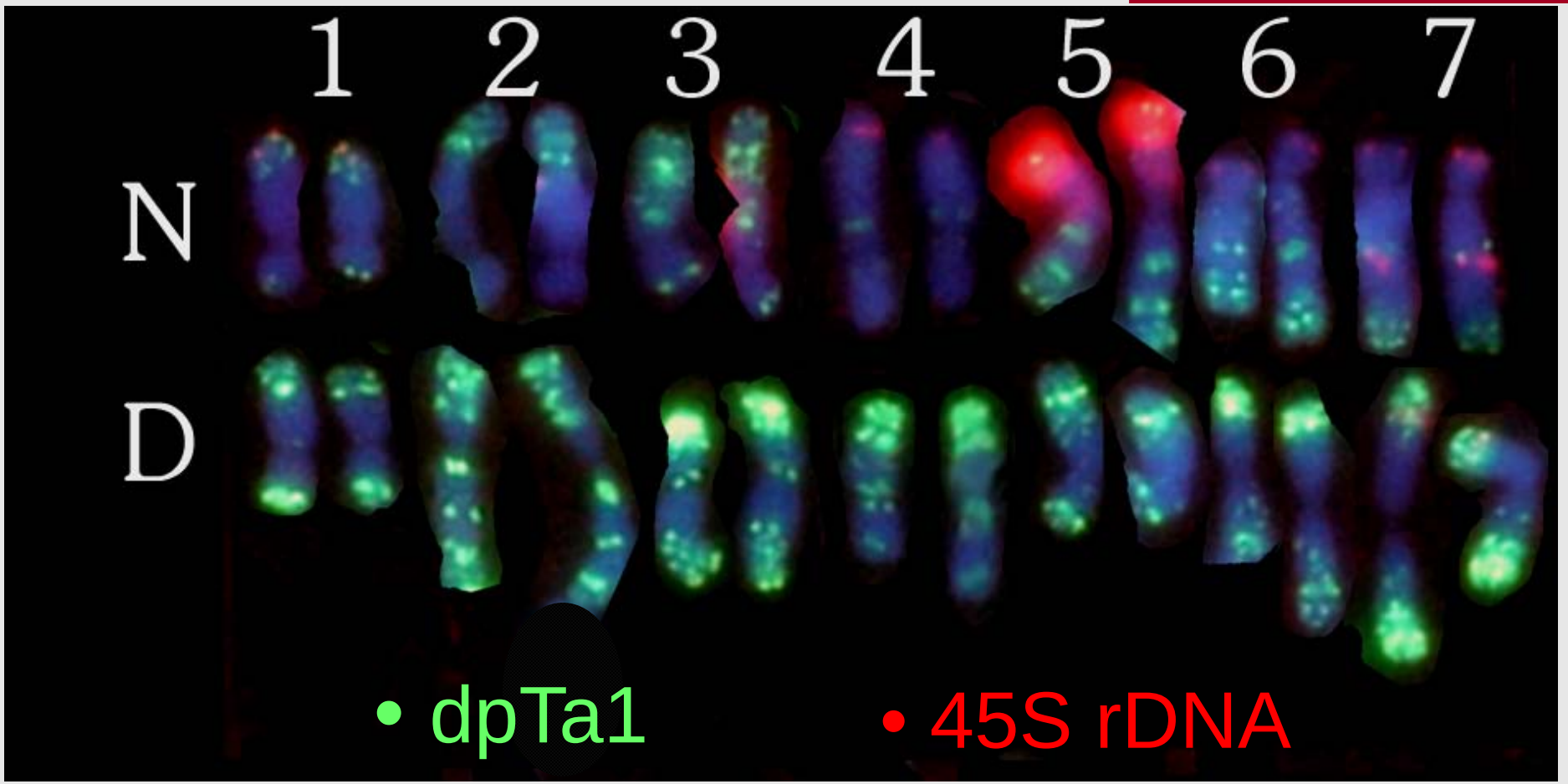
Wheat Species Evolution



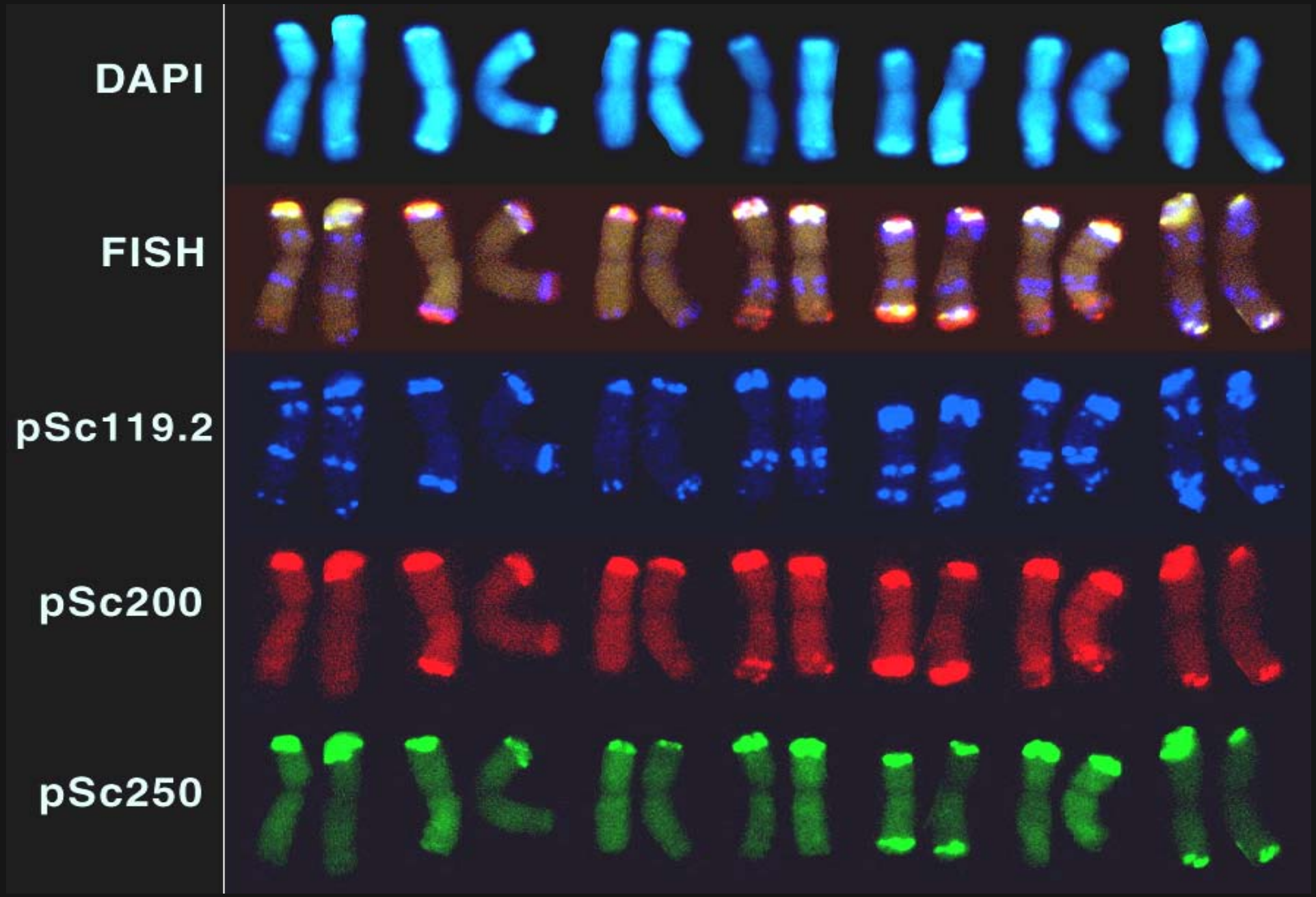
Differences between genomes



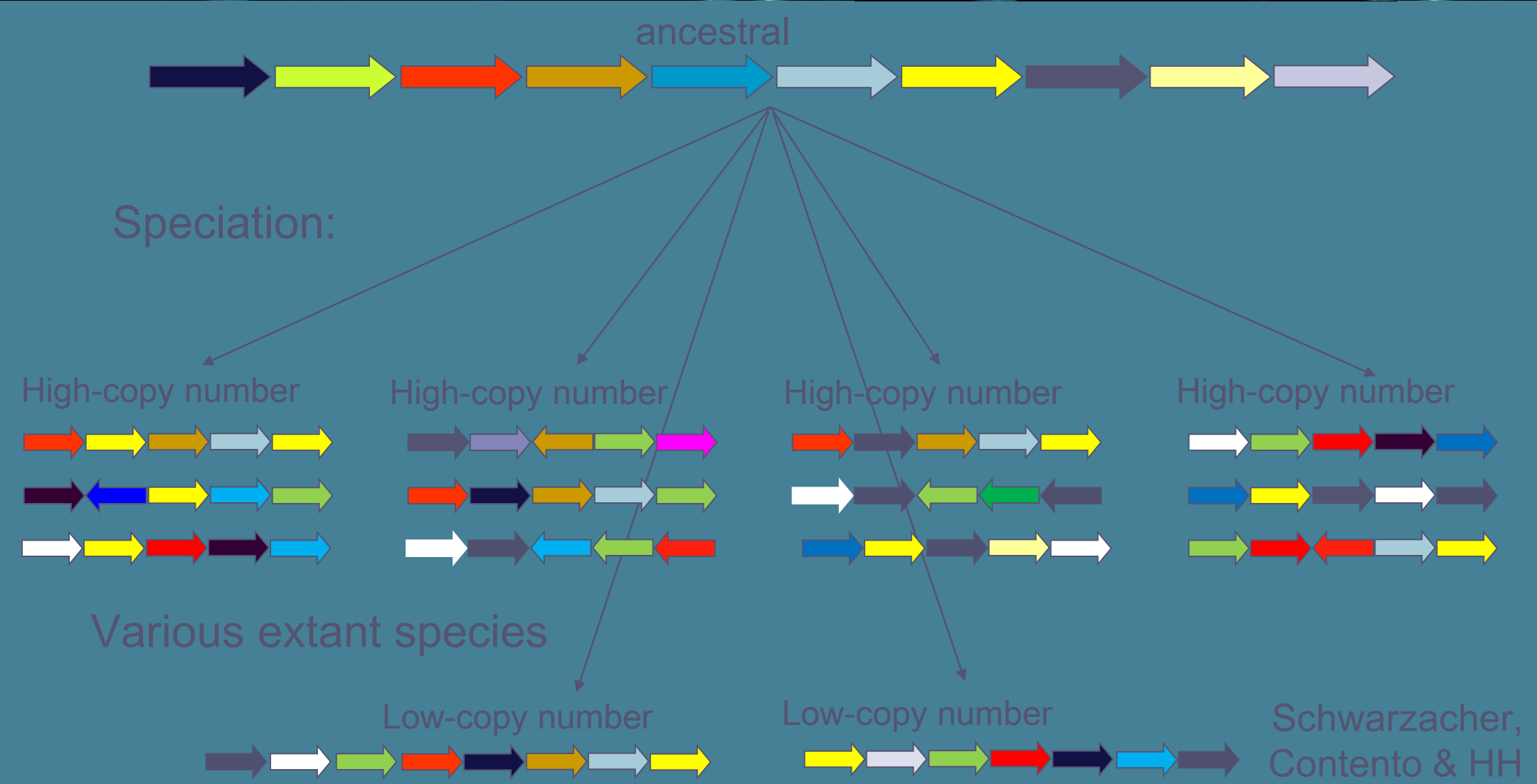
Major differences in the nature and amount of repetitive DNA: new & old



Rye: subtelomereic sequences



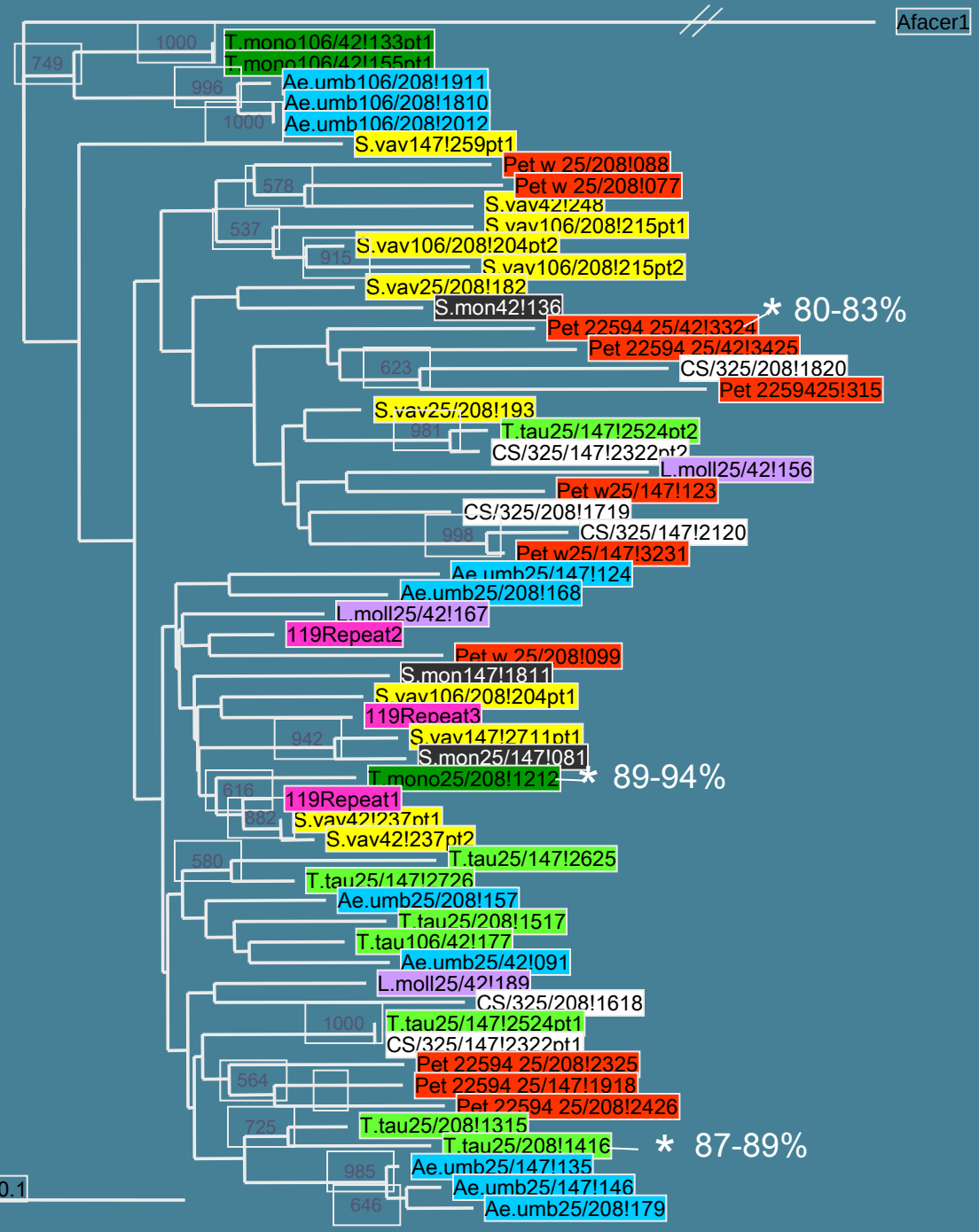
119.2 and the 120bp repeat family in cereals



Schwarzacher, Contento & HH 2009

High copy and low copy spp: no significant homogenization

120bp repeat unit family in *Triticum*, *Aegilops* and *Secale* species



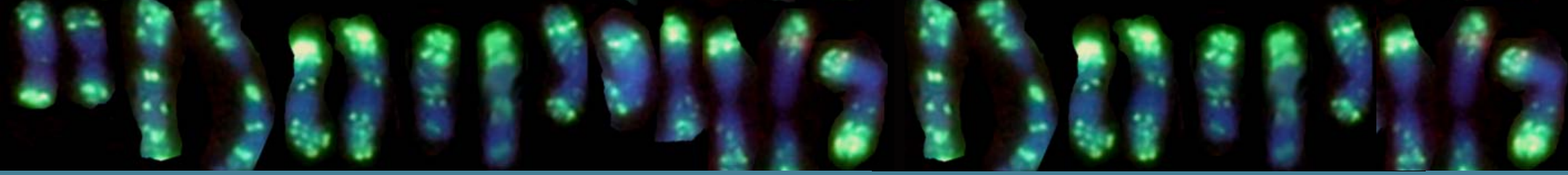
* 80-83%

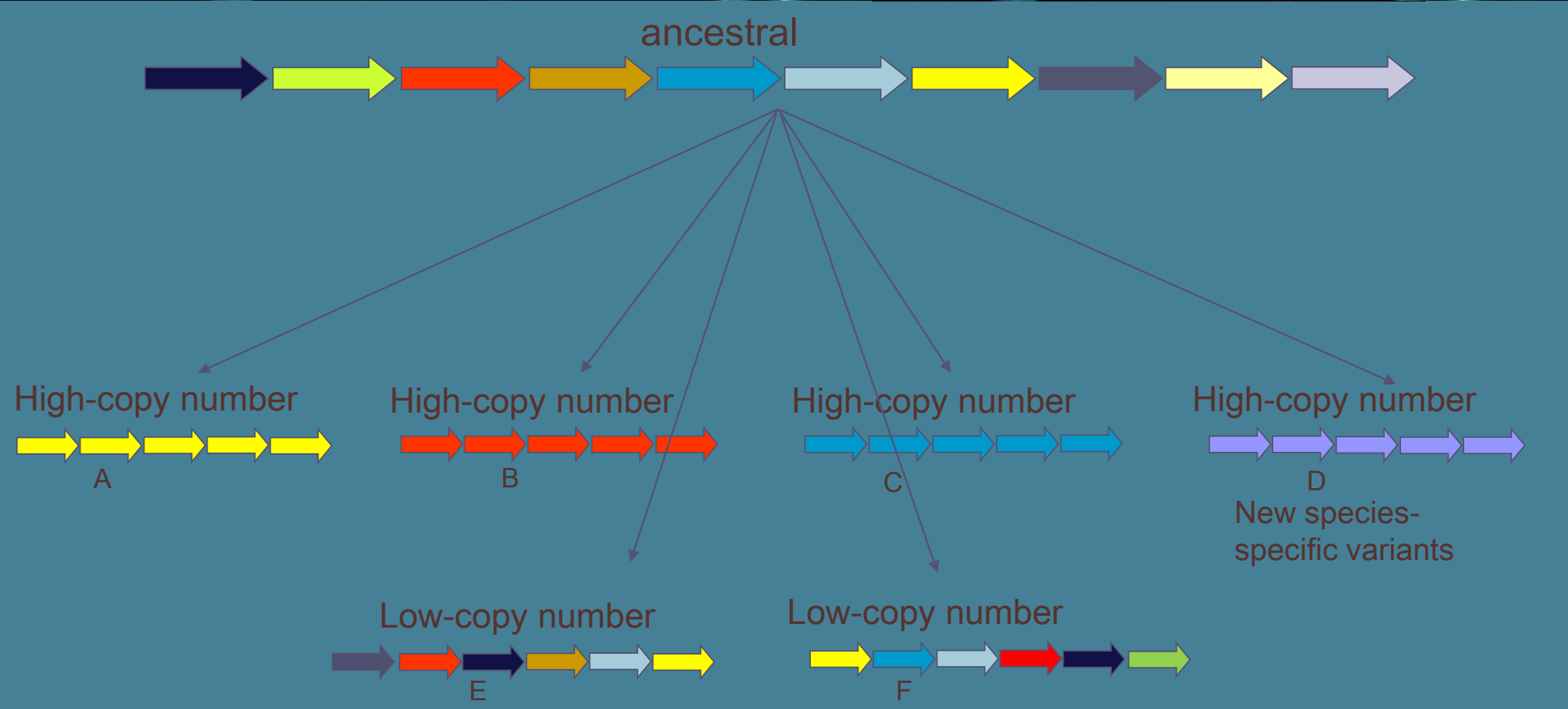
* 89-94%

* 87-89%

* Sequences used for *in situ* hybridization

Contento, Heslop-Harrison, Schwarzacher 2005





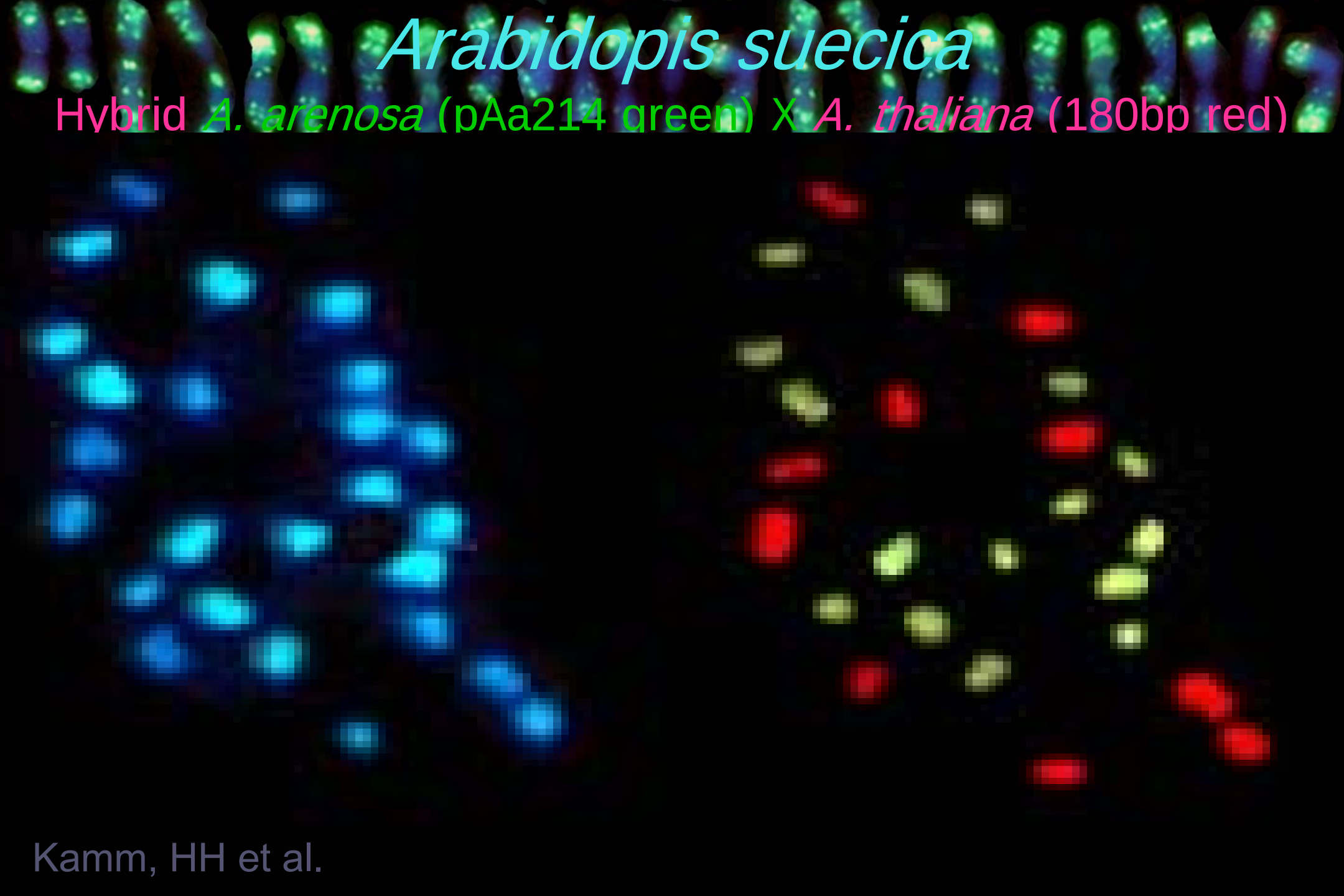
High copy spp: homogenized old (ABC) or new (D) variants

Low copy spp: most old variants in low copy number (EF)

See Kuhn, HH et al. 2009. Heredity & 2008. Chr. Res.

Arabidopis suecica

Hybrid *A. arenosa* (pAa214 green) X *A. thaliana* (180bp red)



Kamm, HH et al.

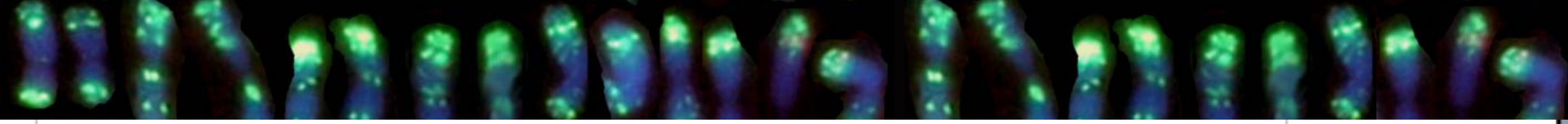
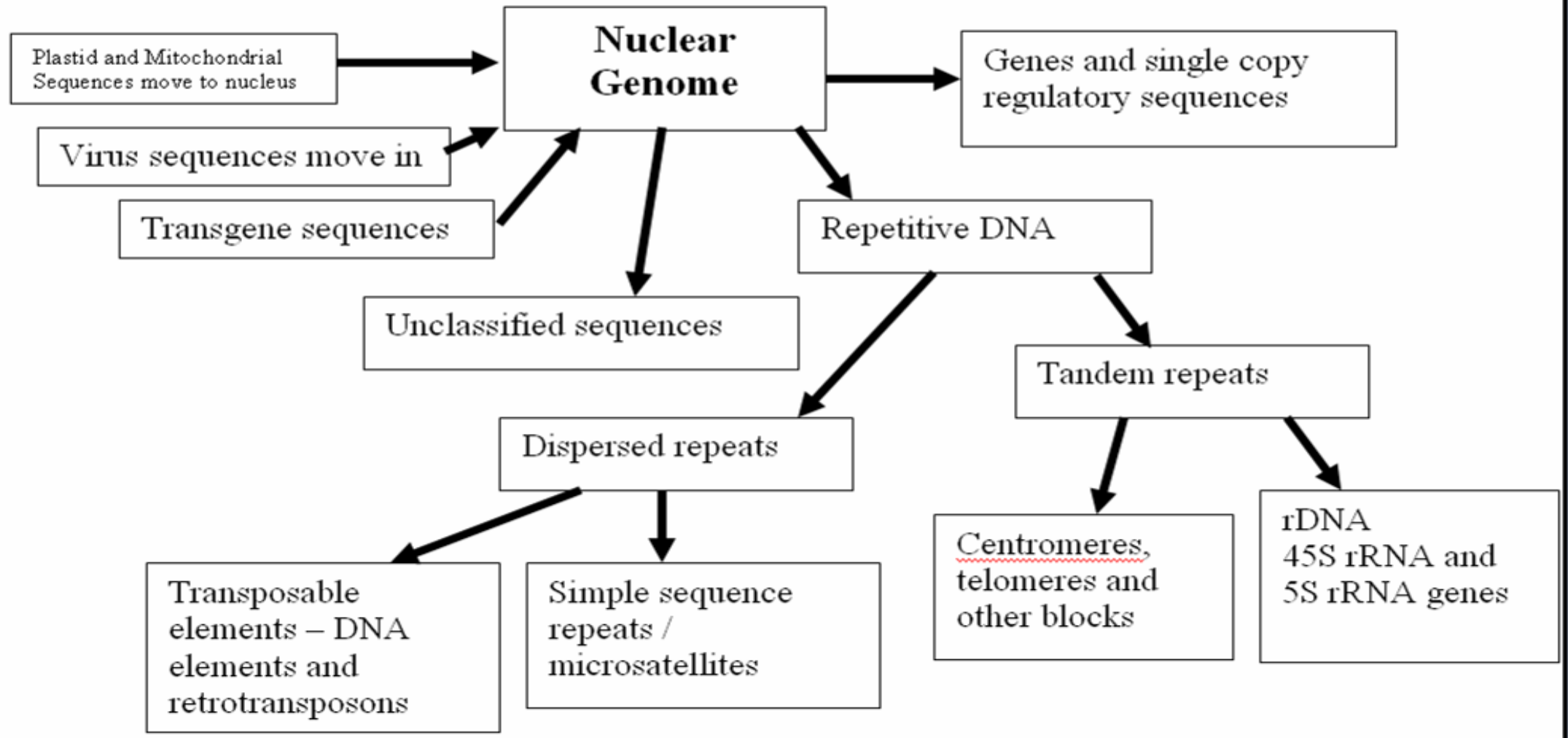
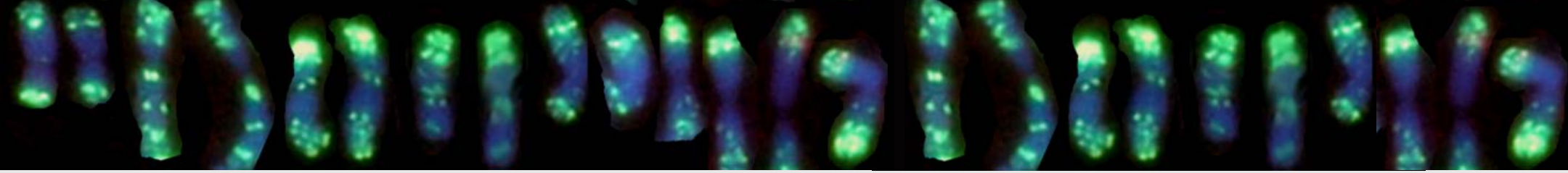


Figure 2. Components of the Nuclear Genome and their Relationships



Heslop-Harrison & Schmidt 2007. Encyclopedia of Life Sciences

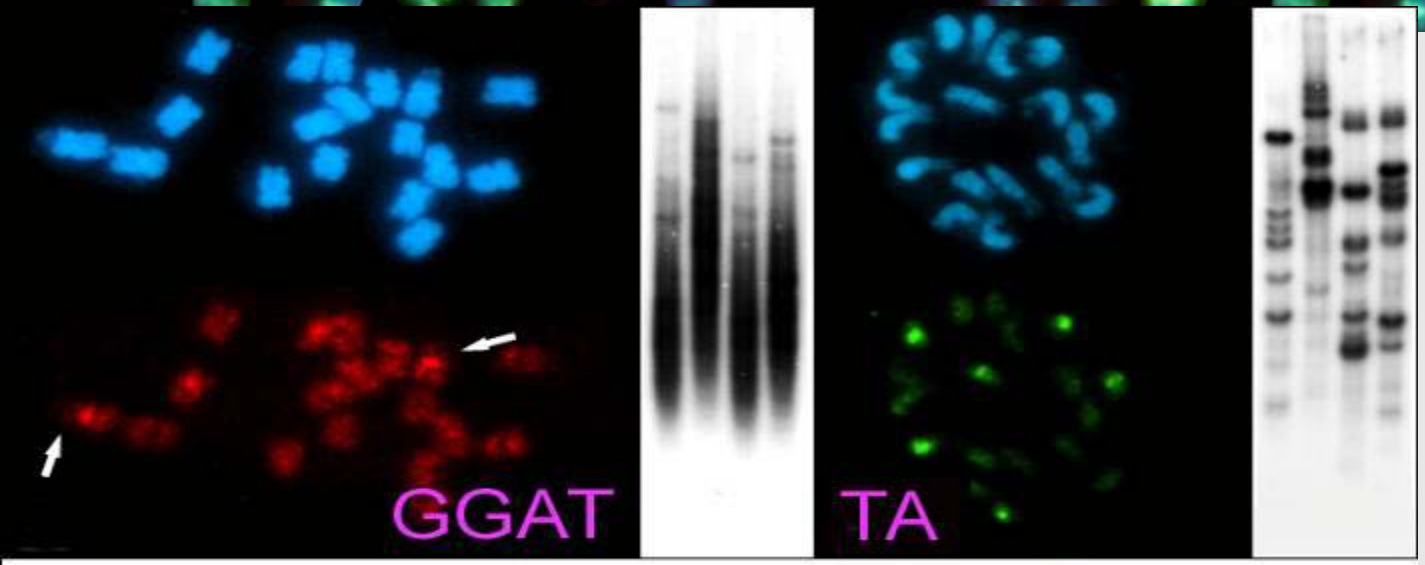


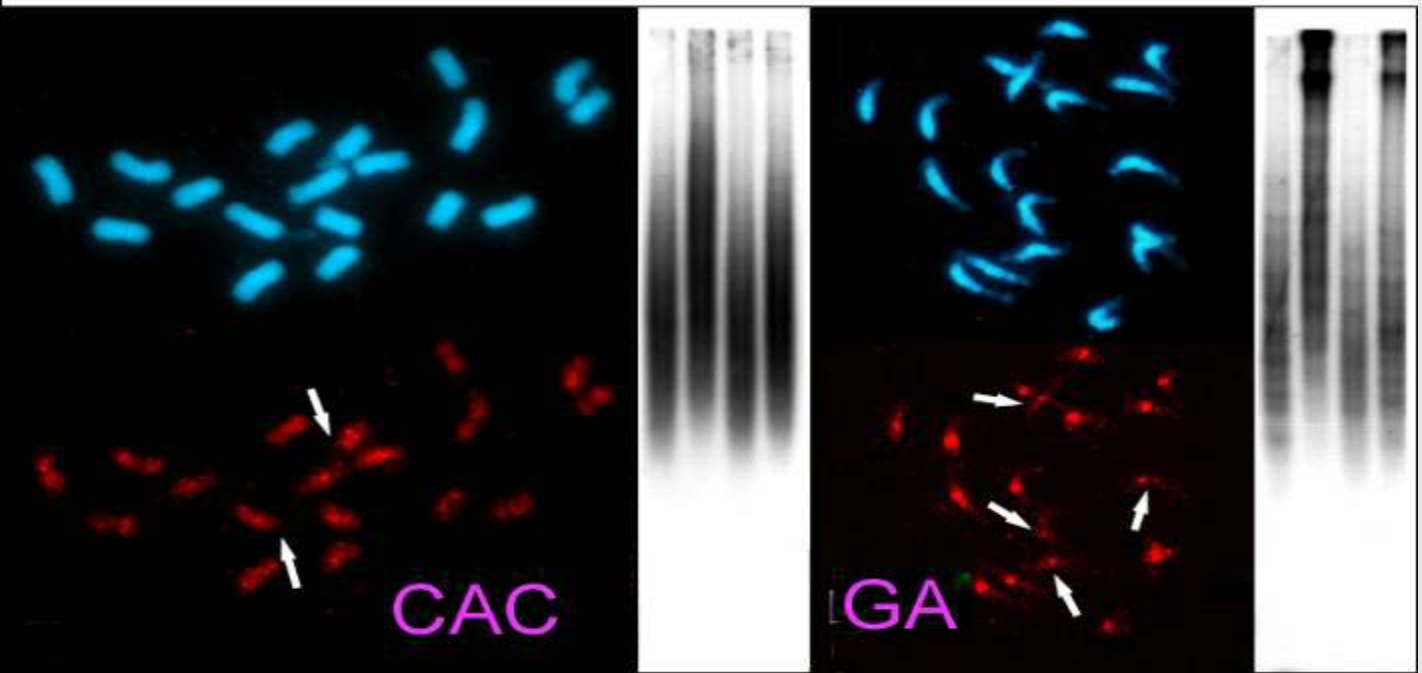
Simple sequence repeats

- GGCTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA GAGAGATGGTCGTAATG
- Flanked by unique sequences (SSR/microsatellite markers) or
- Part of other repetitive elements

- Dispersed OR clustered in genome
- SSR markers are dispersed!

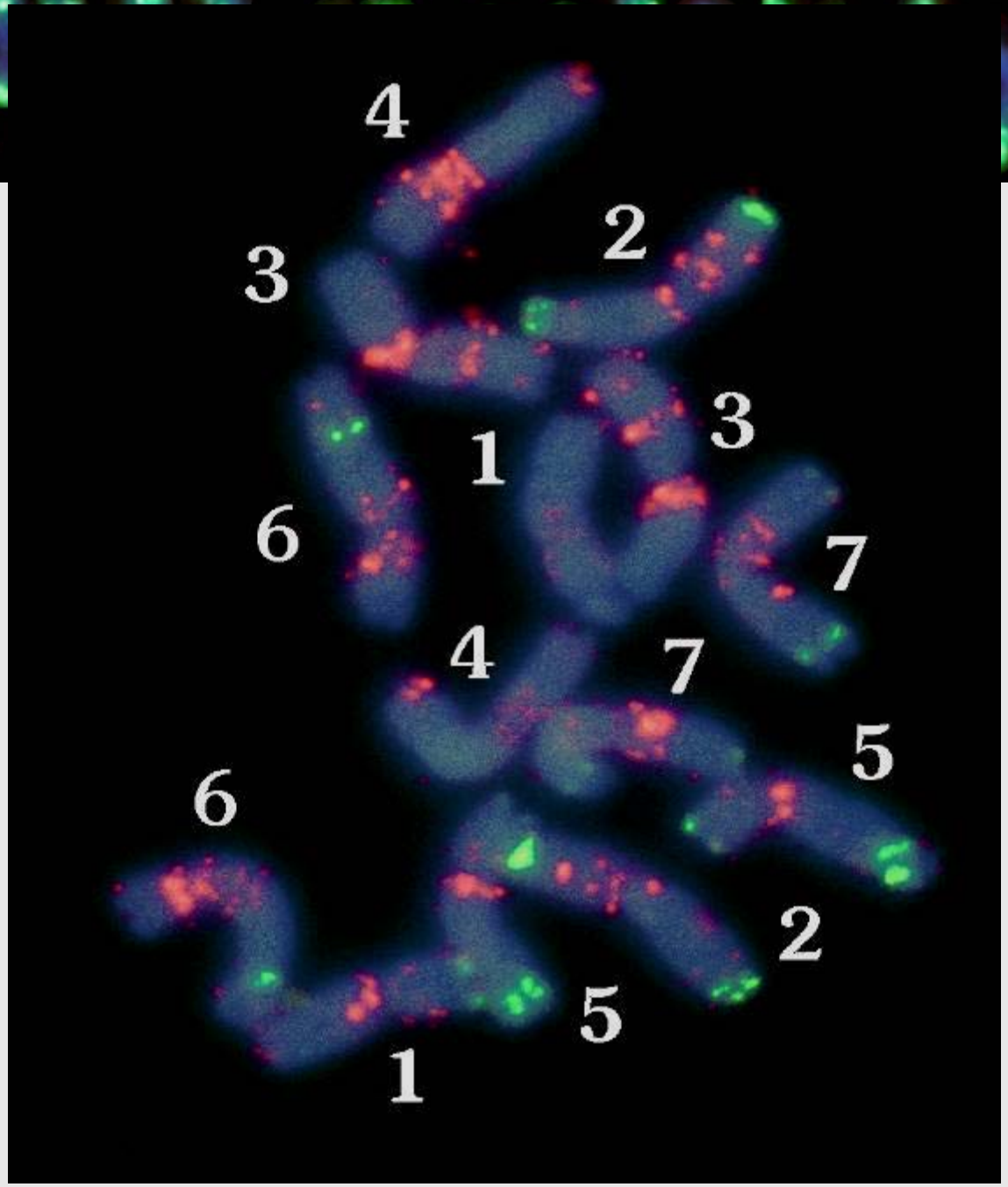
Simple Sequence Repeats

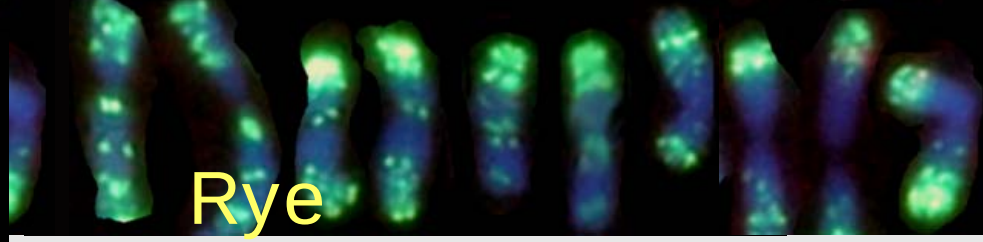




Sugar beet: Characteristic organization of each motif

Schmidt, HH et al.





Rye

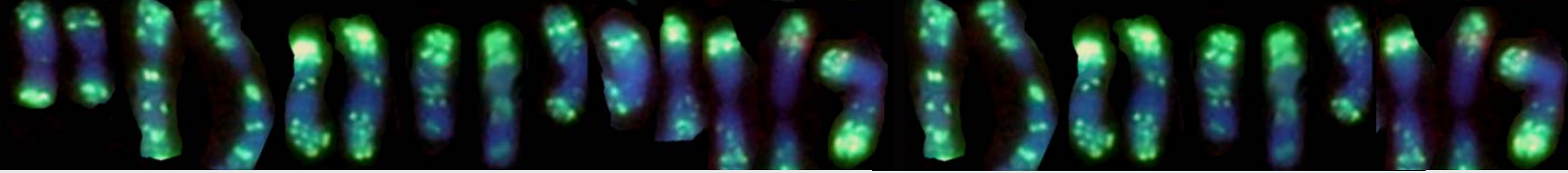
Secale cereale

2n=14

DAPI

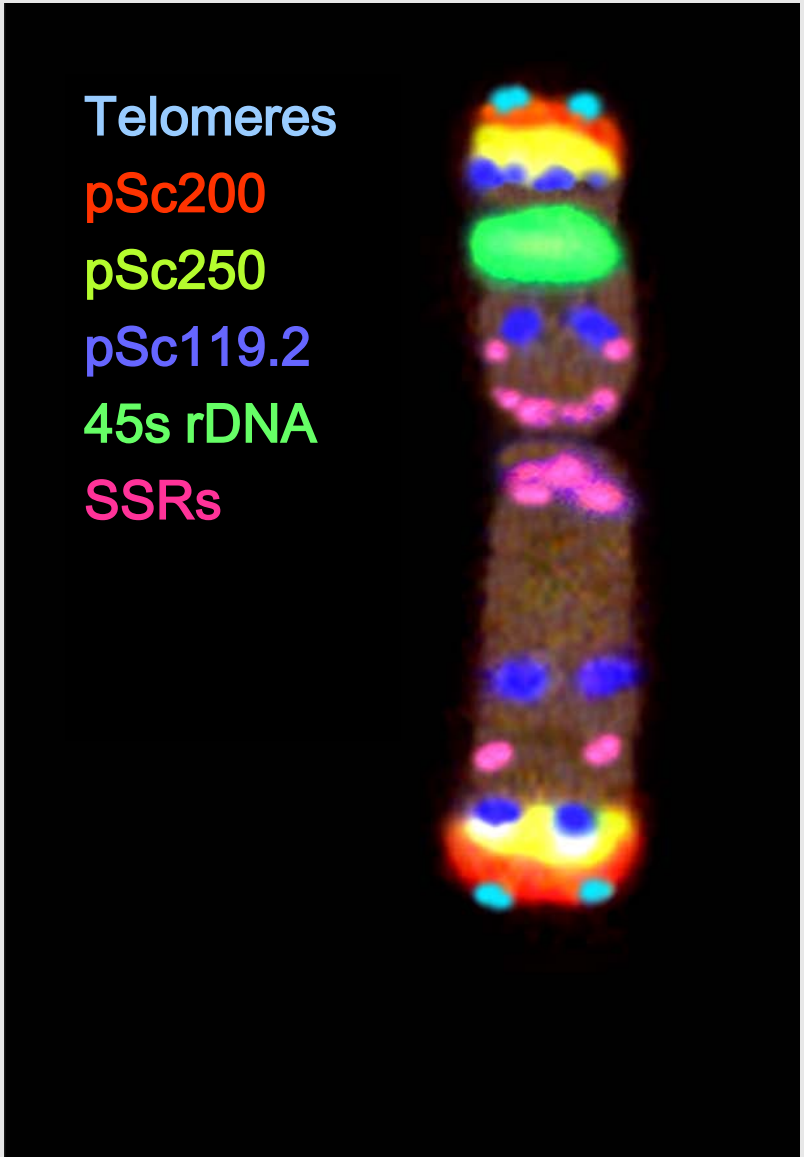
FITC/Alexa 488

Cy3/Alexa 594

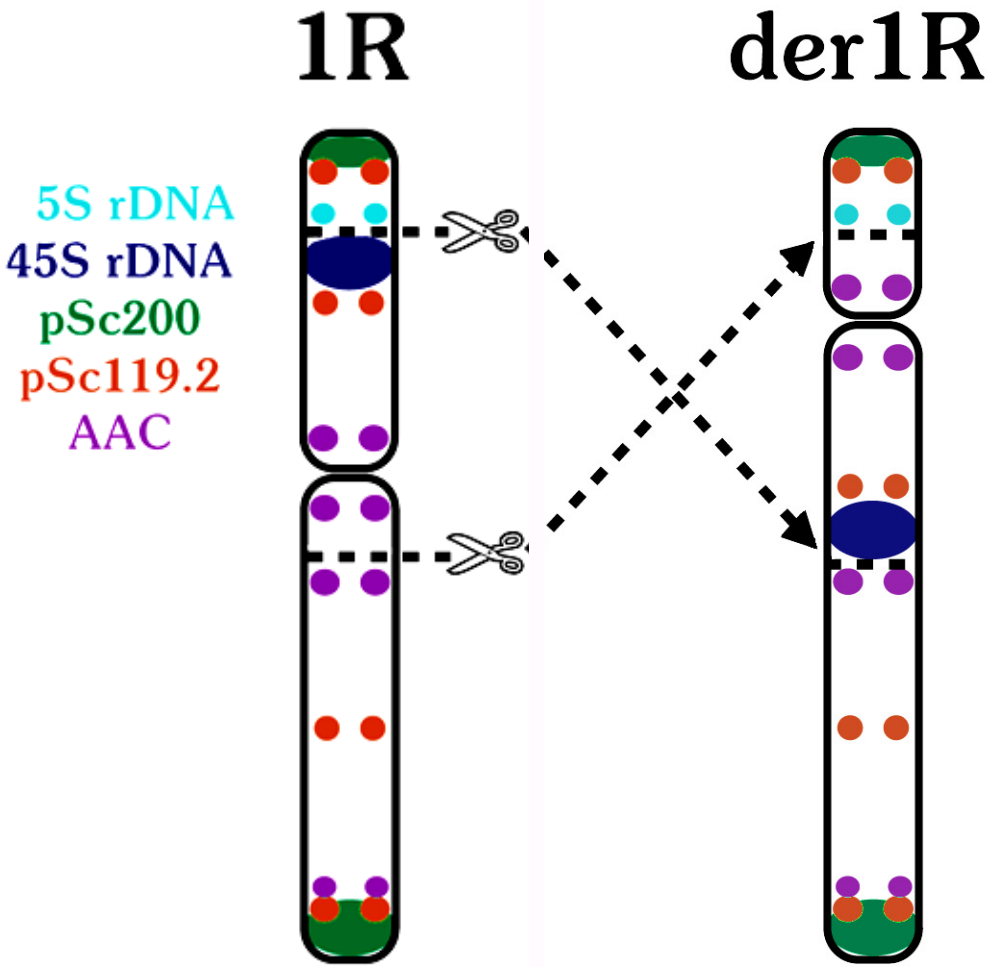


Chromosome model

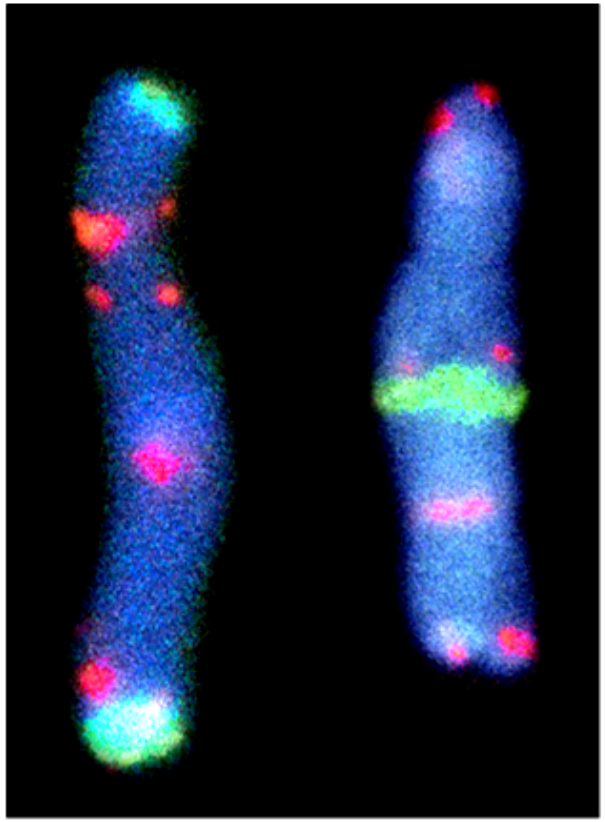
1R of rye



Derivative chromosome 1R of Lines 7-102 and 7-169



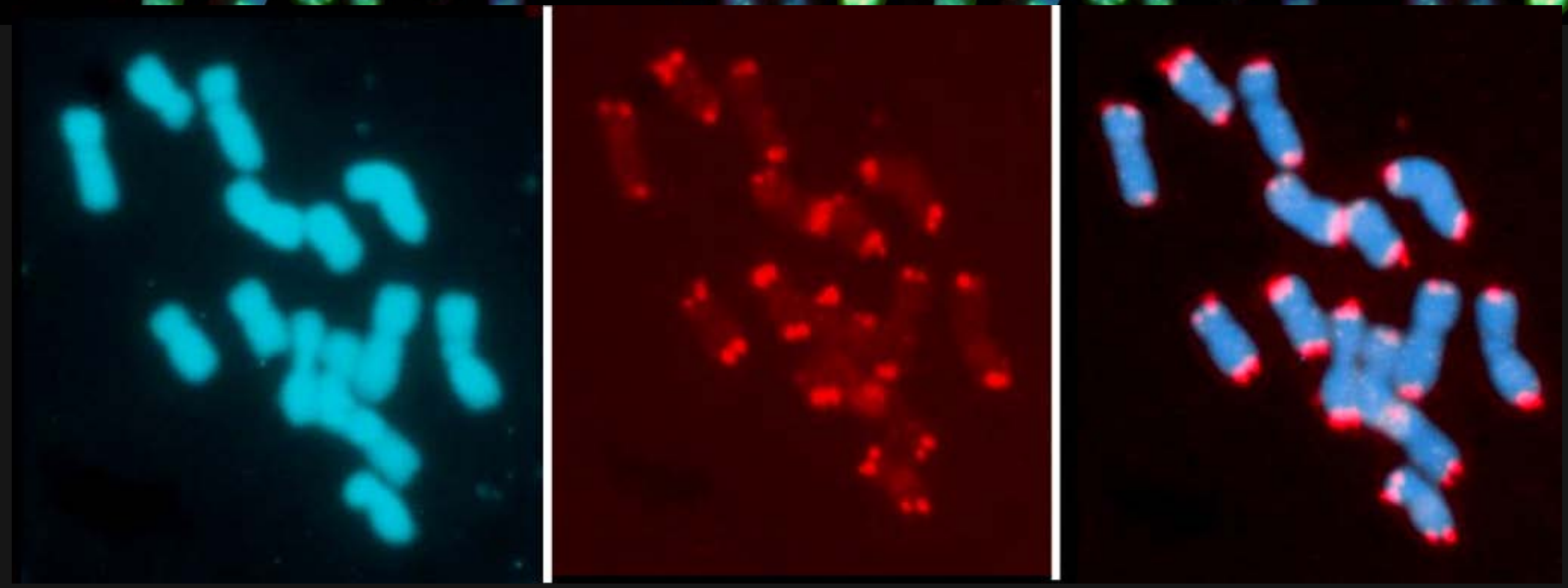
Forsstrom and Schwarzacher 2000



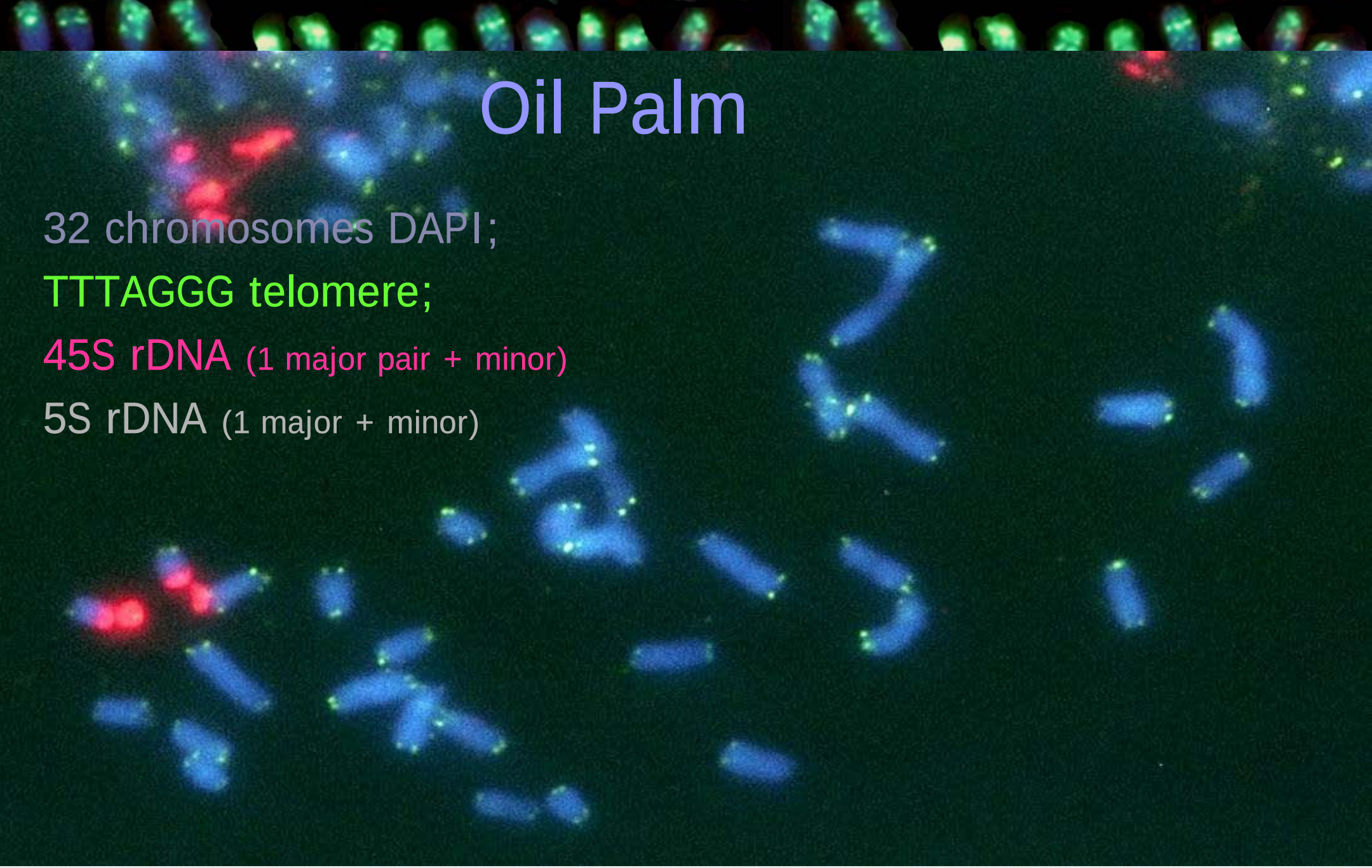
AAC
pSc200

pSc119.2
pTa71

Telomere (TTTAGGG)n



- Universal in eukaryotes with only a few exceptions
- Dynamic
- Number of repeats varies: tissue, age and chromosome
- Added by telomerase



Oil Palm

32 chromosomes DAPI;

TTTAGGG telomere;

45S rDNA (1 major pair + minor)

5S rDNA (1 major + minor)

The Linear Chromosome

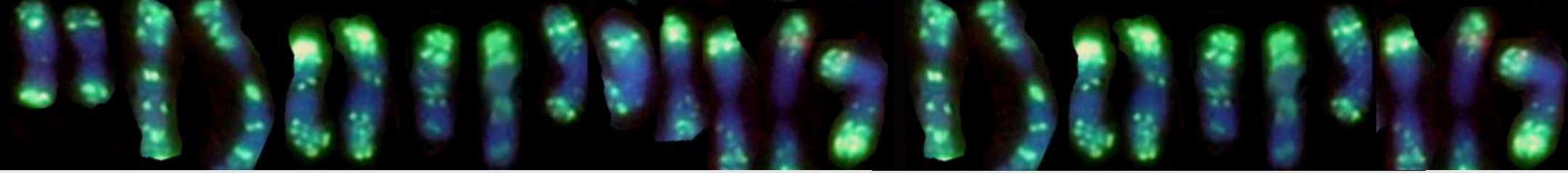
Tandem repeats

Retroelements
Simple sequence repeats

Terminal repeats

Genes

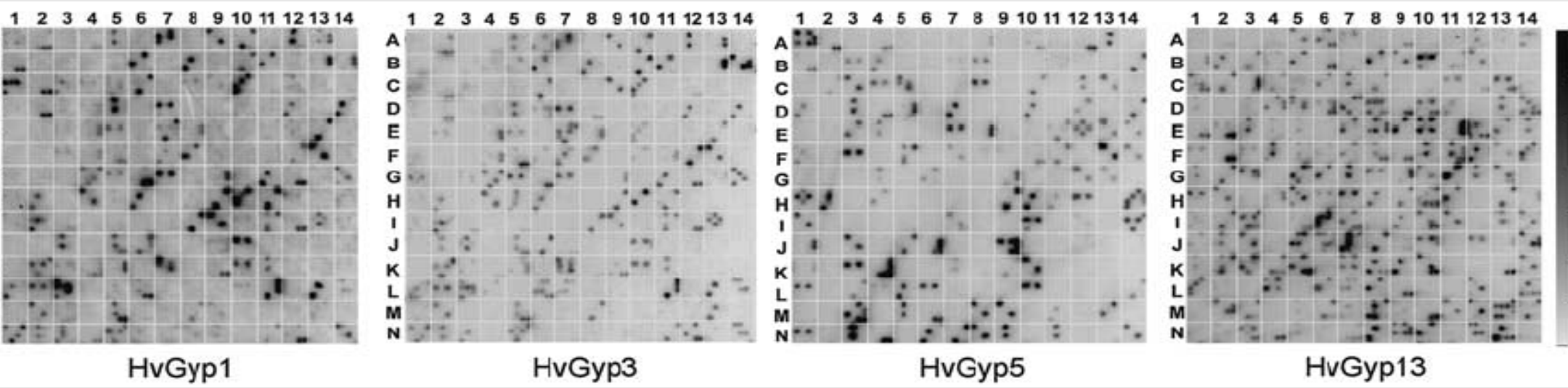
Schmidt & Heslop-Harrison 1998



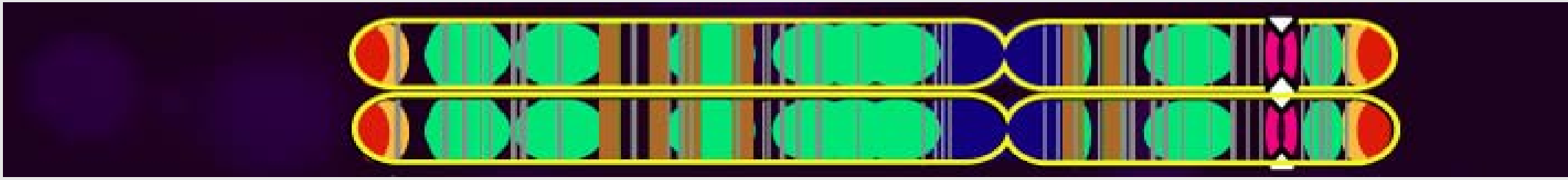
Repetitive Sequences

- The majority of the genomic DNA in most species (95% sometimes)
- Tandem Repeats
- Simple Sequence Repeats
- Dispersed Repeats
- Functional Repeats
- Retroelements

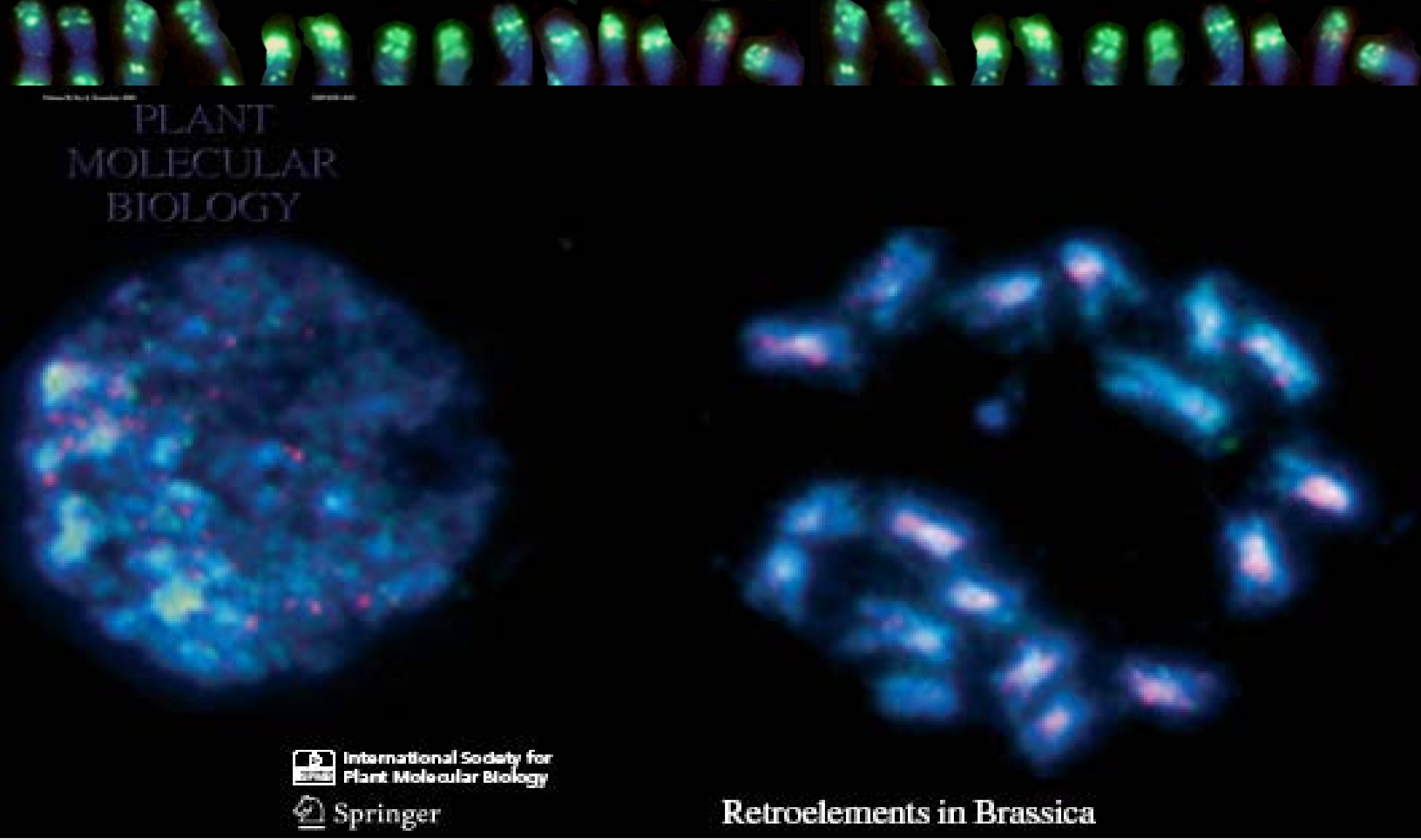
Retroelement abundance and diversity in barley



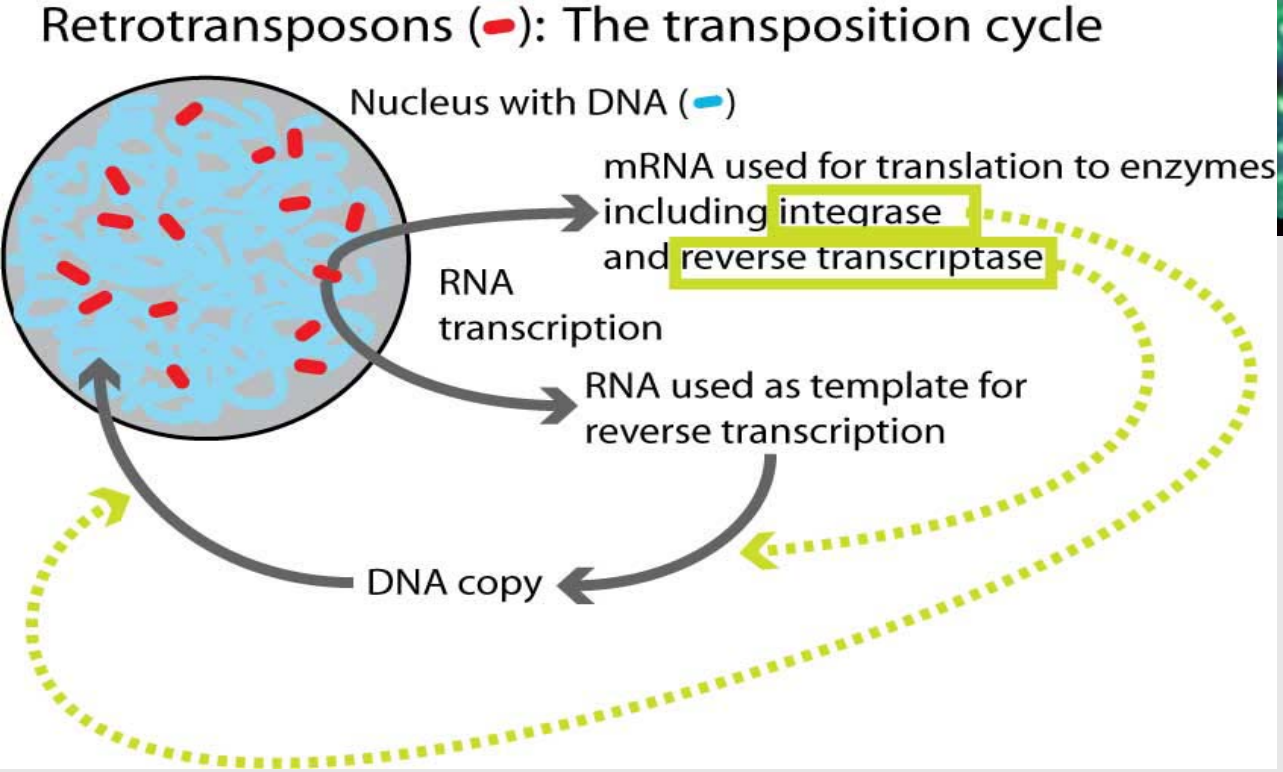
Gypsy elements are present in 25% of all BAC clones

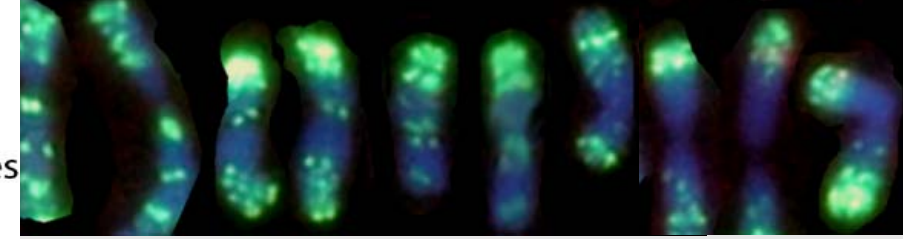


Barley gypsy: Vershinin, Druka, Kleinhofs, HH: PMB 2002; cf Brassica Alix & HH PMB 2005



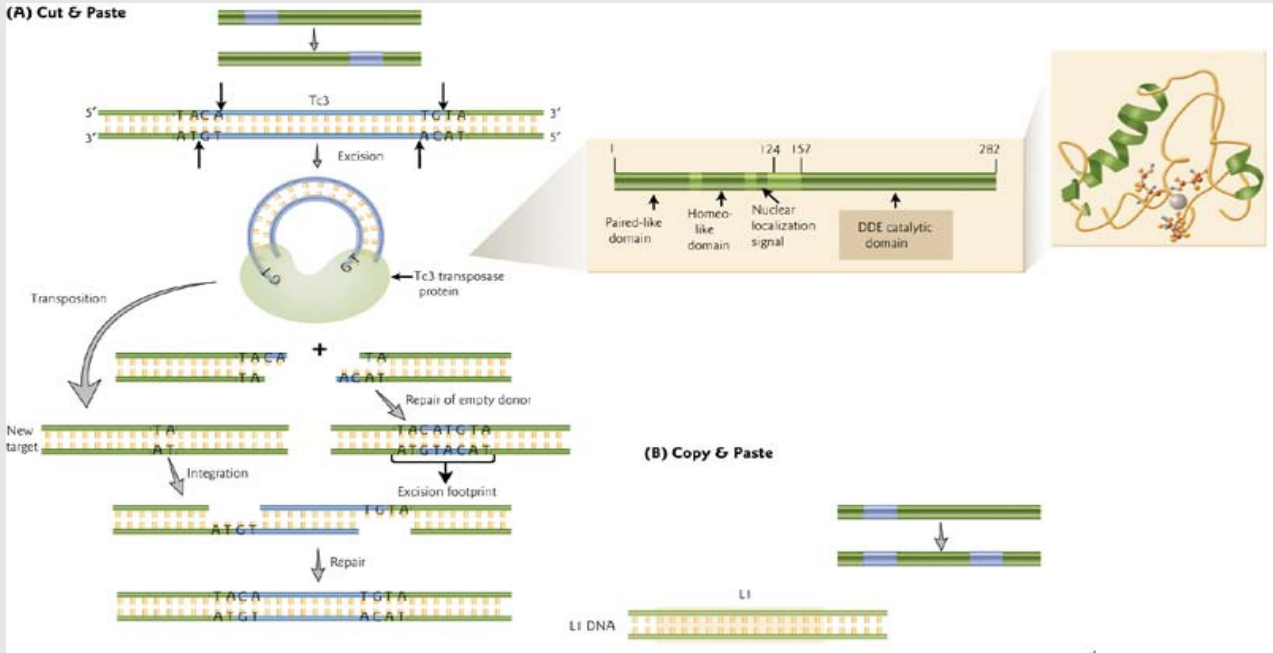
Alix et al. 2005





DNA transposons
Class II transposable elements
Cut-and-paste

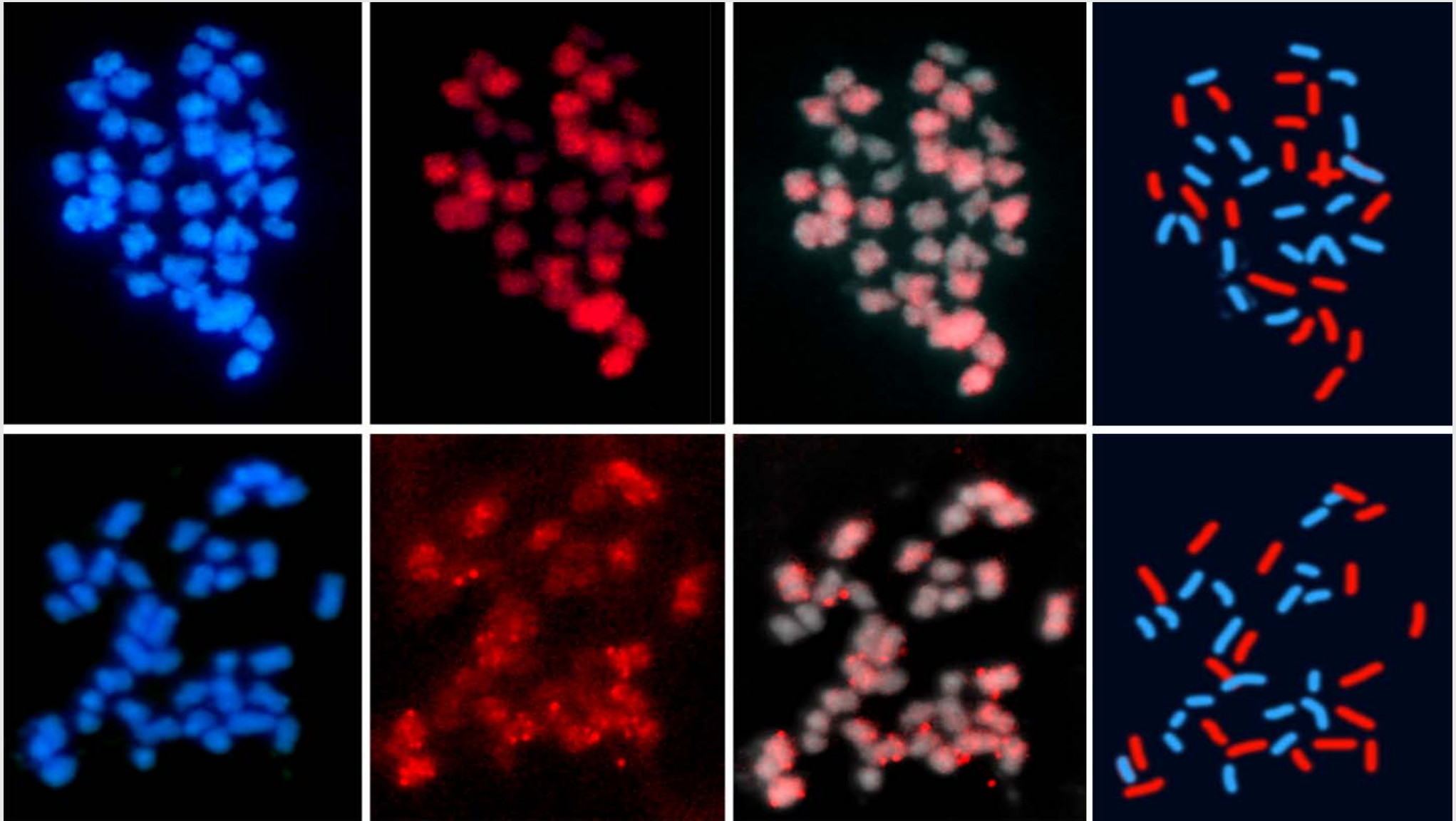
Retrotransposons
Class I transposable elements
RNA intermediate



Genome Specificity of a CACTA (*En/Spm*) Transposon

B. napus **(AACC, 2n=4x=38) – hybridized with C-genome CACTA element red**

B. oleracea (CC, 2n=2x=18) **B. rapa (AA, 2n=2x=20)** Alix & HH 2008



LINE Retrotransposon
(non-LTR Retrotransposon)

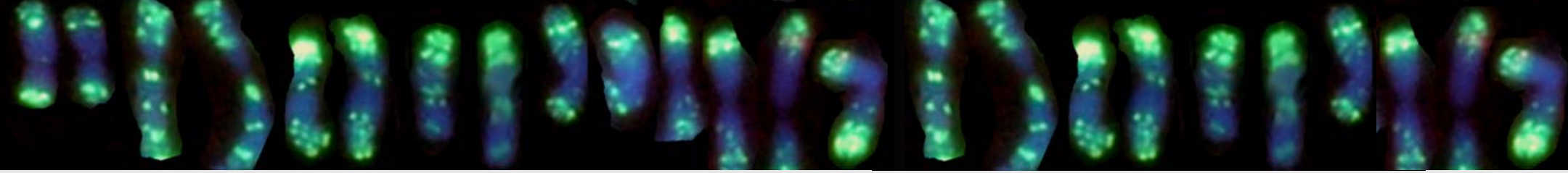
Gypsy
(LTR Retrotransposon)

Copia
(LTR Retrotransposon)

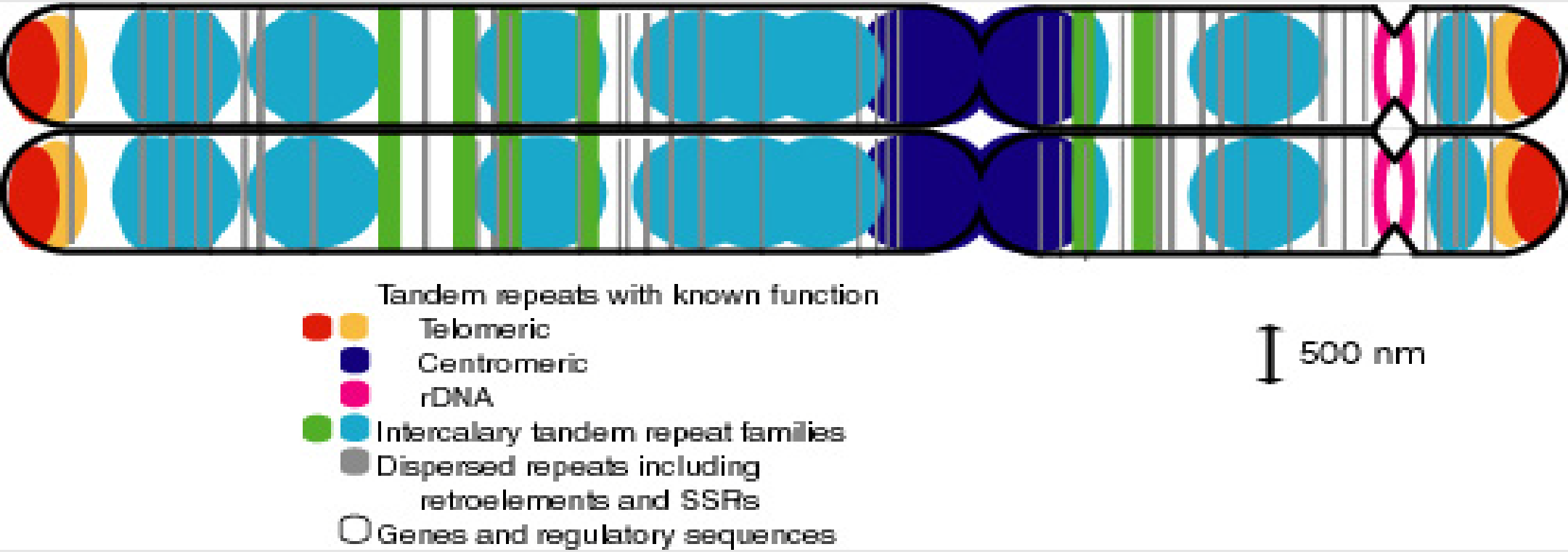
Retrovirus

Common structure of Retroelements

gag – core particle component
en – endonuclease
rt – reverse transcriptase
LTR – long terminal repeat
env – envelope glycoprotein



The Chromosome Model



Schmidt & HH Trends Plant Sci

Bos taurus taurus vs *Bos taurus indicus*:

2n=60, XY

But: B. taurus submetacentric Y

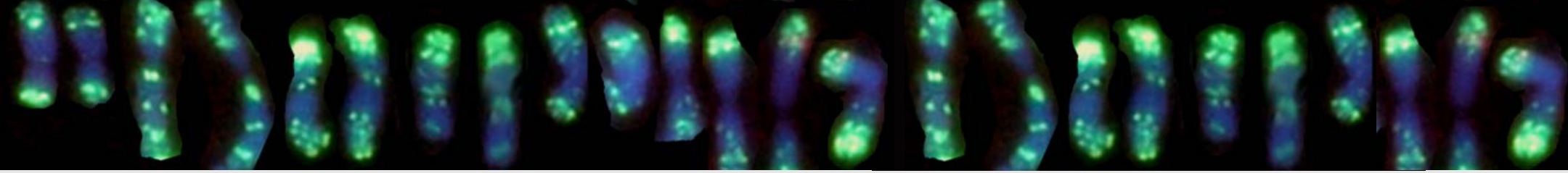
B. indicus acrocentric Y

Bovidae

Cattle, sheep, goats, and antelopes

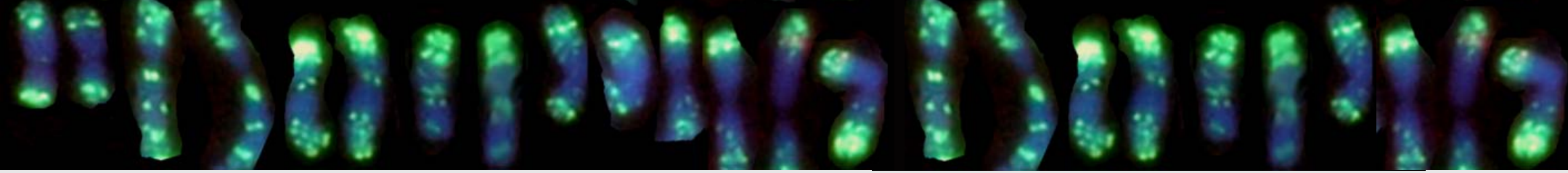
- Bovinae (oxen, cattle, buffalos, eland, kudu, and relatives)
- Alcelaphinae (hartebeests, wildebeests, and sassabies)
- Hippotraginae (addax, roan antelopes, sable antelopes, oryxes)
- Caprinae (sheep, goats, muskox, chamois, and relatives)
- *Pantholops hodgsonii* (chiru)
- *Aepyceros melampus* (impala)
- Cephalophinae (duikers)
- Reduncinae (reedbucks, waterbuck, kob, puku, and lechwes)
- *Pelea capreolus* (common rhebock)
- Antilopinae (gazelles, dik-diks, steenboks, and their relatives)
- *Neotragus* (dwarf antelopes)
- *Oreotragus oreotragus* (klipspringer)
- Miscellaneous fossil bovids †

http://tolweb.org/Bovidae/50878



Bovidae – Family

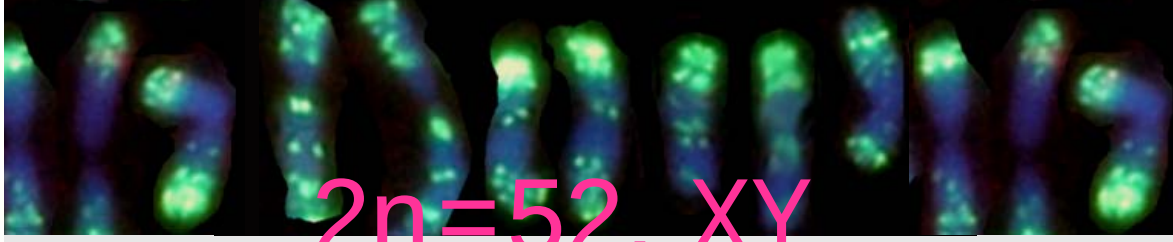
- Mammals
  - Order Artiodactyla (=Even-toed ungulates)
  - 3 groups: the Suiformes (pigs, peccaries, hippopotamuses), Tylopoda (camels, llamas) and Ruminantia (cattle, goats, sheep, deer, antelopes, giraffes)
  - 9 families (13 tribes) including Bovidinae
    - Family Bovidae
      - c. 137 species
      - Last species (new genus) discovered in 1992



Bovidae family

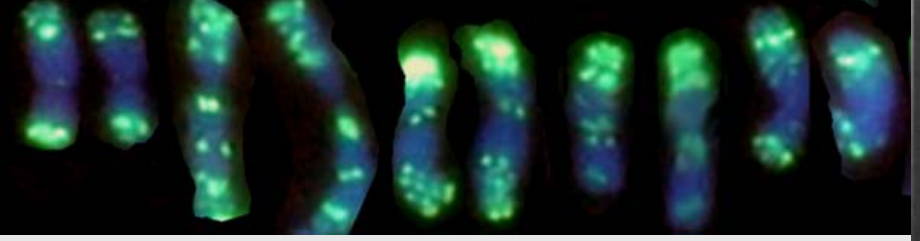
- 2n ranges from 30 to 60 in different species

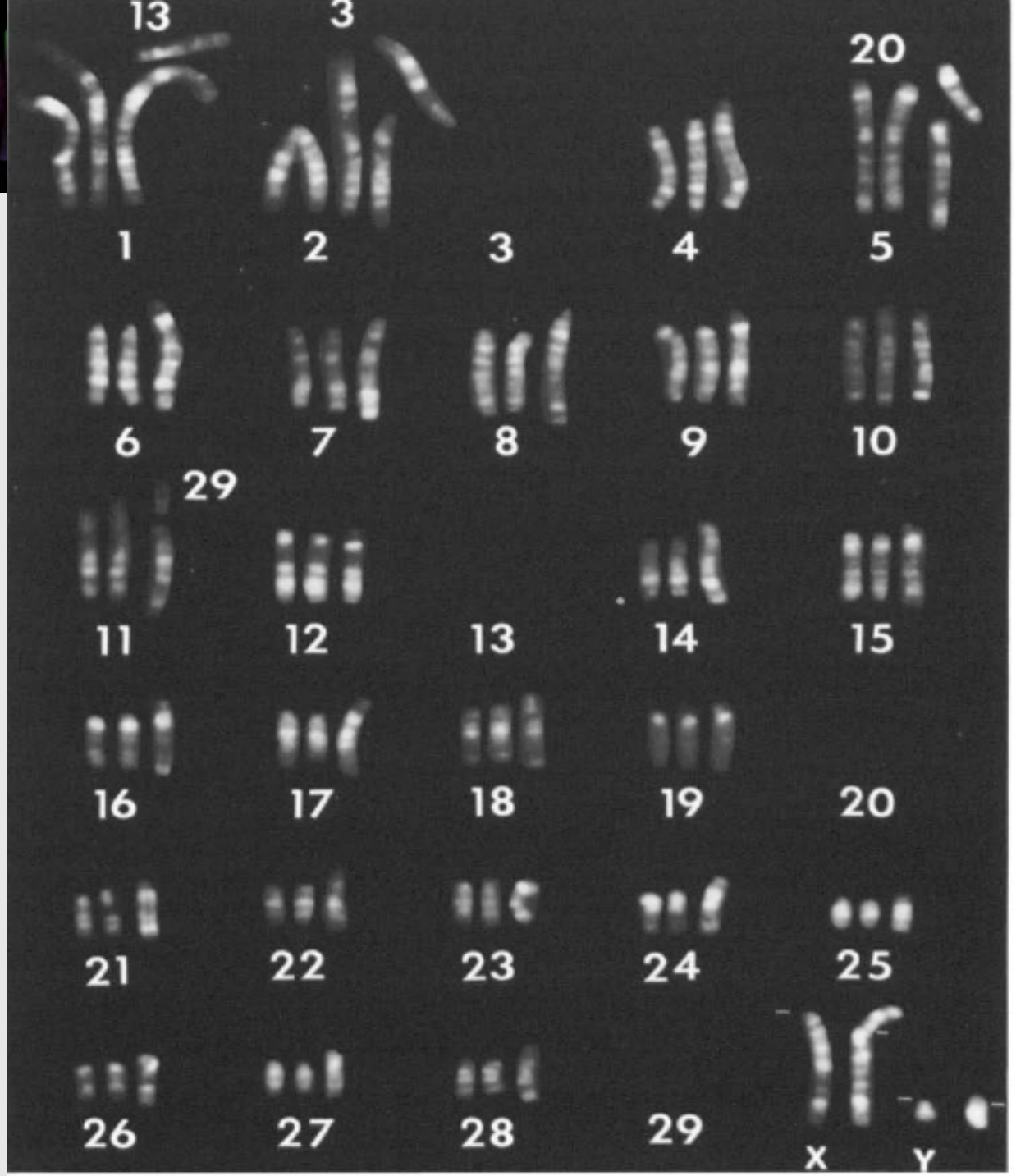
- (Galagher & Womak 1992)



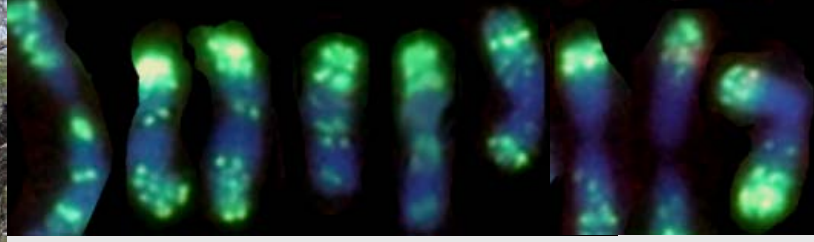
2n=52, XY
including 4
bi-armed
chromosomes = 58
autosomal
chromosome arms
+X,Y

- *Syncerus caffer* (African Buffalo or Cape Buffalo), a bovid from the family of the Bovineae





- Male *Syncerus caffer* QFH band karyotype (left 2 chrs) with cattle chrs to right
- Gallagher & Womak 1992



Tragelaphus strepsiceros or greater kudu

2n=31, X1 X2 Y
26 biarmed chromosomes, three acrocentric chromosomes (inc. X1), acrocentric X and a biarmed Y

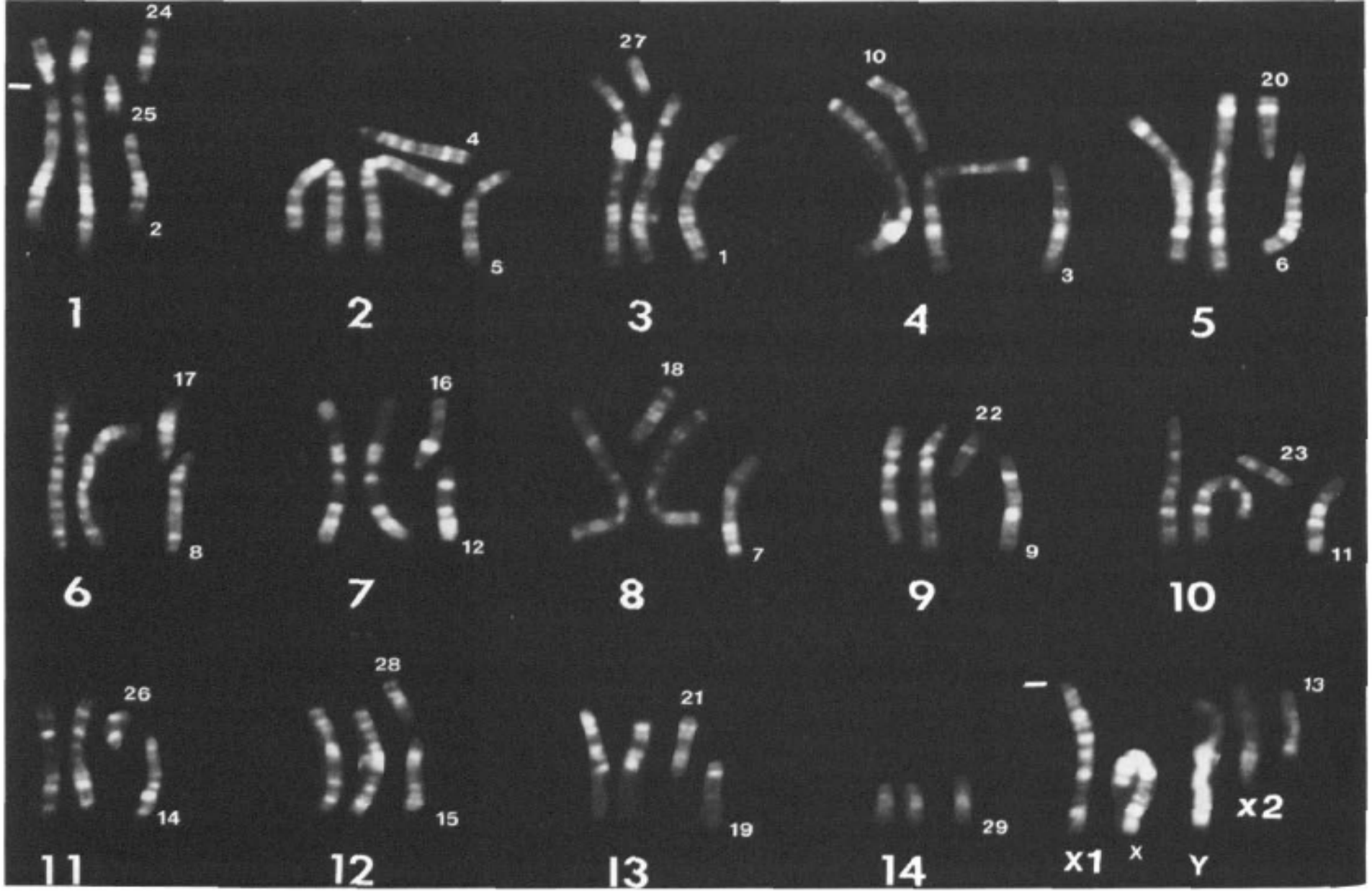
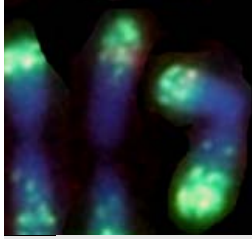
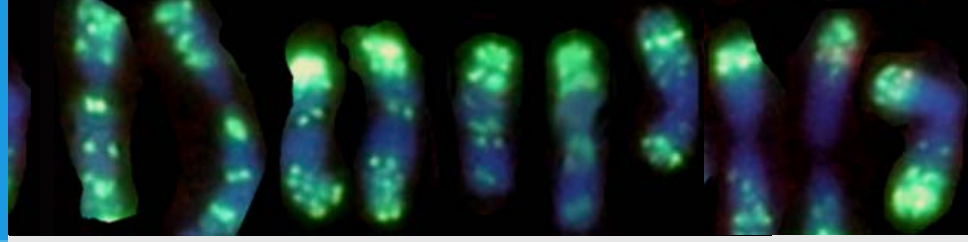


Figure 4. A male *Tragelaphus strepsicerus* (greater kudu) QFH-band karyotype ($2n = 31$) consisting of 26 biarmed autosomes, three acrocentric autosomes (one labeled as X2), an acrocentric X1, and a biarmed Y (the ancestral Y is fused to cattle equivalent autosome 13). The autosomal pairs are arranged and numbered (large numbers) according to relative size. The domestic cow equivalent chromosomes are arranged to the right of the greater kudu autosomes and are numbered (small numbers are placed toward the telomeric ends of the domestic cow acrocentric autosomes) according to the Reading Conference (1980) standard. The banding pattern of cattle chromosome 25 does not precisely match the region of kudu chromosome 1 to which we believe it is homologous, but this placement is the only way we found to account for cattle 25 within the kudu karyotype. The greater kudu sex chromosomes and equivalent cattle chromosomes are arranged from left to right as X1 (greater kudu ancestral X), cattle X, greater kudu Y, greater kudu X2, and cattle autosome 13. White lines are positioned at the centromere of some chromosomes.

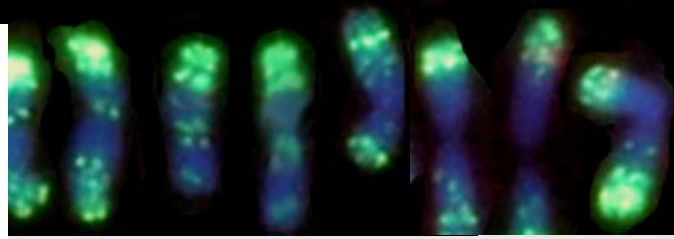


Gallagher & Womack 1992



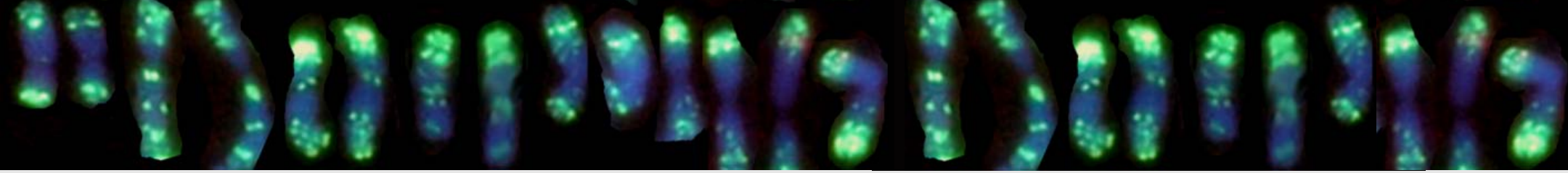
- Sheep *Ovis aries*

2n=54, XY
three pairs
biarmed
chromosomes
60 autosomal
arms



- Goat
- Sheep
- Cattle
- Chromosome homologies and centromeric fusions

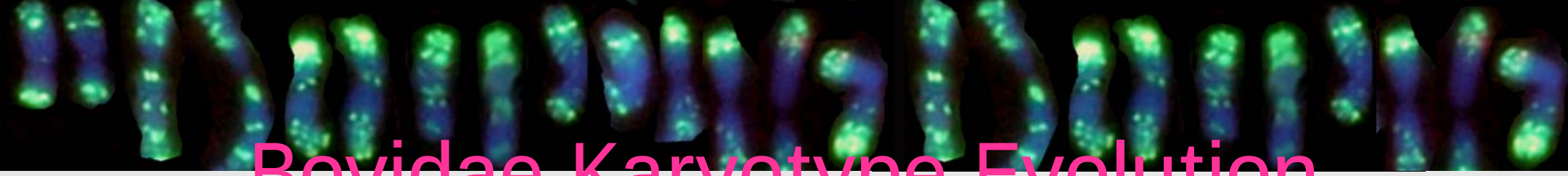
- Paul Popescu



Bovidae Karyotype Evolution

- 2n ranges from 30 to 60 in different species
- BUT:
- Almost all have 58 autosomal chromosome arms and two sex chromosomes

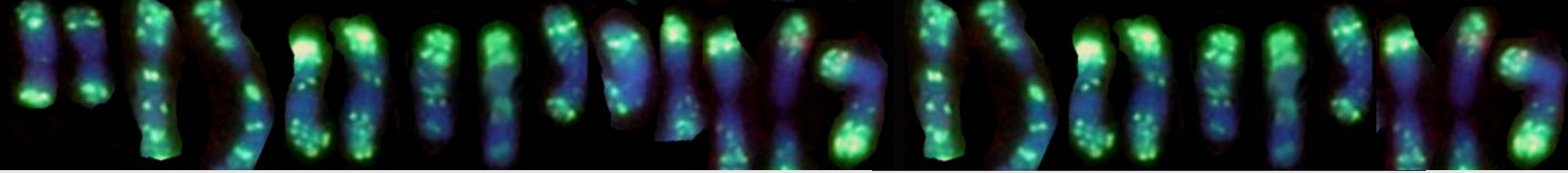
- (Galagher & Womak 1992)



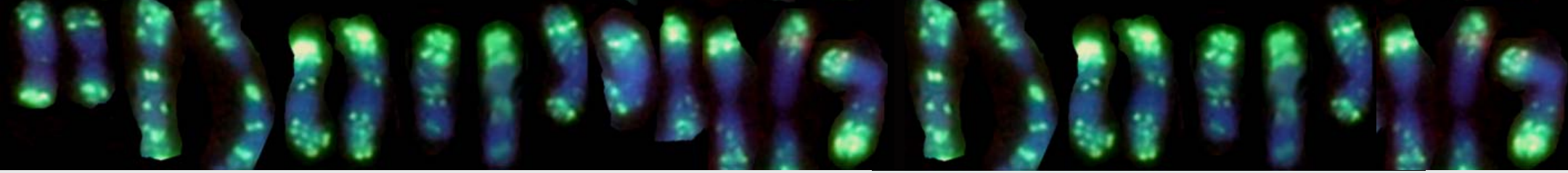
Bovidae Karyotype Evolution

- Almost all have 58 autosomal chromosome arms and two sex chromosomes but 2n from 30 to 60
- Chromosome arm homologies extensive BUT homologous biarmed chromosomes are rare
- Reproductive isolation (and speciation) may have followed centric fusion

- (Galagher & Womak 1992)

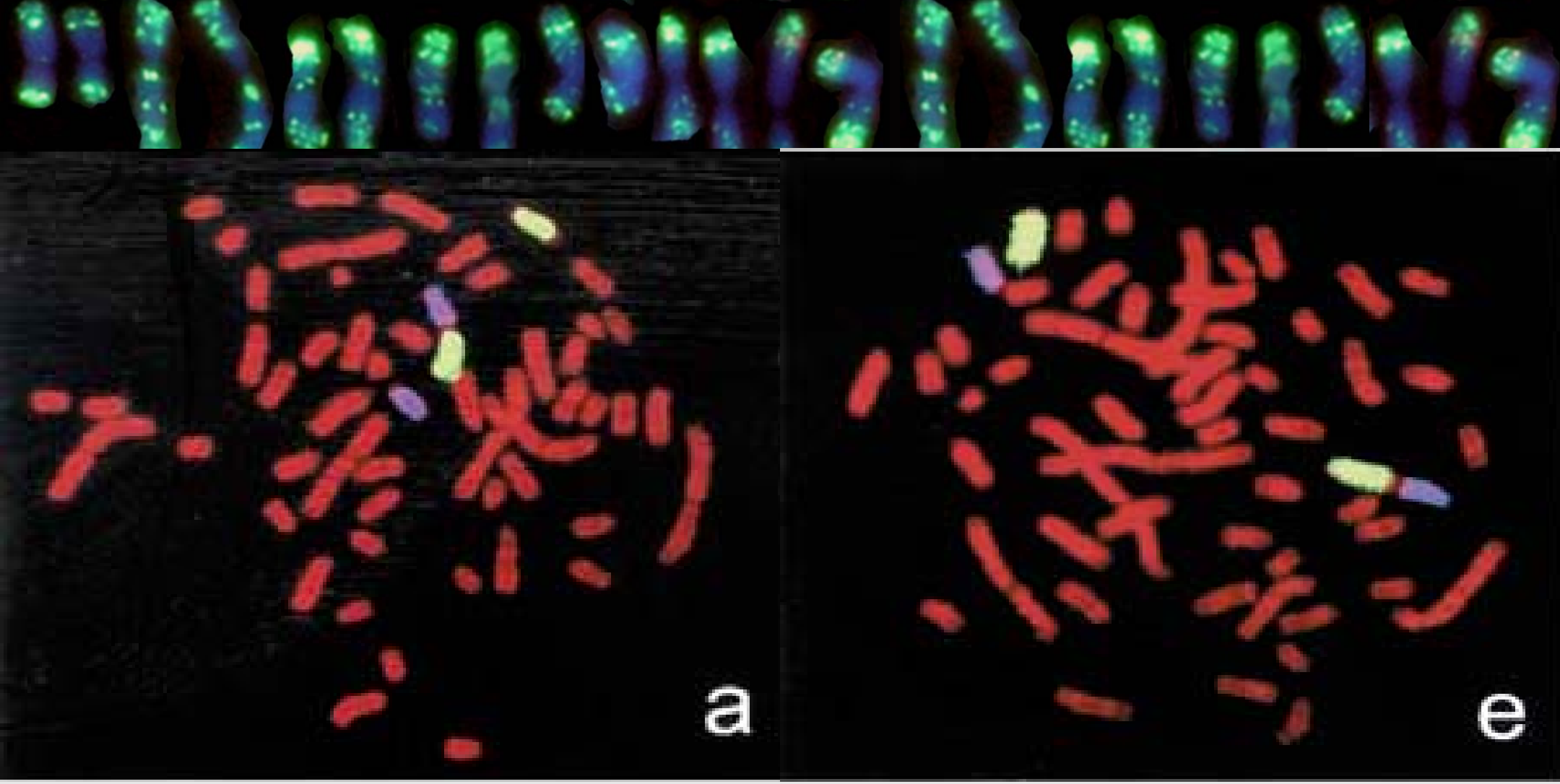


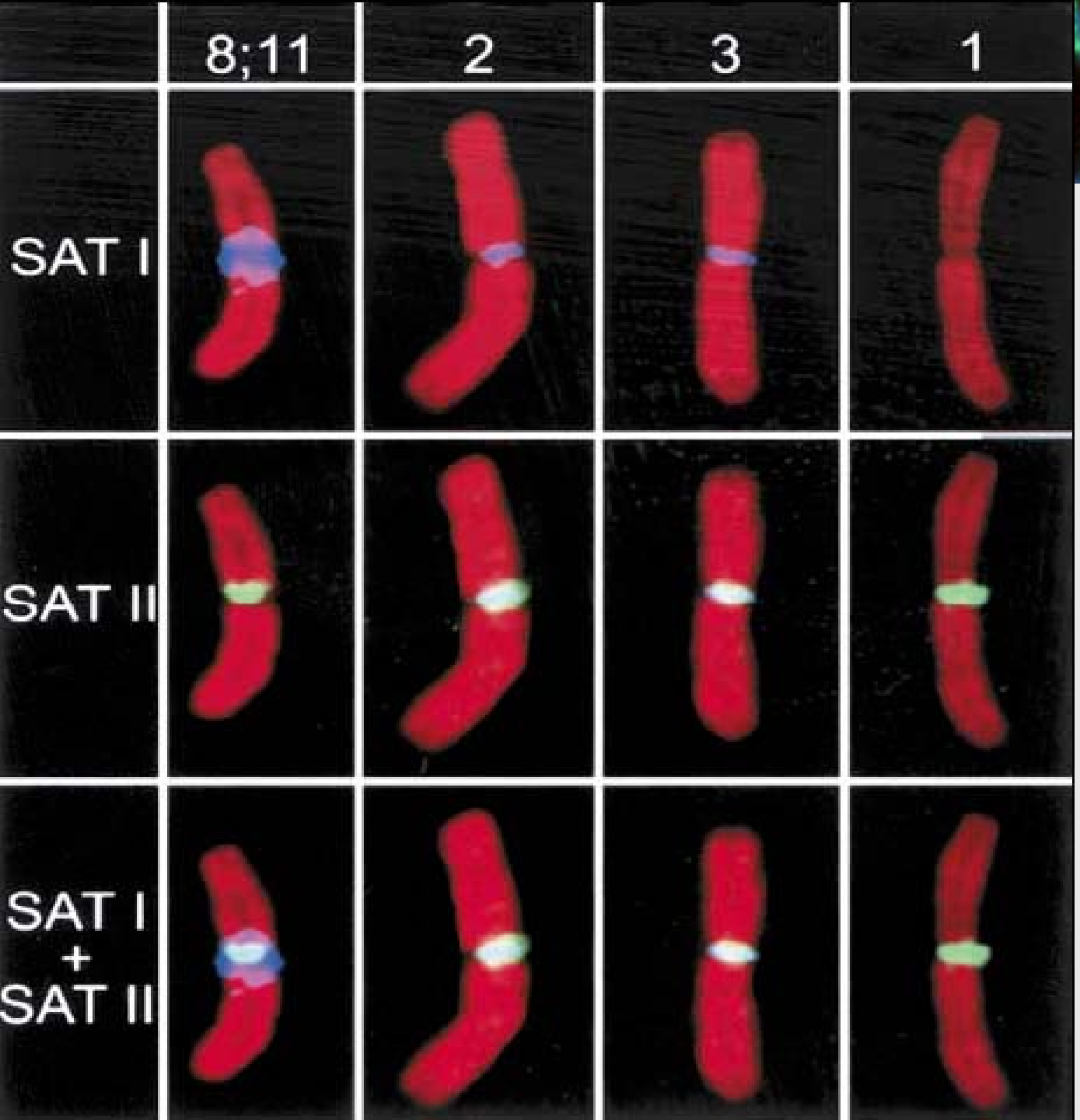
Do we see chromosome fusion now?



Do we se

Molecular cytogenetic analysis and centromeric satellite organization of a novel 8;11 translocation in sheep: a possible intermediate in biarmed chromosome evolution. 2003. Chaves, Adega, Wienberg, Guedes-Pinto, Heslop-Harrison

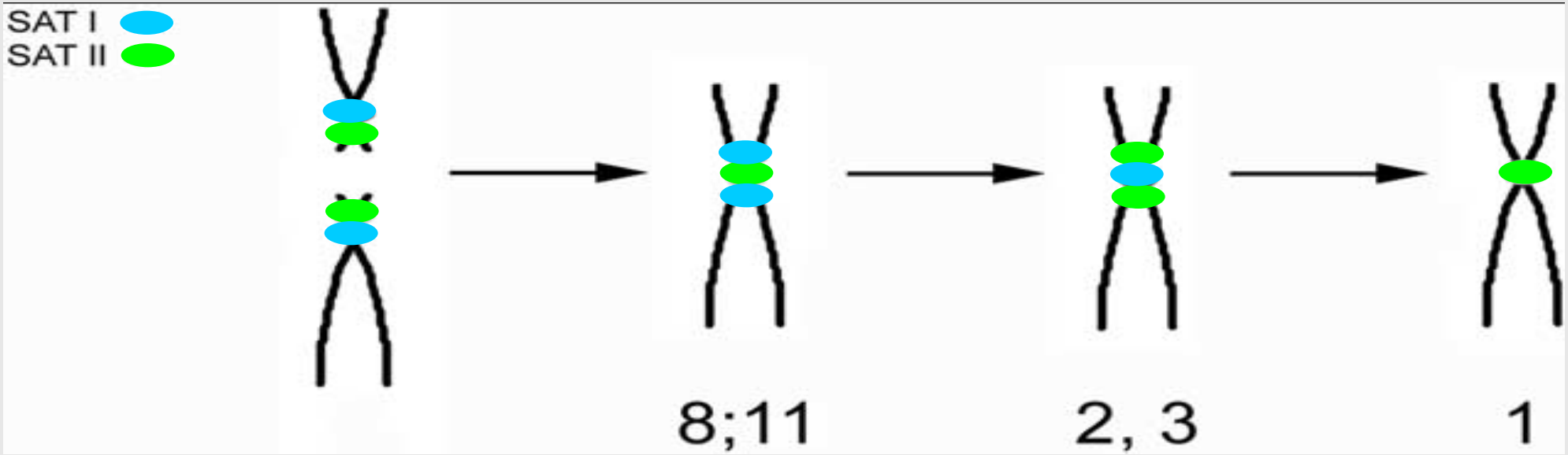

a
e



- Satellite I and II probes in the biarmed chromosomes of the sheep with 2n = 53, XY.

- Chr (8;11), 2, 3, 1 are ordered from the most recent to the postulated evolutionarily oldest chromosome

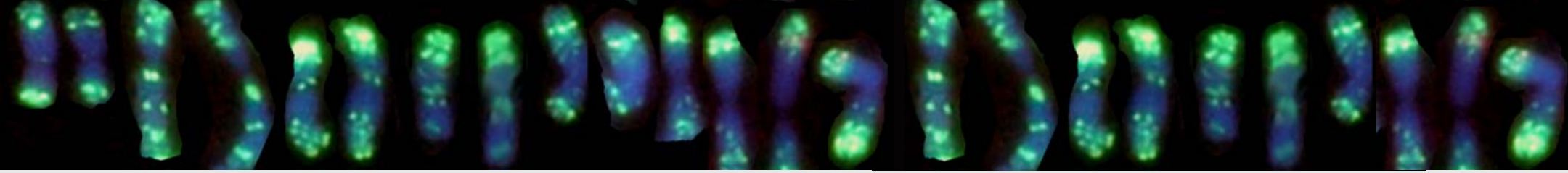
- t(8;11) showed satellite I proximal on both arms with satellite II covering the centromere, while the evolutionarily derived fusion leading to Chrs 2 and 3 showed the opposite configuration, not obviously derived by a simple fusion. Chr 1 has lost the satellite I hybridization patterns. The novel t(8;11) provides strong evidence for an intermediate step in evolution of the biarmed chromosomes in sheep.



How many chromosomes?

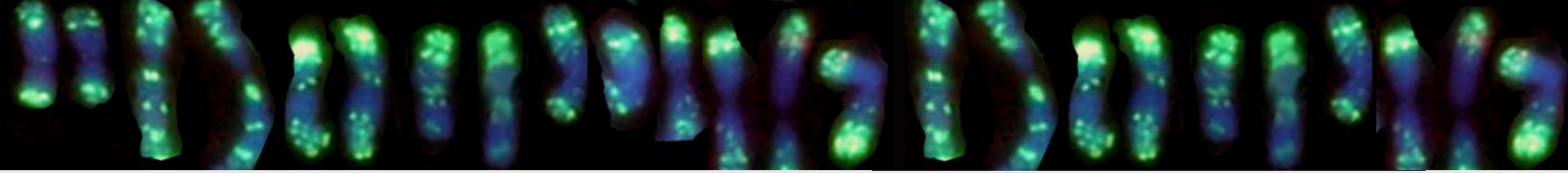
- Is the number constant in a species?

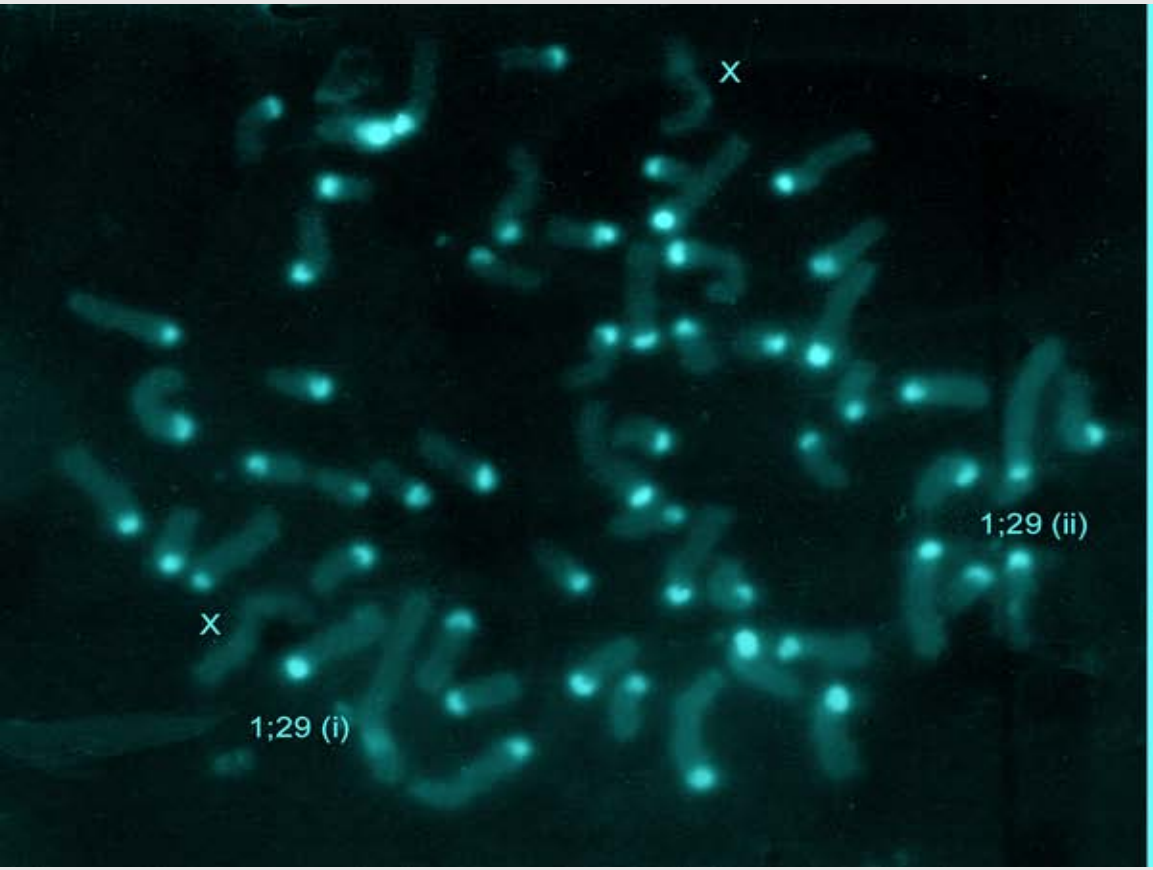
- Cattle 2n=60
  - but some individuals have 2n=58 or 2n=59 because two chromosomes fuse
- Chromosomal evolution is happening now

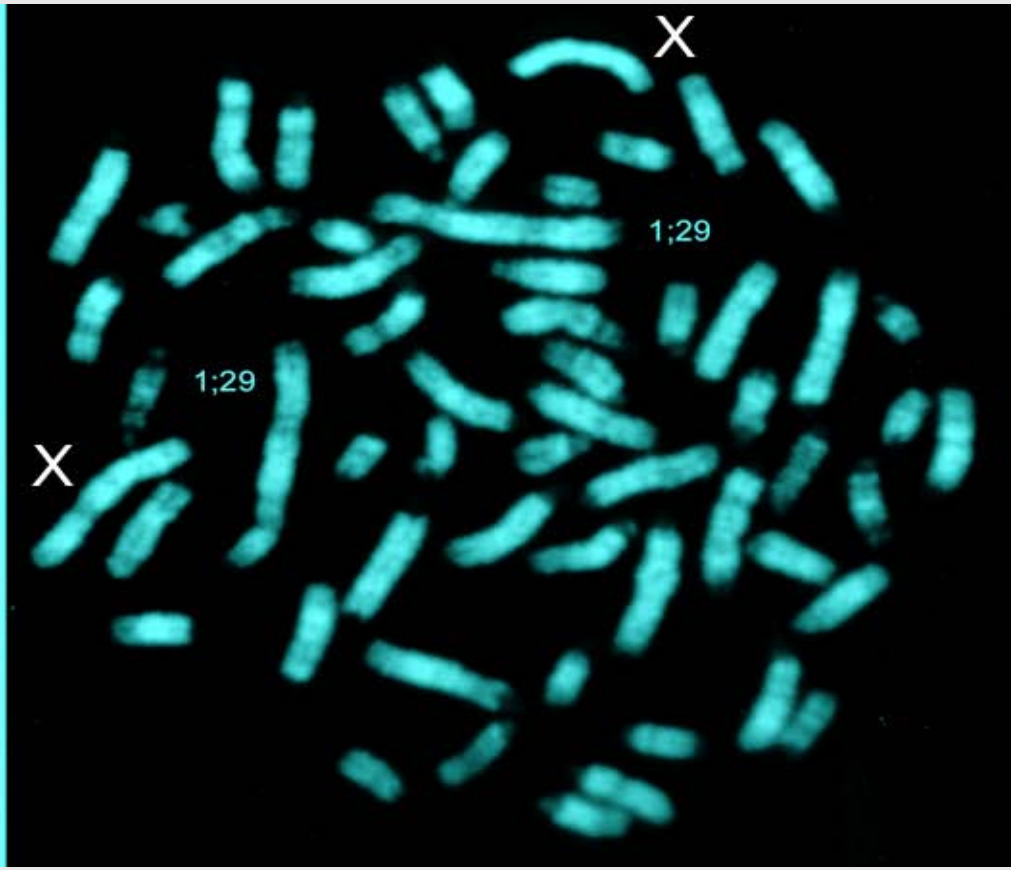


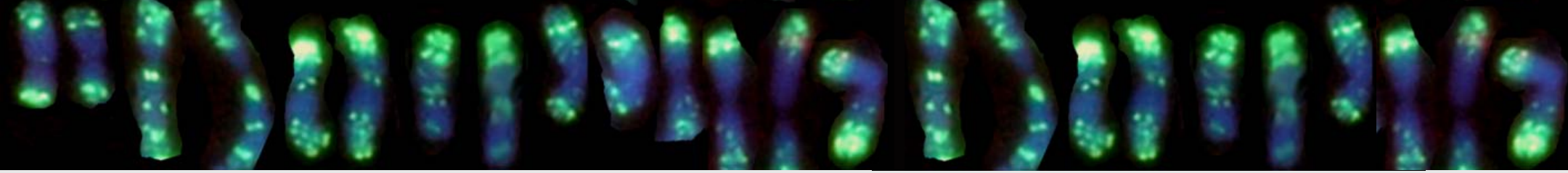
The 1;29 fusion in cattle

- Found in multiple breeds
- Sometimes a founder effect (imported in one bull – e.g. Brahman to Africa)
- But present even in major breeds
- Limited effect on fertility
- Probably positively selected for a difficult-to-score trait

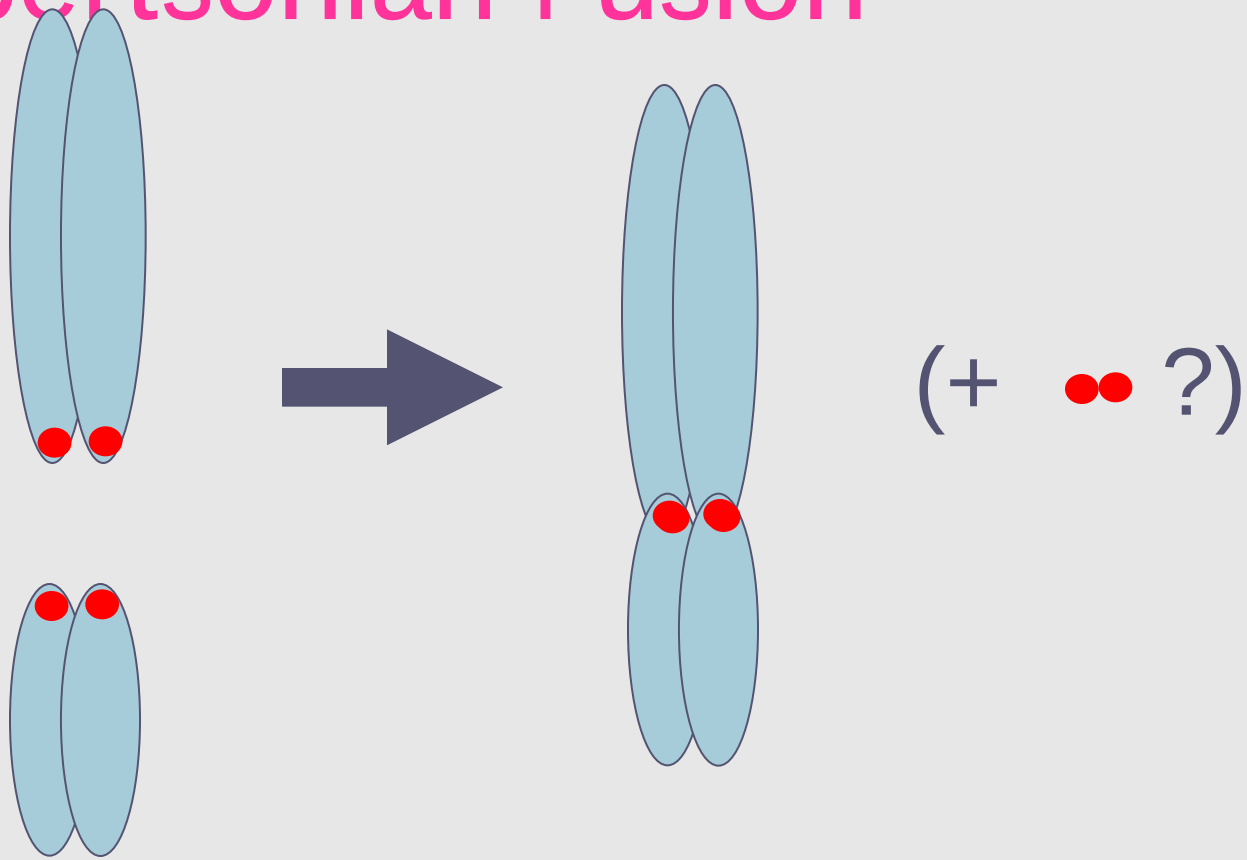



X
1;29 (ii)
X
1;29 (i)

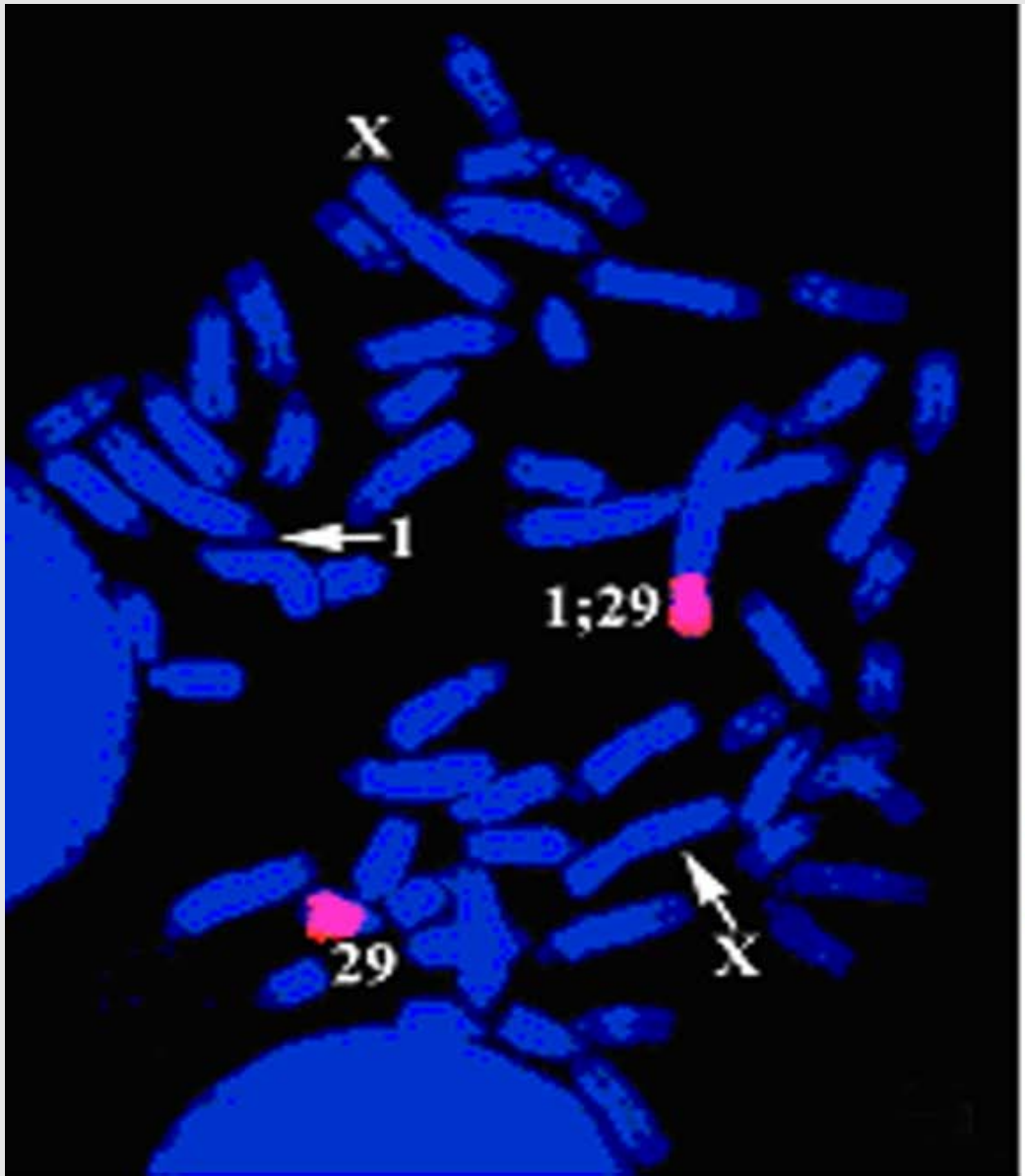

X
1;29
1;29
X

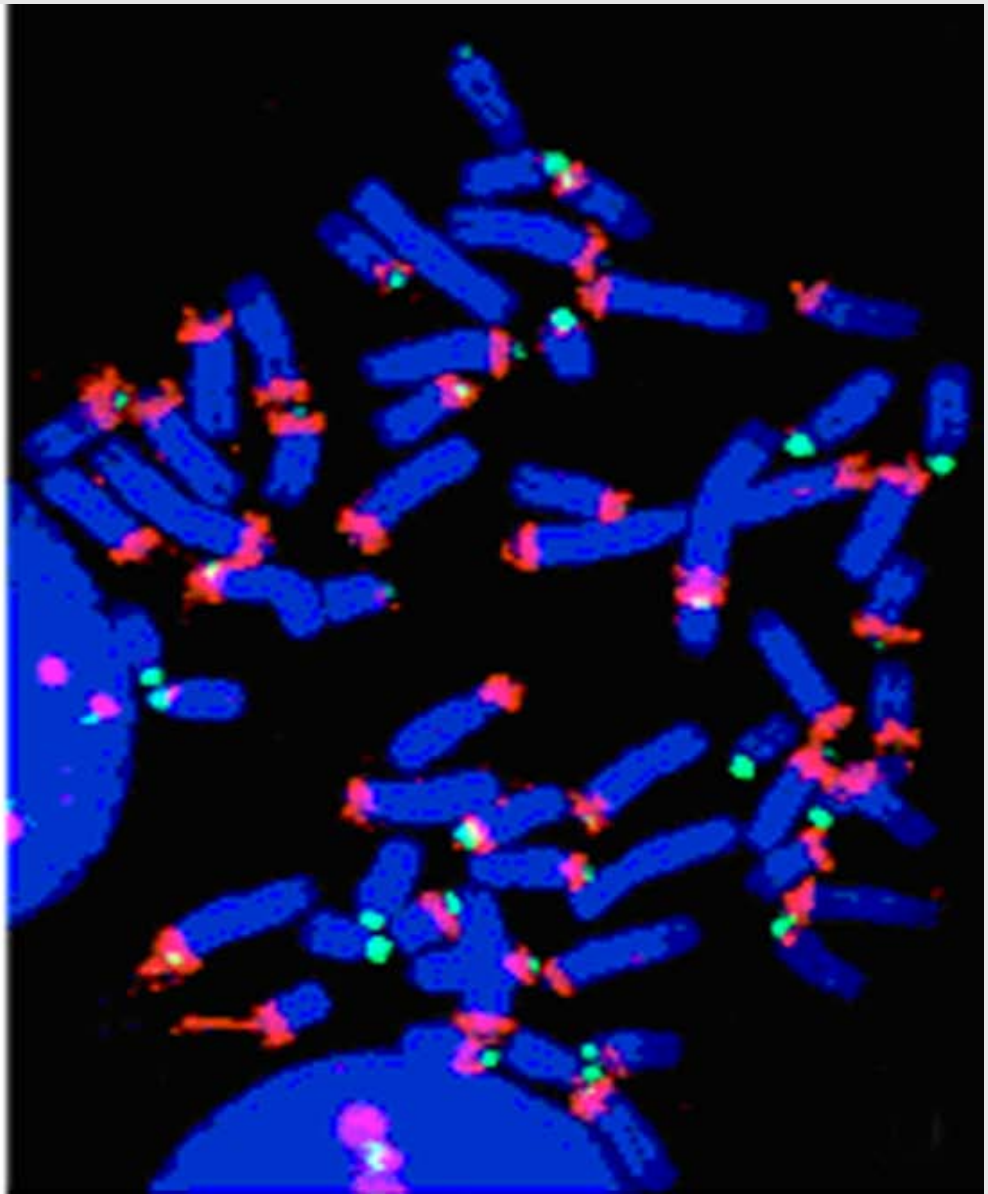


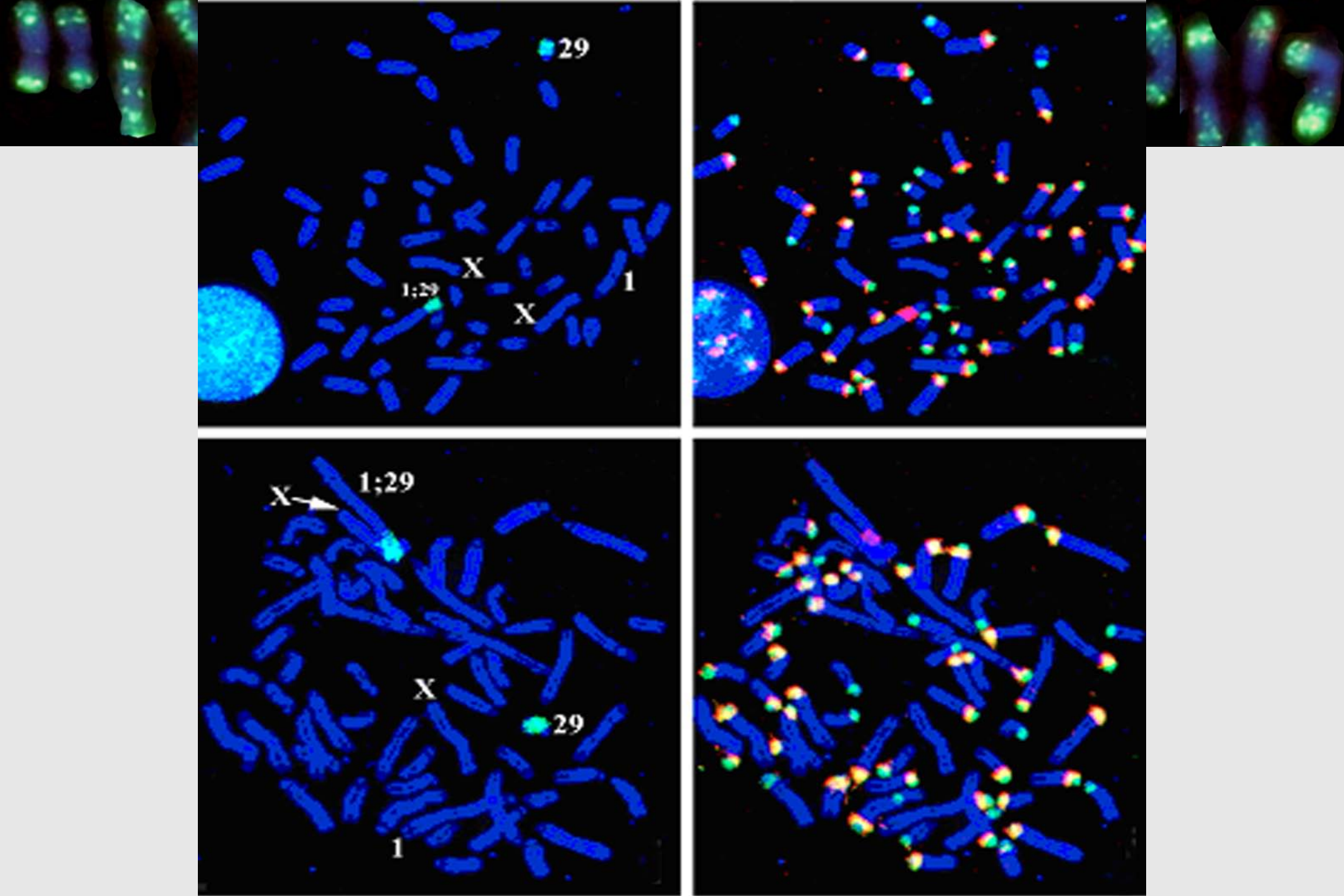
Robertsonian Fusion

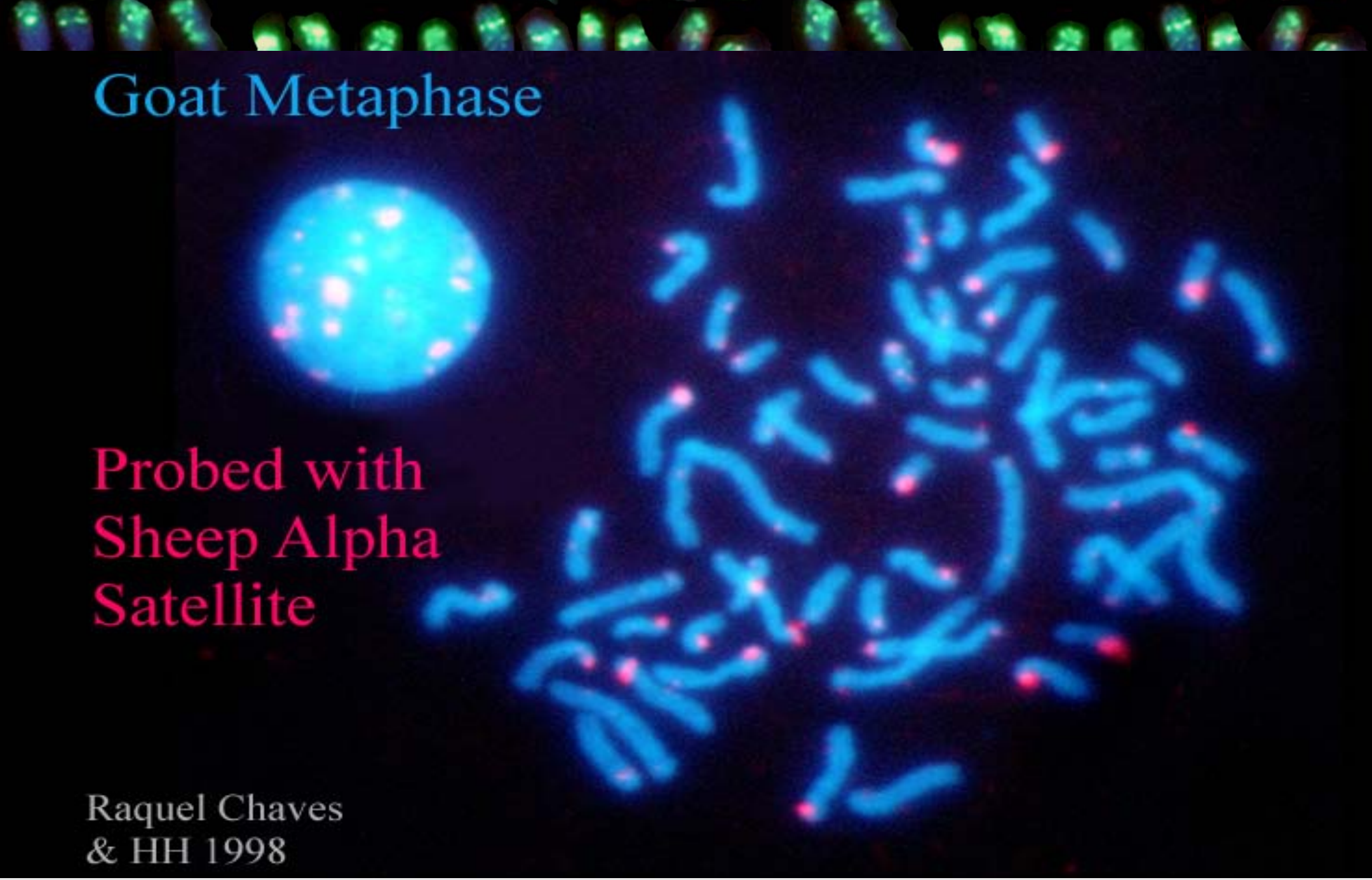


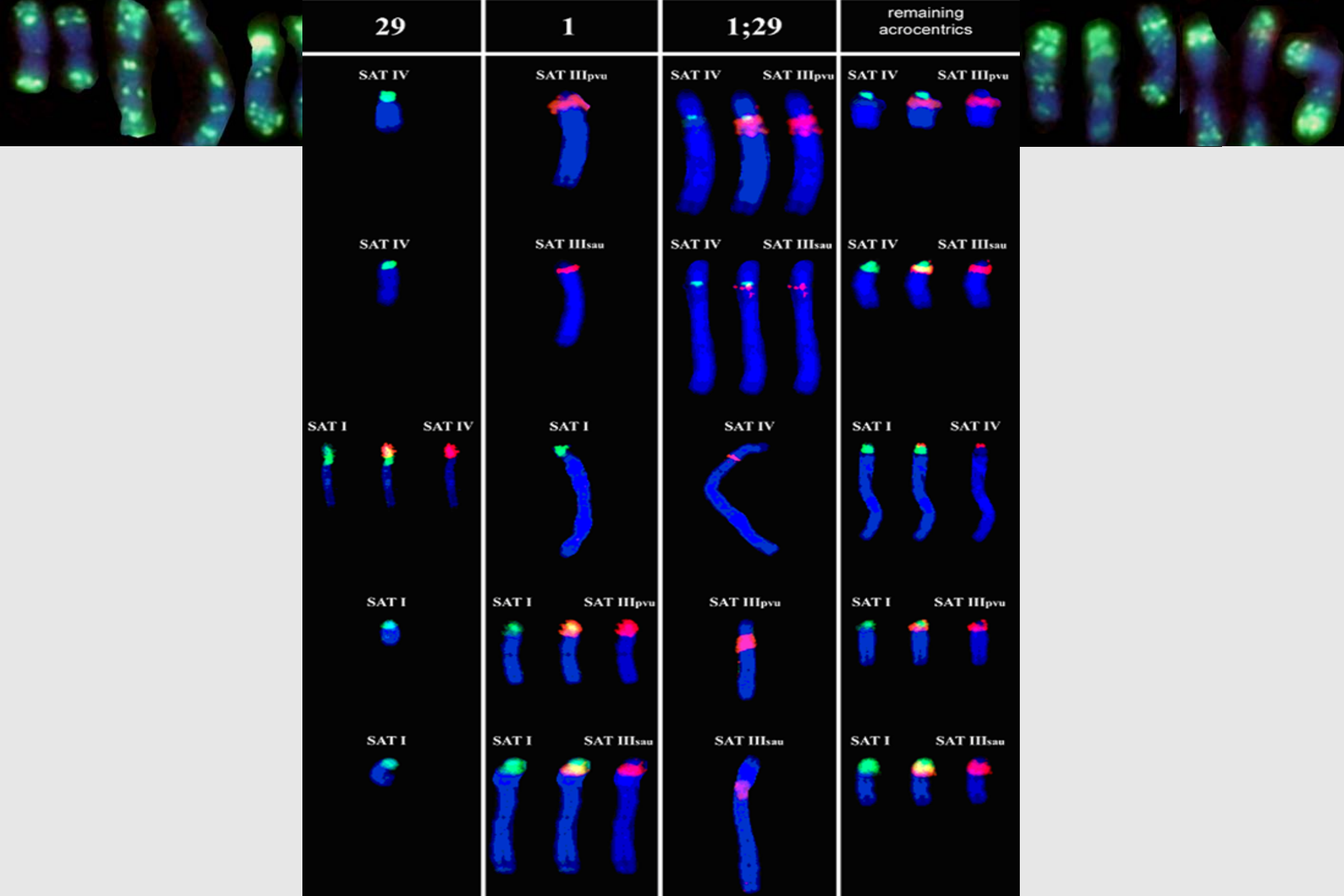
Bovid alpha-satellites and chromosome evolution

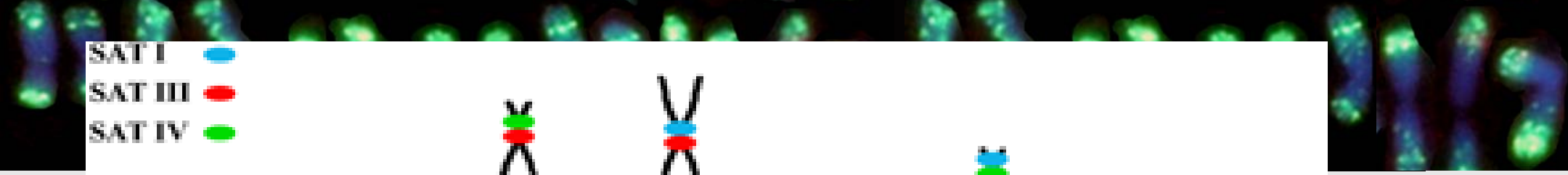


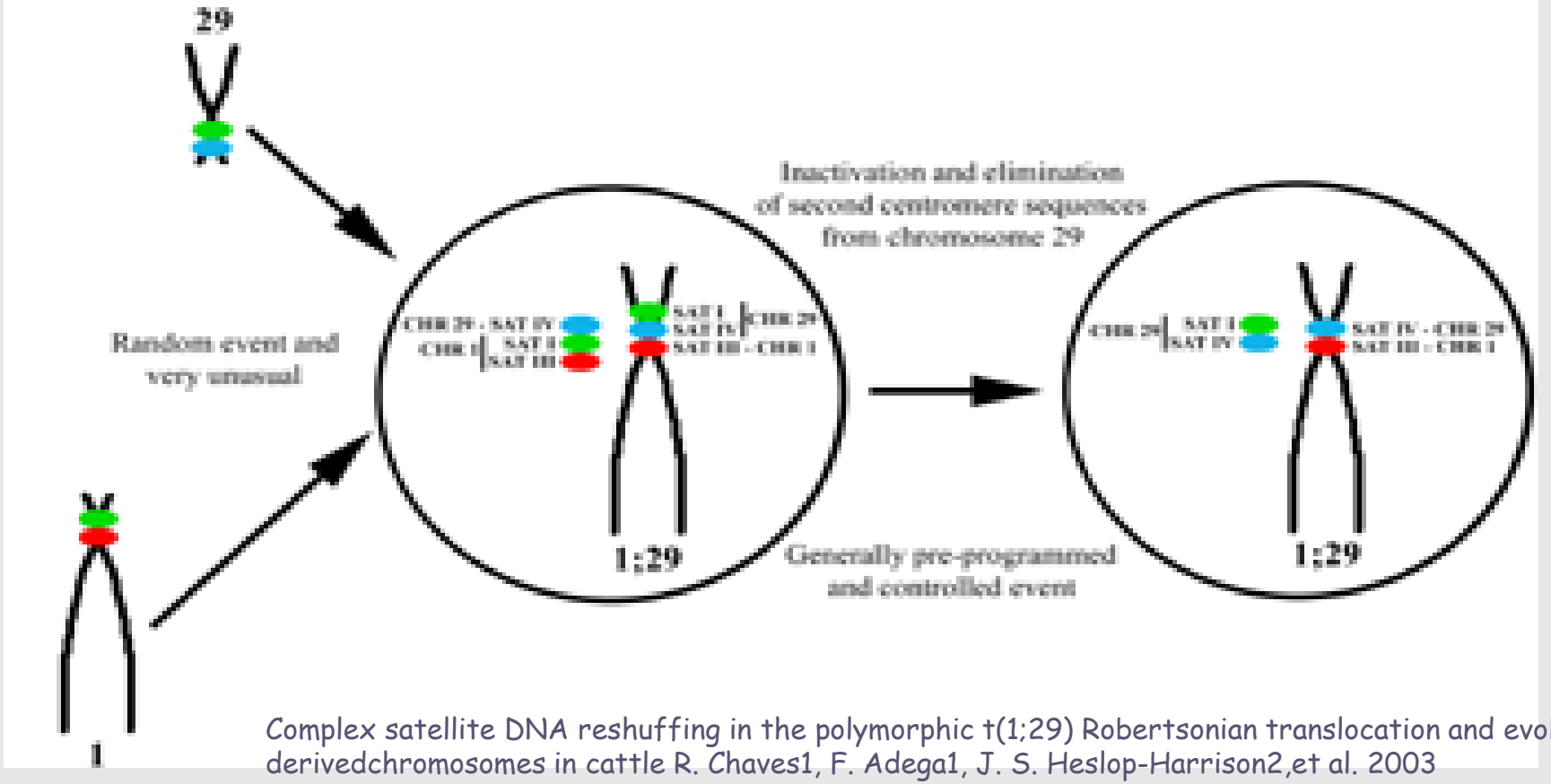



29
X
1;29
X
1
X
1;29
29
1

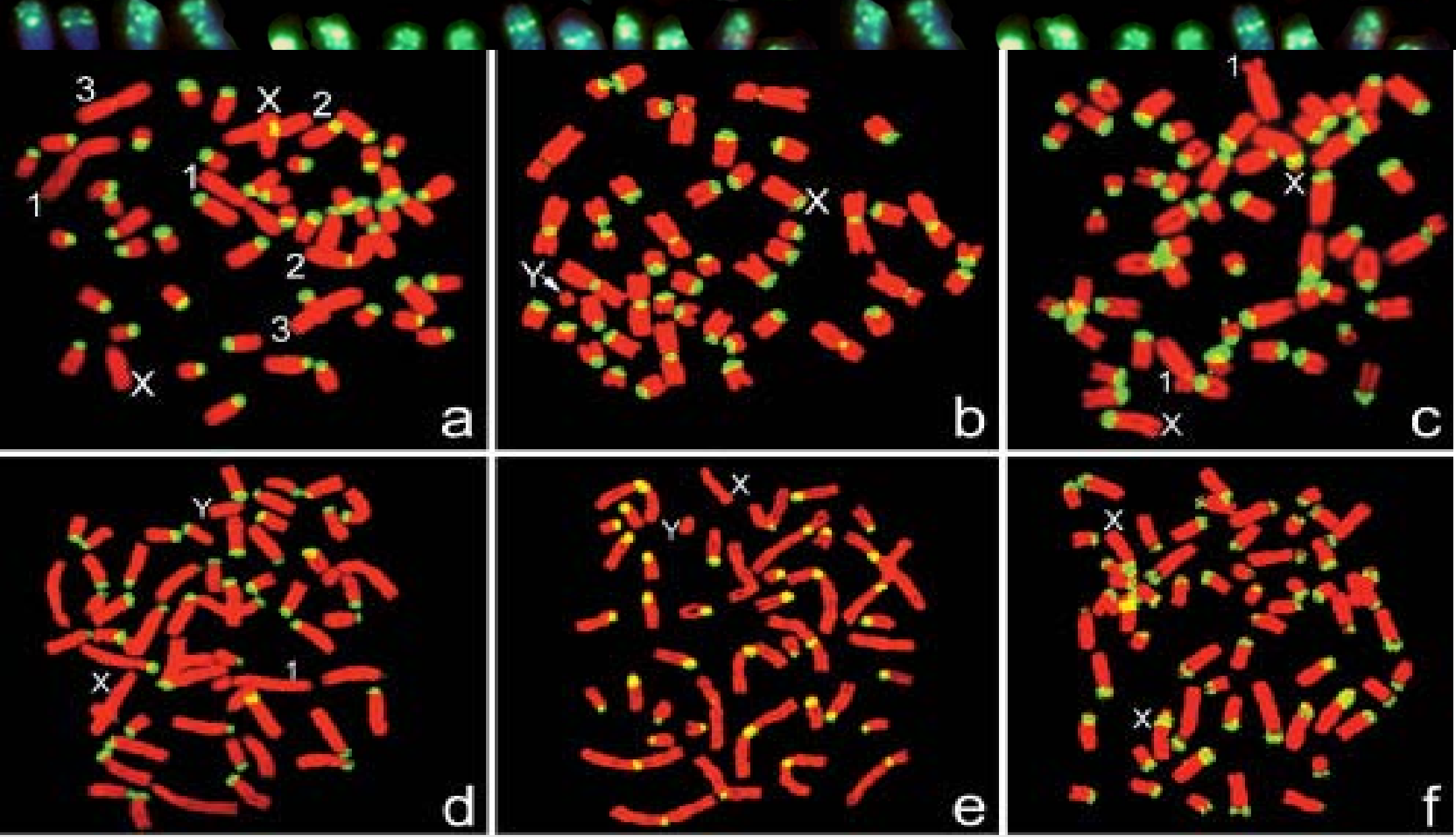

Goat Metaphase
Probed with
Sheep Alpha
Satellite
Raquel Chaves
& HH 1998

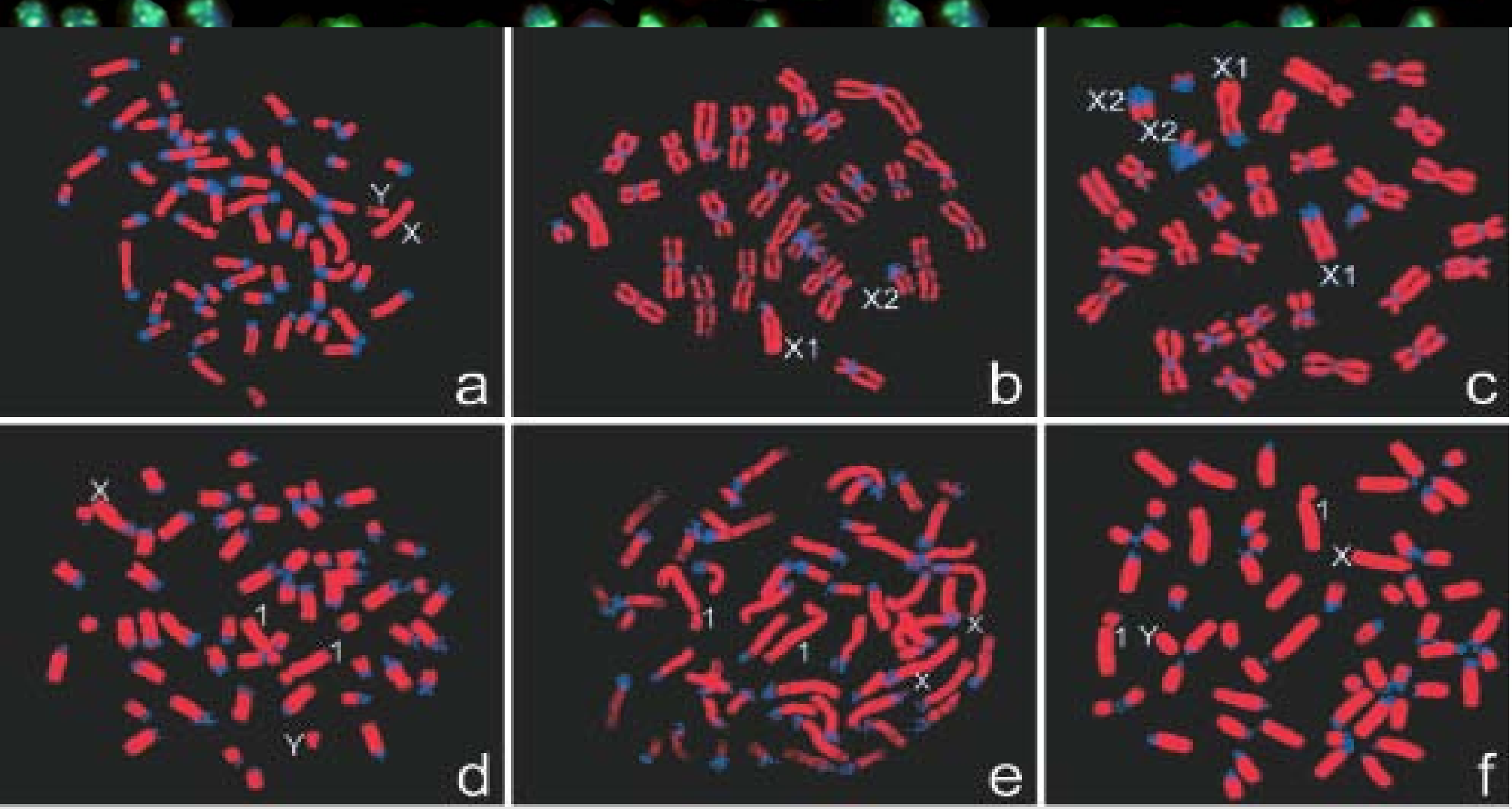

29
1
1;29
remaining acrocentrics
SAT IV
SAT IIIpvu
SAT IIIsau
SAT I

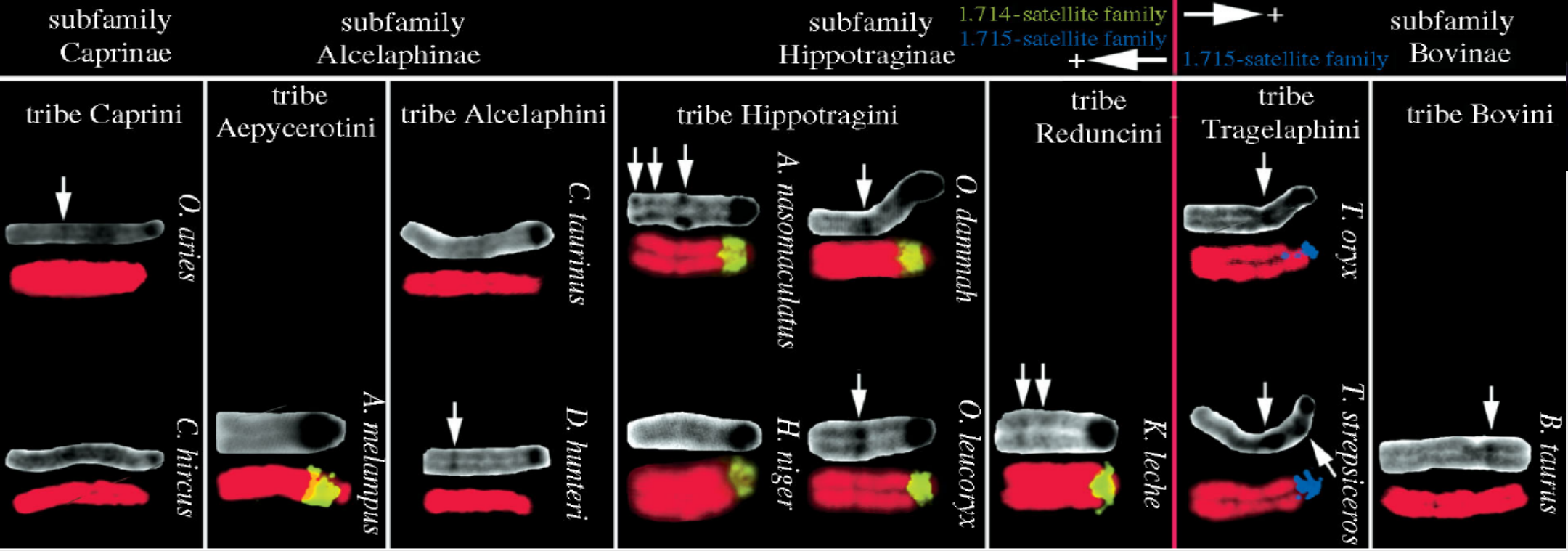




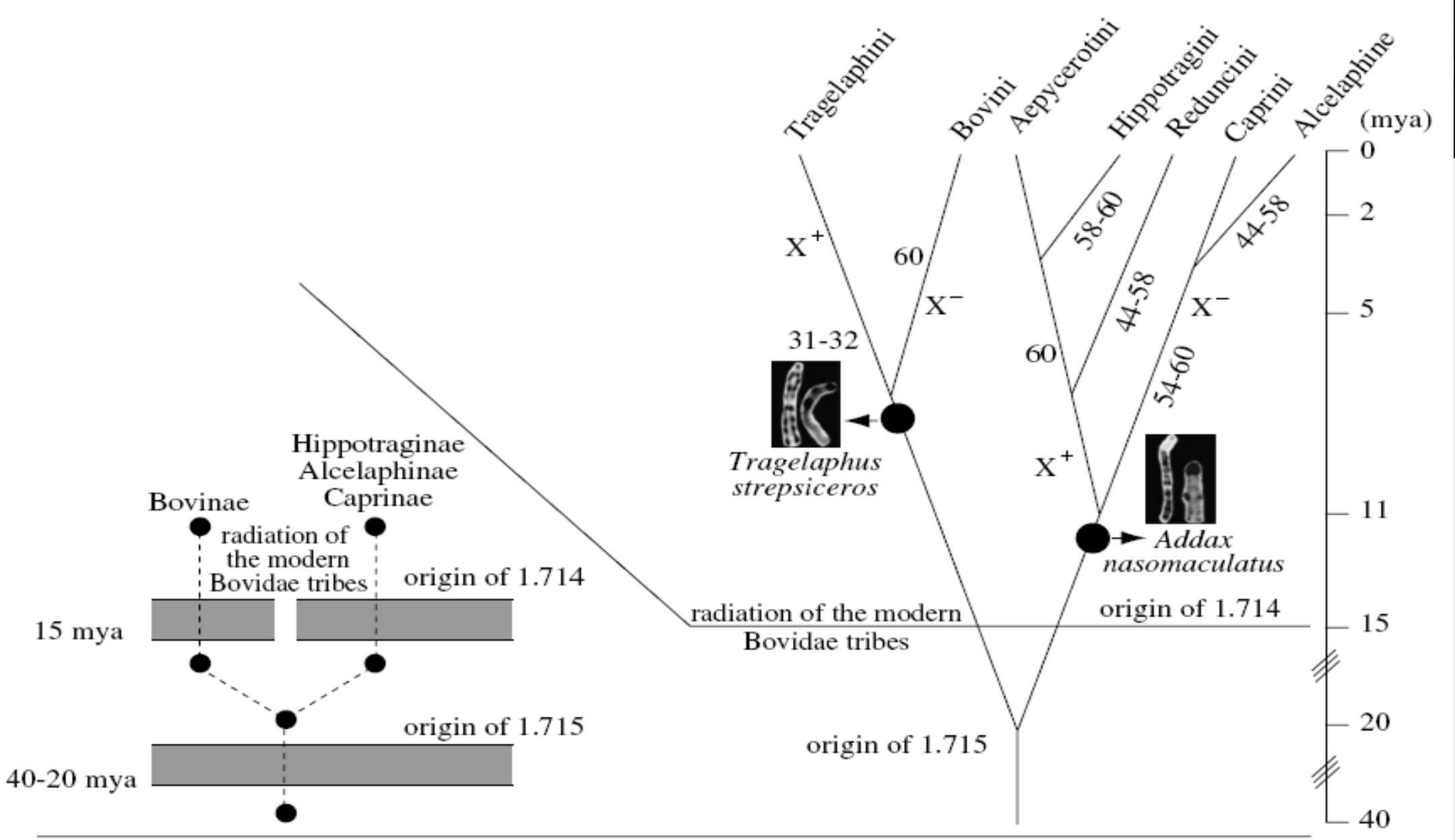
Complex satellite DNA reshuffing in the polymorphic t(1;29) Robertsonian translocation and evolutionarily derivedchromosomes in cattle R. Chaves1, F. Adega1, J. S. Heslop-Harrison2,et al. 2003


3
X
2
1
1
2
3
X
a
X
Y
b
1
X
1
X
c
Y
1
X
d
Y
X
e
X
X
f

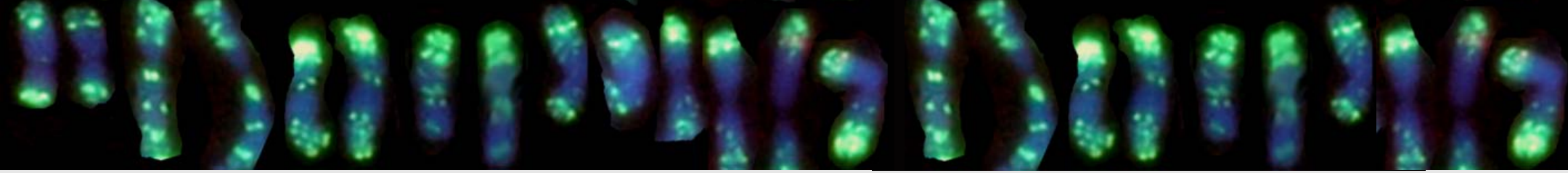

Y
X
a
X2
X1
b
X1
X2
X2
X1
c
X
1
1
Y
d
1
1
X
X
e
1
1 Y
X
f



Hybridization of sheep (clone pOaKB9) and cattle (pBtKB5) DNA satellite I probes to the X chromosome of most representative species listen in table 1. Bovinae subfamily shows only hybridization with the cattle satellite I and only in the X chromosome's centromeric regions of the tribe Tragelaphini was there signal from the cattle satellite I. Metaphases of subfamilies Hippotraginae, Alcelaphinae and Caprinae show positive in situ hybridization signals with both sheep and cattle satellite I probes. However, only the X chromosome centromeric regions of the Tribes Reduncini, Hippotragini and Aepycerotini show positive in situ hybridization signals with both satellite probes



Phylogenetic relationships and the primitive X chromosome inferred from chromosomal and satellite DNA analysis in Bovidae Raquel Chaves1,*, Henrique Guedes-Pinto1 and John S. Heslop-Harrison Proc Roy Soc B 2005

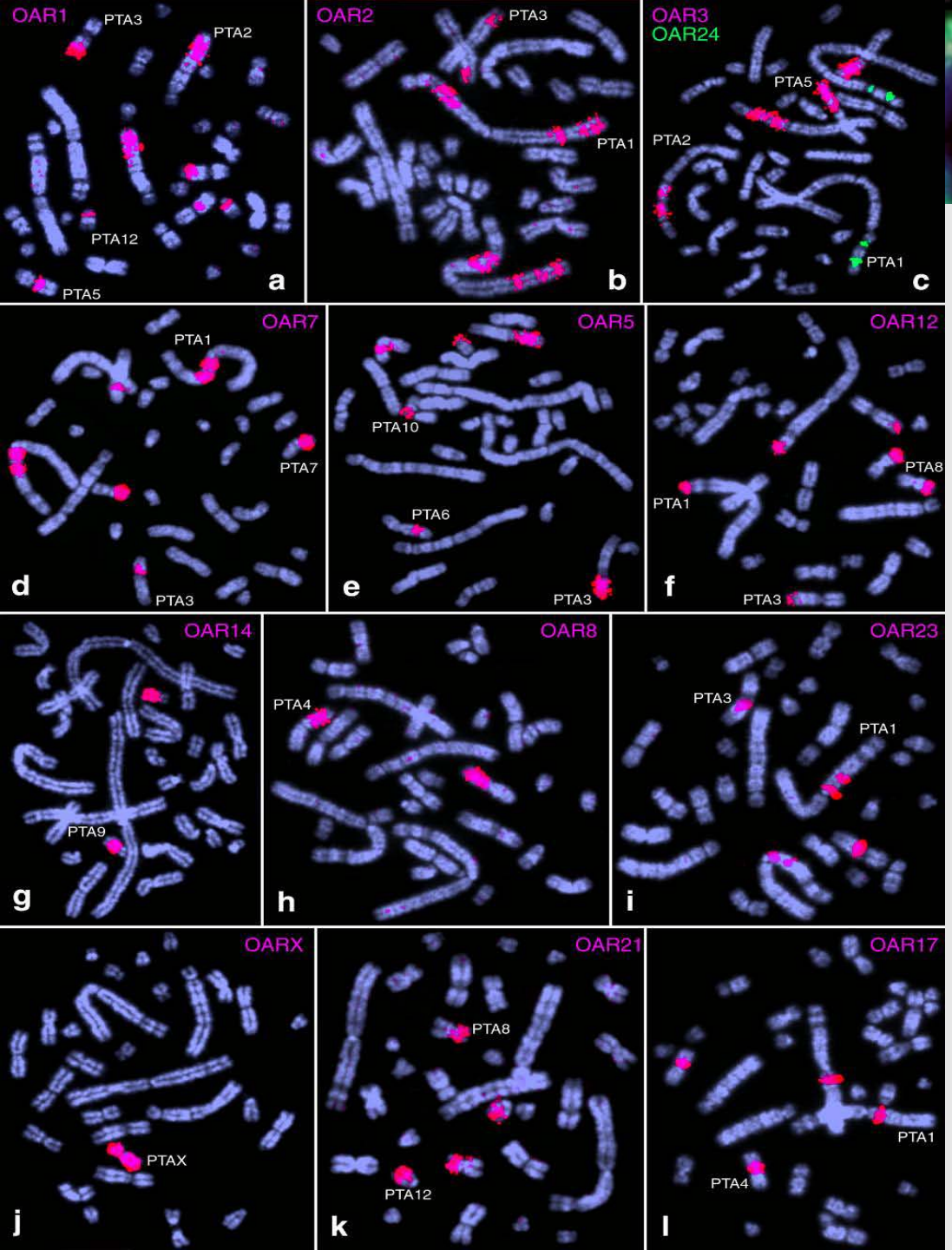


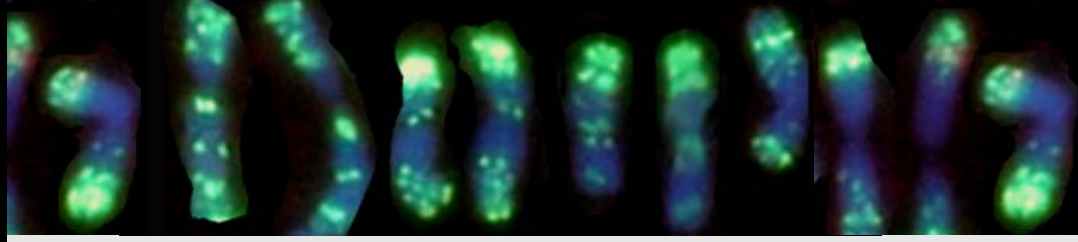
Bovidae – Family

- Mammals
  - Order Artiodactyla (=Even-toed ungulates)
  - 3 groups: the Suiformes (pigs, peccaries, hippopotamuses), Tylopoda (camels, llamas) and Ruminantia (cattle, goats, sheep, deer, antelopes, giraffes)
  - 9 families (13 tribes) including Bovidinae
    - Family Bovidae
      - c. 137 species
      - Last species (new genus) discovered in 1992

Translocation in Sus

High-resolution comparative chromosome painting in the Arizona collared peccary (Pecari tajacu, Tayassuidae): a comparison with the karyotype of pig and sheep Filomena Adega, Raquel Chaves, Andrea Kofler, Paul R. Krausman, Julio Masabanda, Johannes Wienberg & Henrique Guedes-Pinto. Chromosome Research 2006

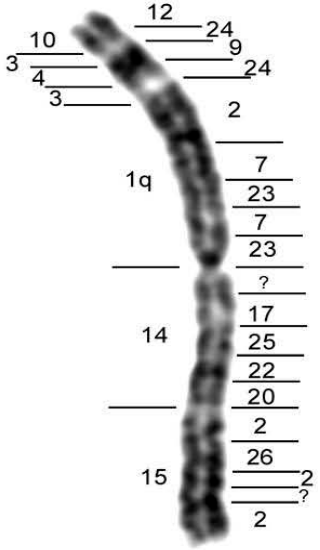




Translocation in Sus

Complex
Chaves 2005

SSC OAR



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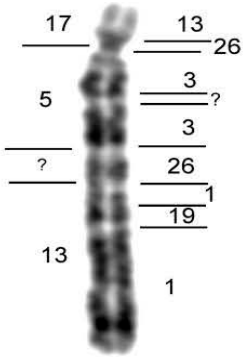

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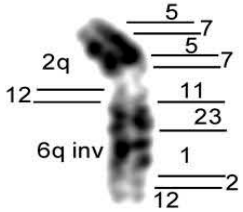

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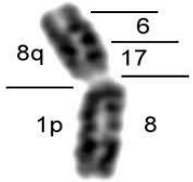

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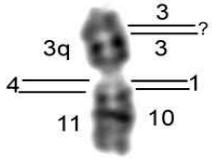
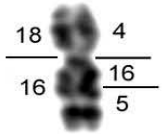


5 [1qter+11]



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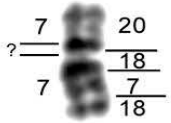

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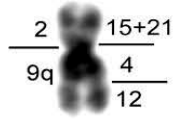

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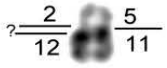

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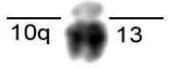

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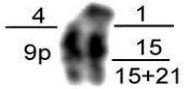
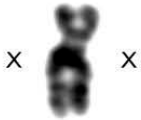


12 [12]

13 [10]

14 [14]



X [X]

Y [Y]

Diversity

- In the genepool
  - Allelic in one species
  - In different genomes
  - In different species
- From recombination
- From new mutations
  - Induced or natural
  - DNA sequence or retroelements

Polyploidy

- **Polyploids** have three or more complete sets of chromosomes
  - diploid 2n=2x
  - triploid 2n=3x
  - tetraploid 2n=4x
  - hexaploid 2n=6x
  - octoploid 2n=8x
- Two types of polyploidy

Autopolyploidy

A x A

⇩

AA

⇩

AAAA

Allopolyploidy

A x B

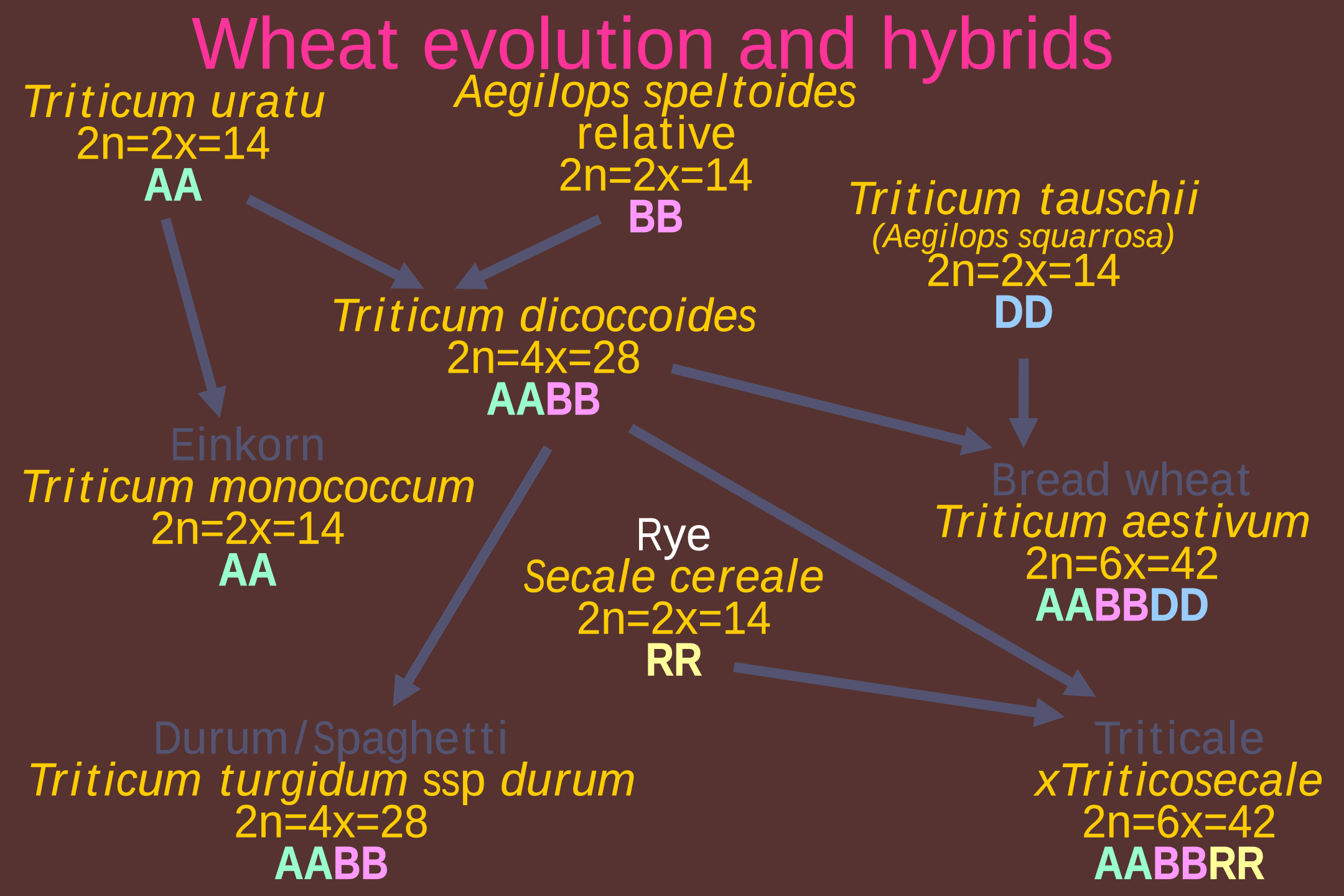
⇩

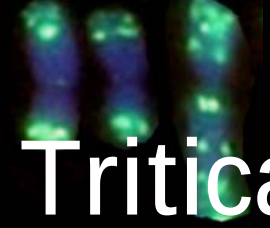
AB

⇩

AABB

Wheat evolution and hybrids





Triticale:
wheat x rye
hybrid

Breeding strategies

AABBDD x RR

ABDR

Double chromosomes

AABBDDRR

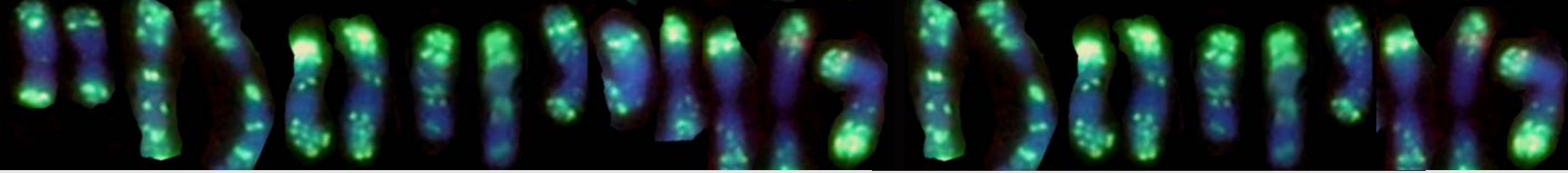
Backcross to wheat

Looses the R chromosomes eventually

AABBDD+1R

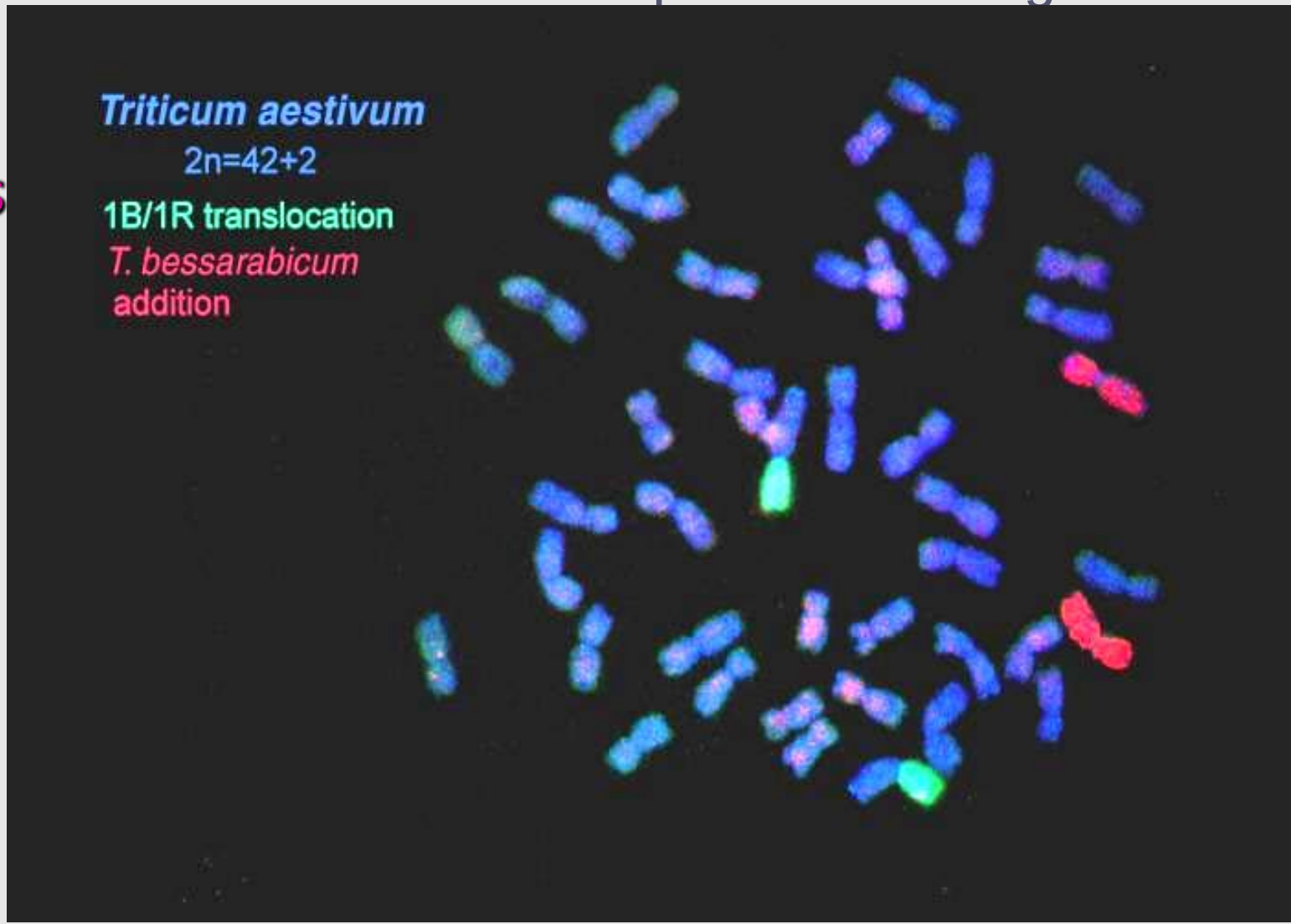
Induce recombination

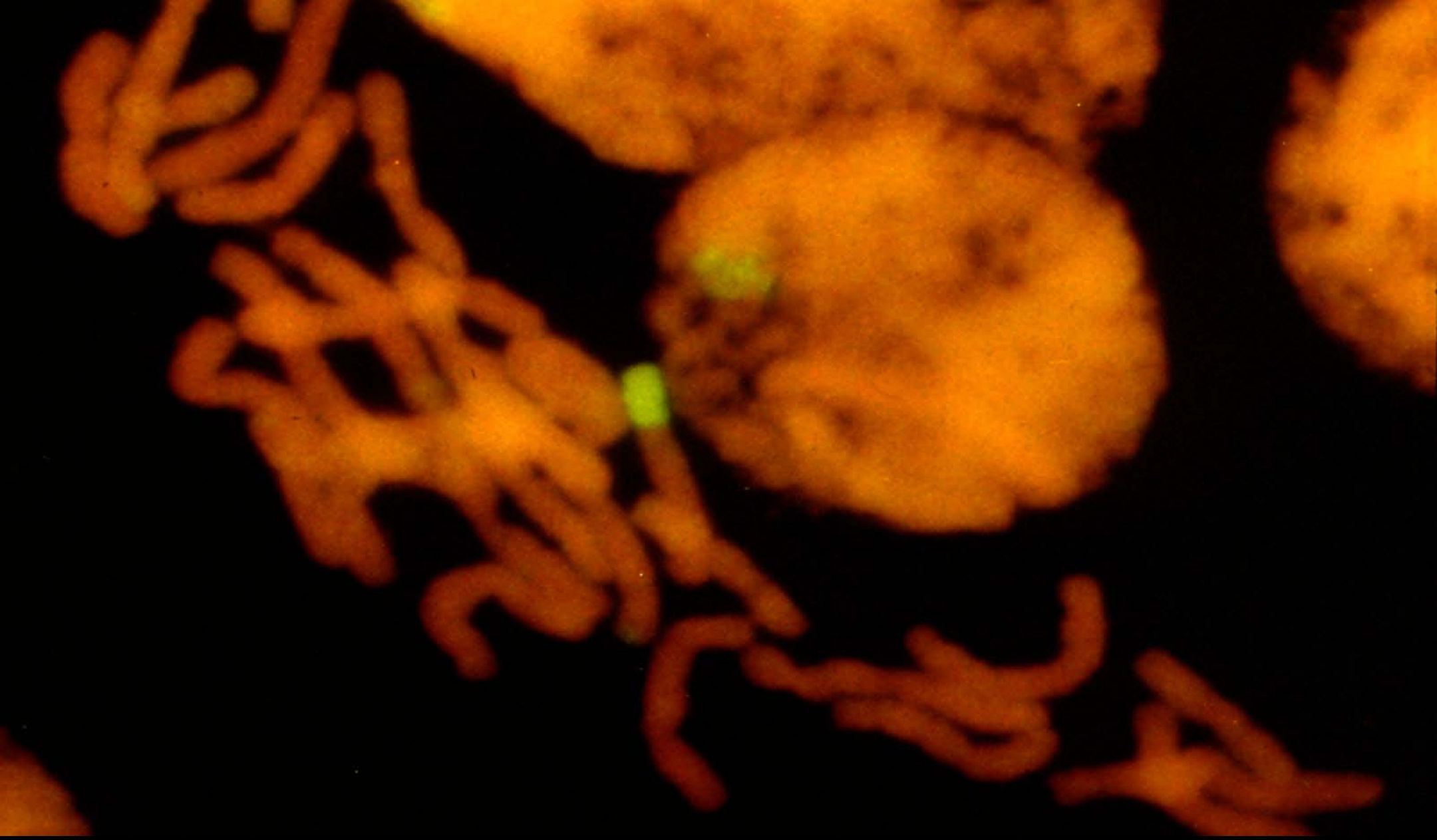
AABBDD including 1BL/1RS

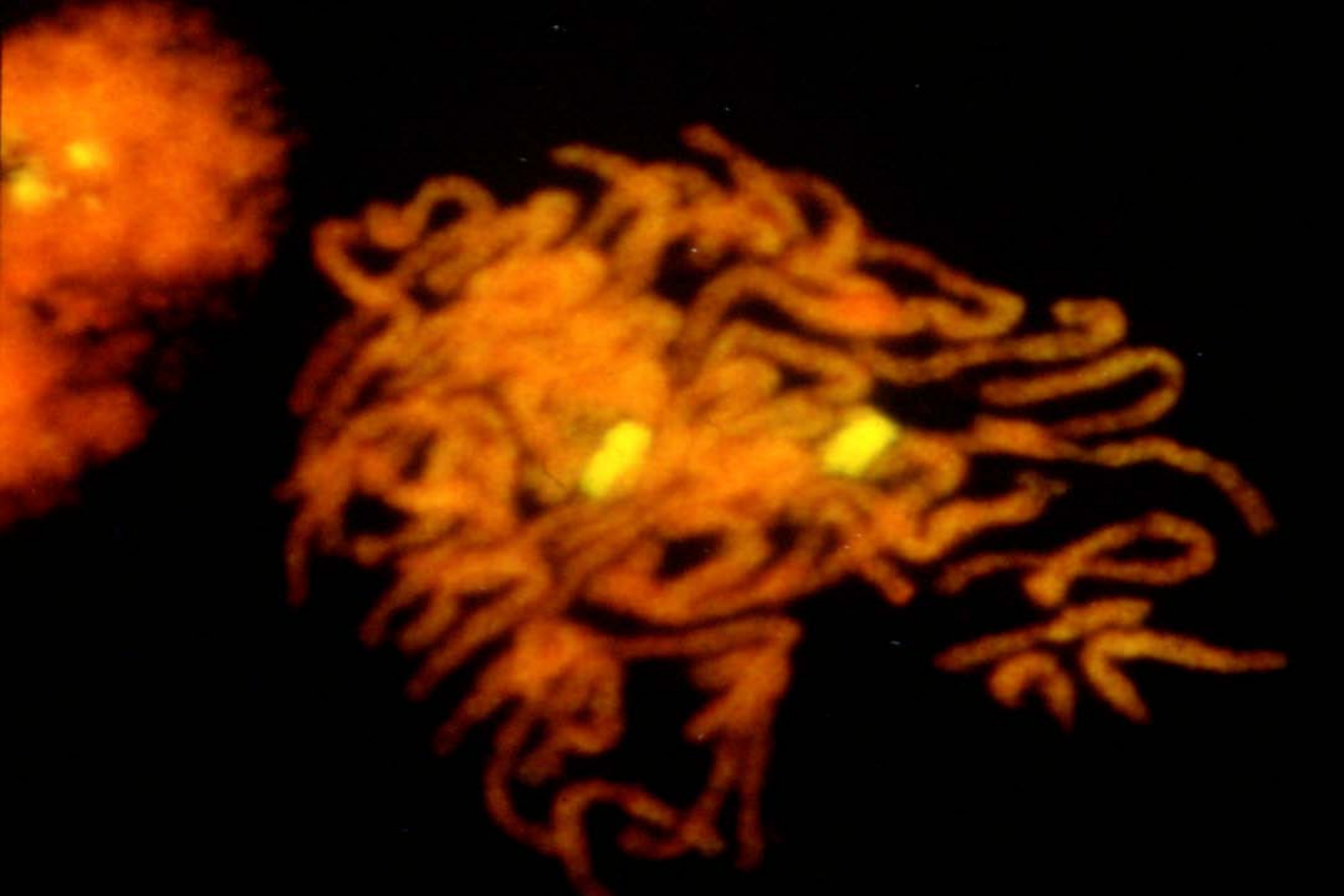


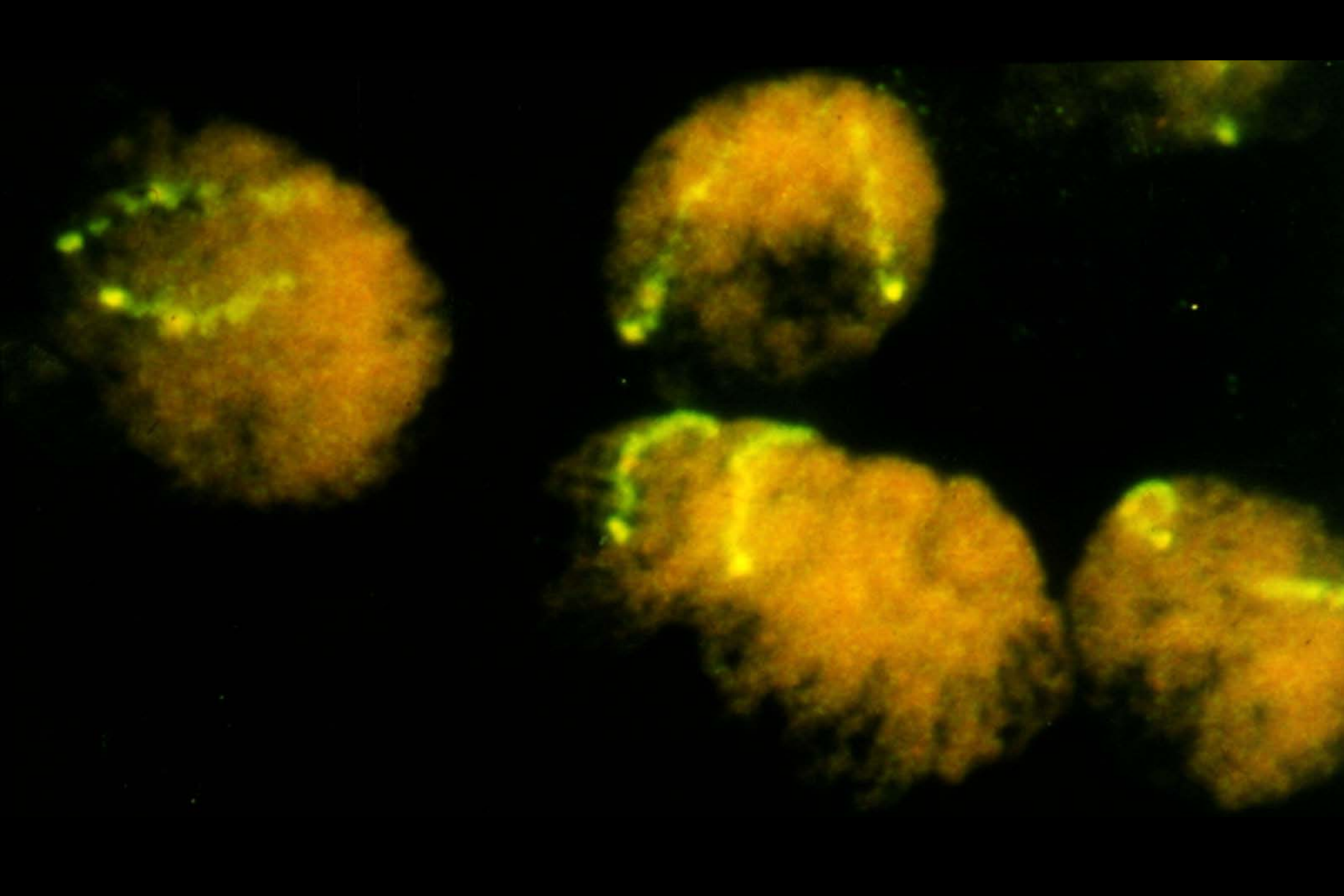
Total genomic DNA can be used as a probe to distinguish

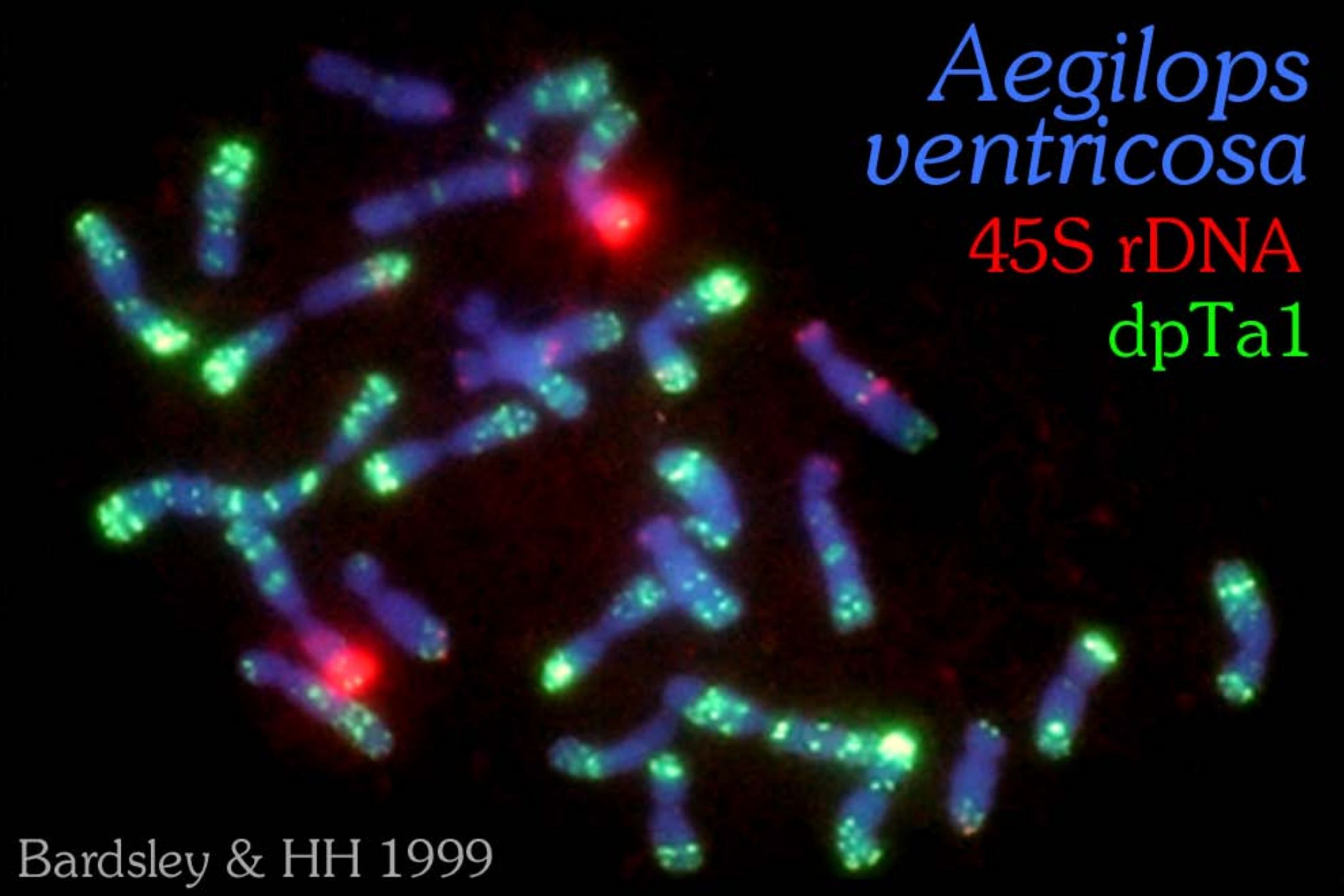
- Genomes in sexual hybrids
- Alien chromosome introgression

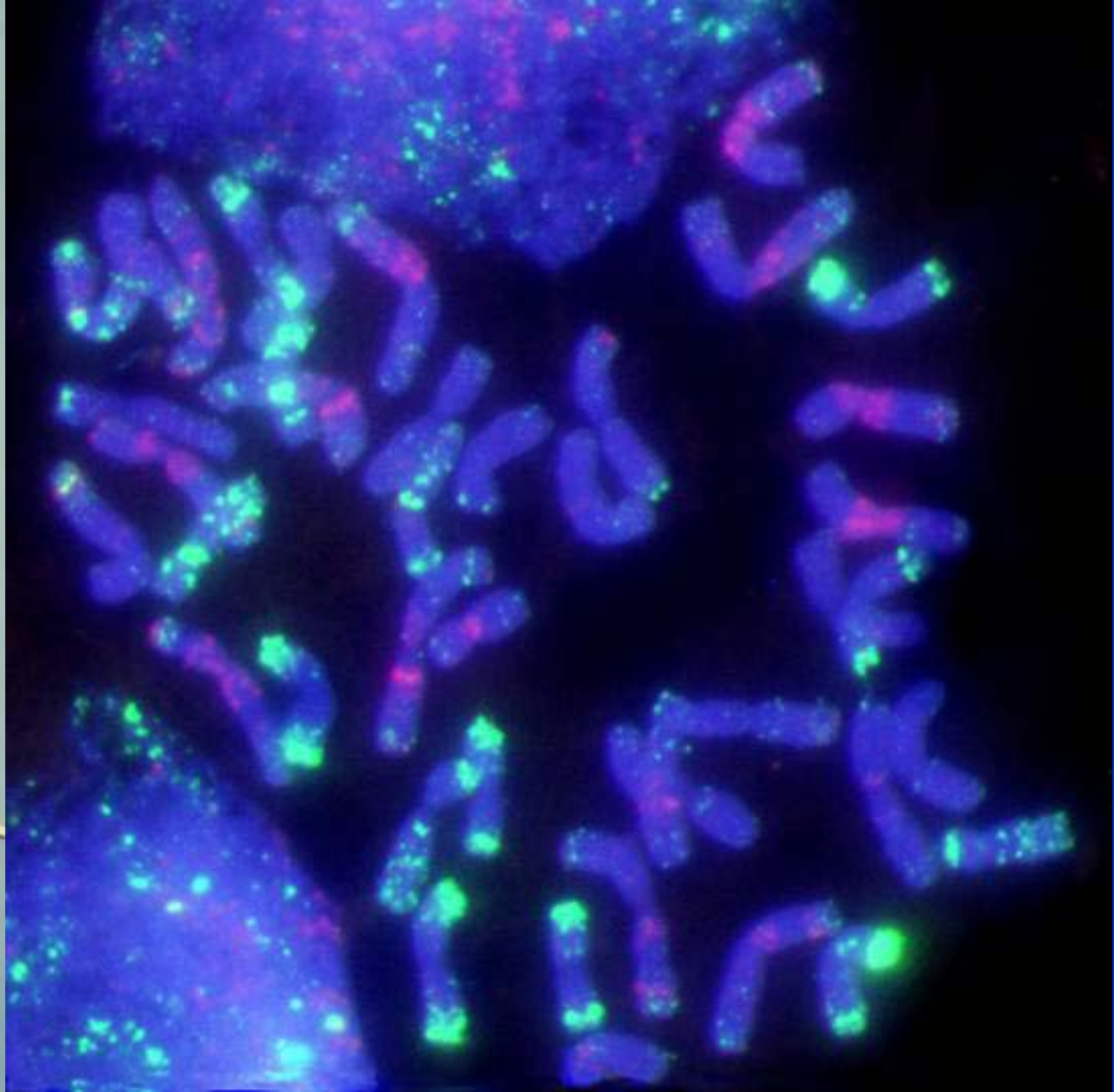




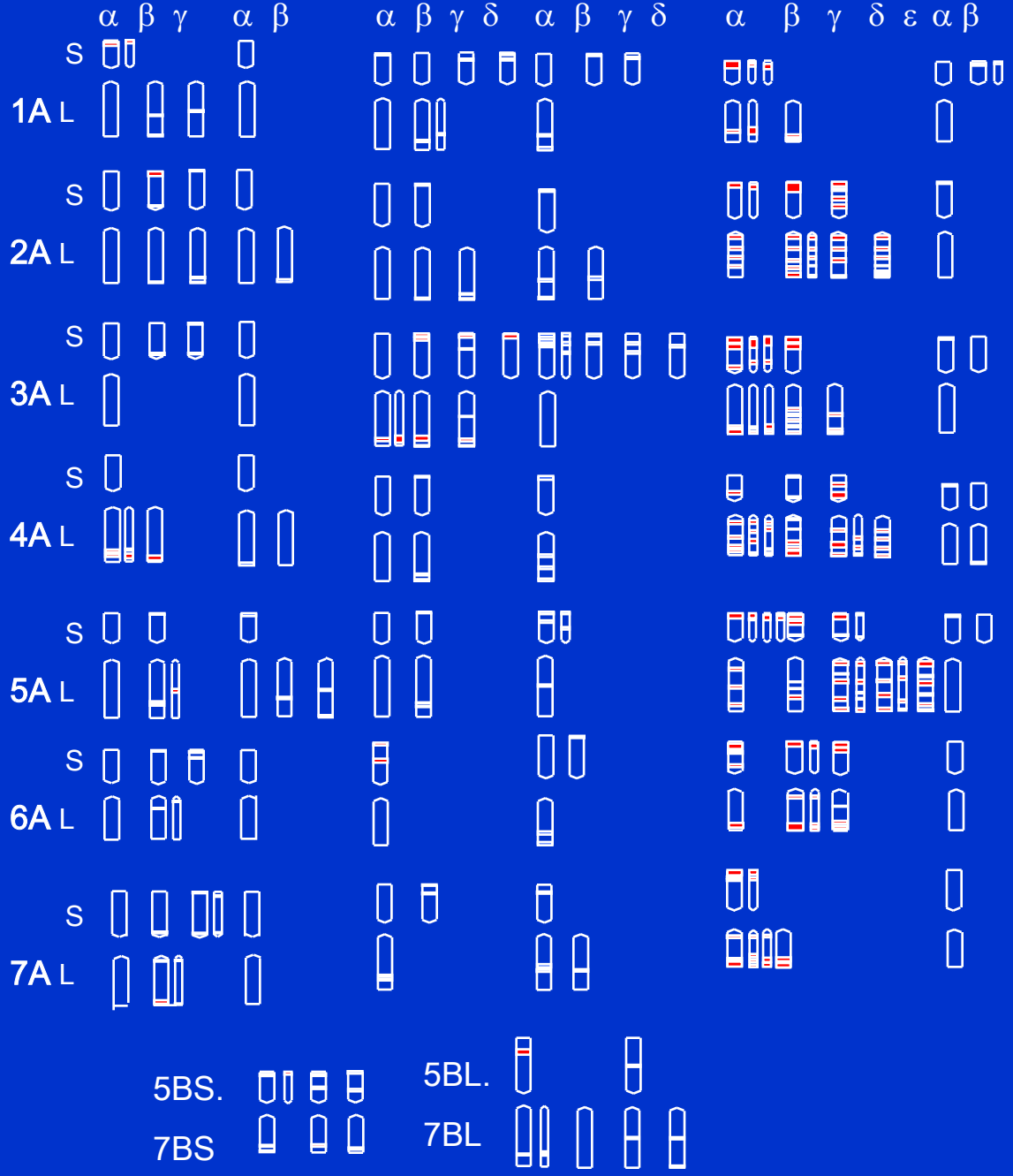





Aegilops
ventricosa
45S rDNA
dpTa1
Bardsley & HH 1999

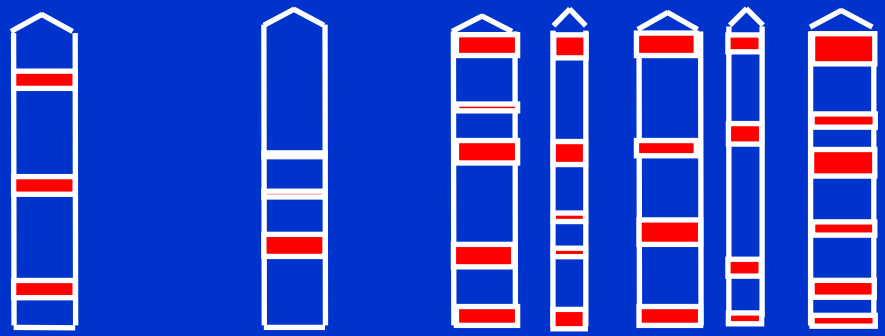


Lodging in cereals
UK July 2007



Multiple dpTa1 variants of each chromosome

e.g. 5DL



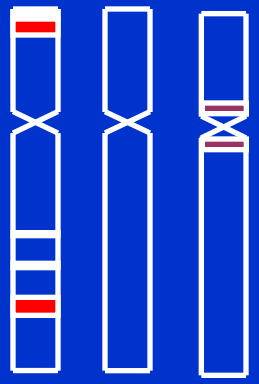
Bardsley, Schwarzacher & HH 2007

Inheritance of Chromosome 5D

Aegilops ventricosa
DDNN

×

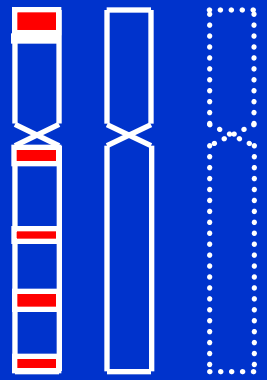
Triticum persicum Ac.1510
AABB

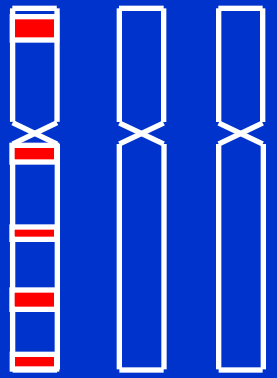


ABDN

AABBDDNN

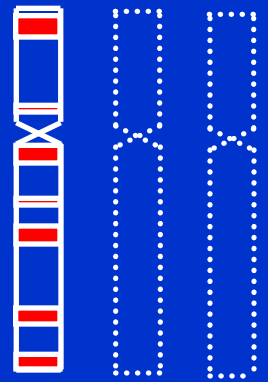
× Marne
AABBDD





VPM1

× Hobbit

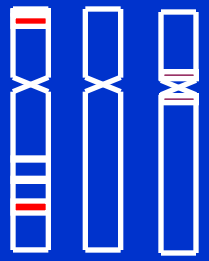


CWW1176-4

dpTa1

Inheritance of Chromosome 5D

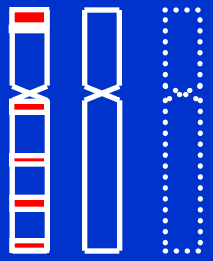
Aegilops ventricosa
DDNN



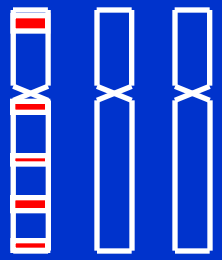
× *Triticum persicum* Ac.1510
AABB

ABDN

AABBDDNN

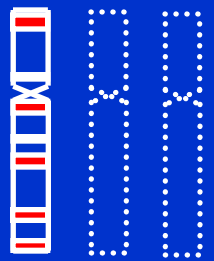


× Marne
AABBDD

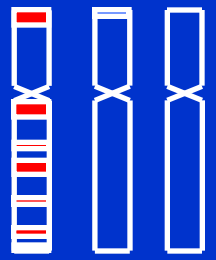


VPM1

× Hobbit

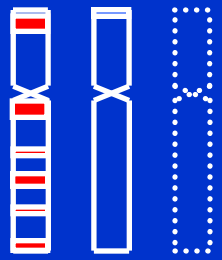


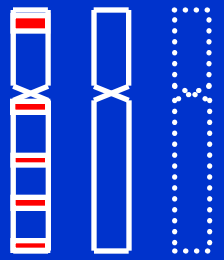
Dwarf A



CWW1176-4

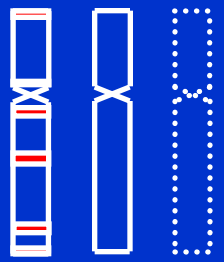
× Virtue





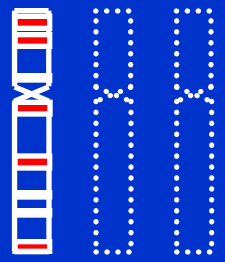
Rendezvous

× {Kraka × (Huntsman × Fruhgold)}



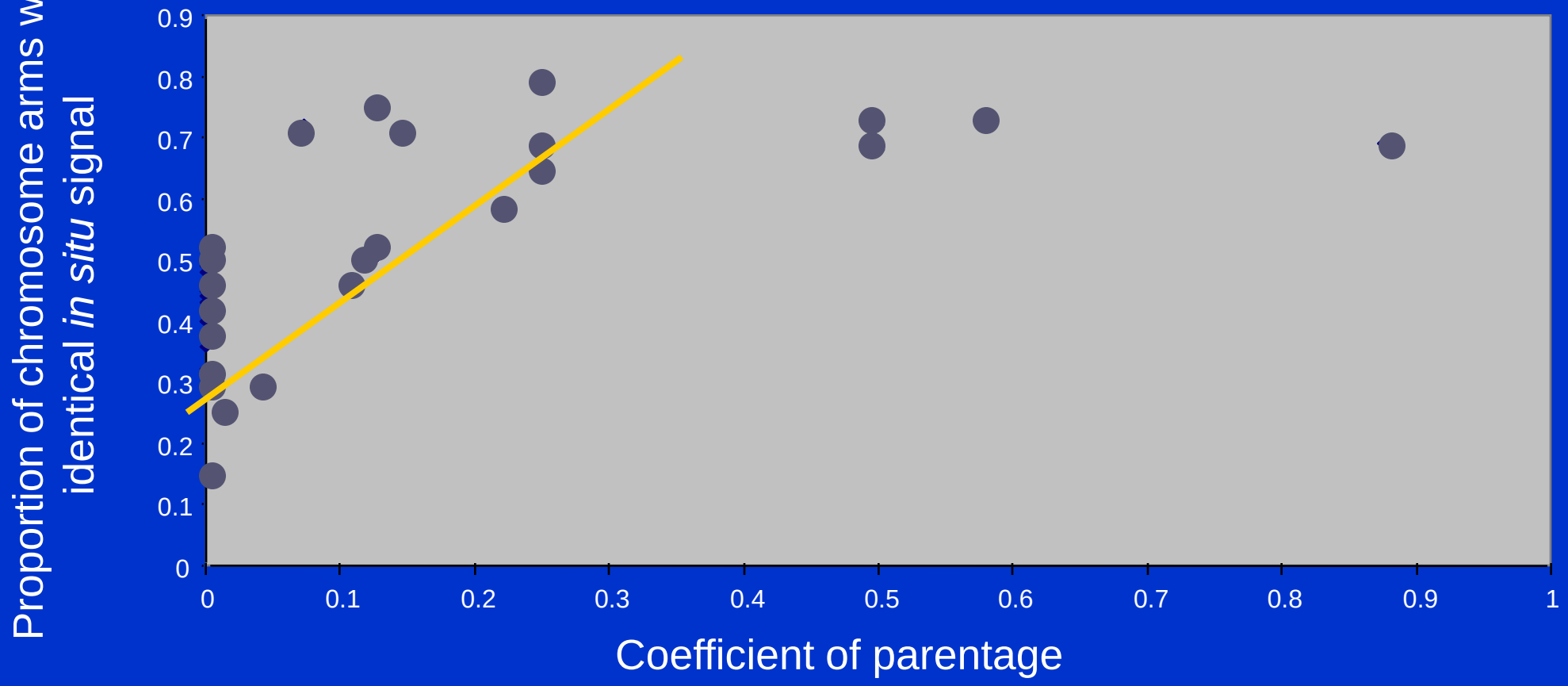
Piko

96ST61

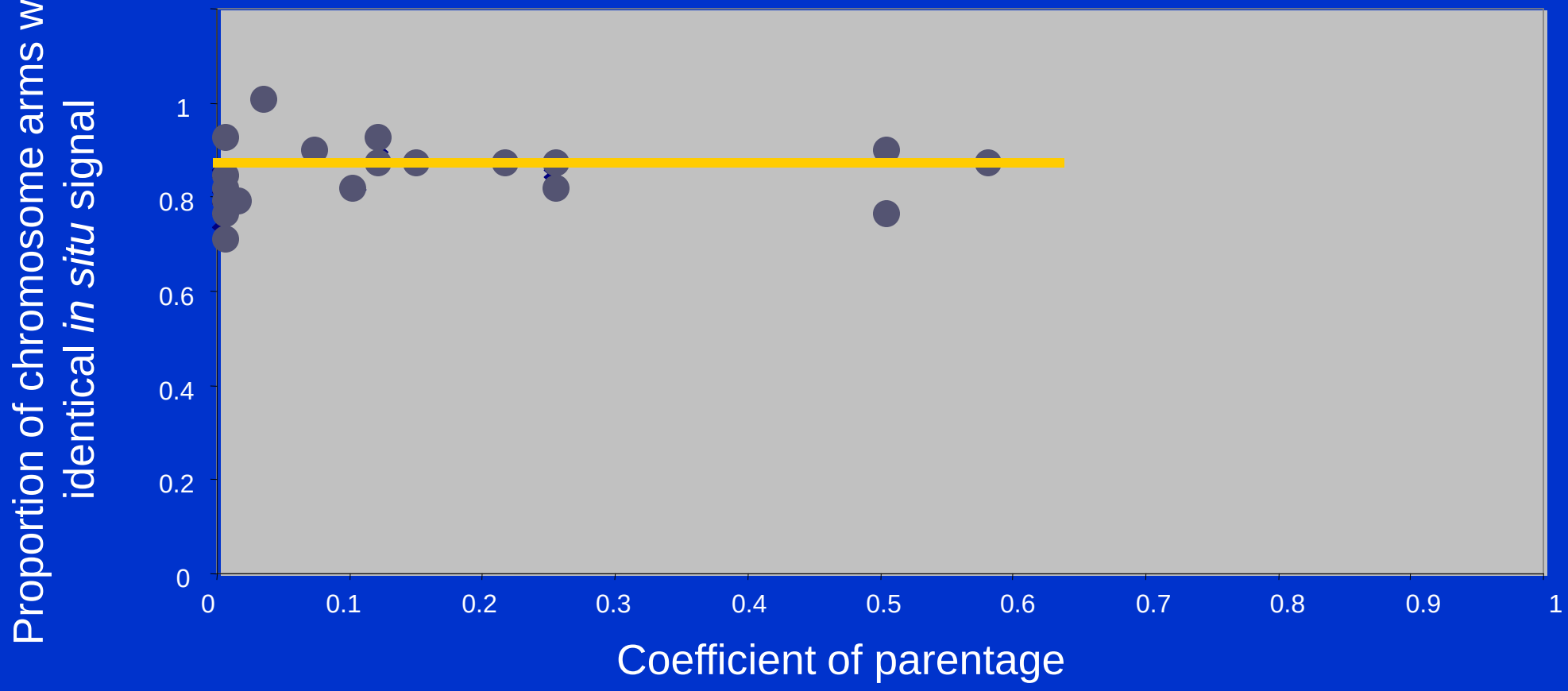


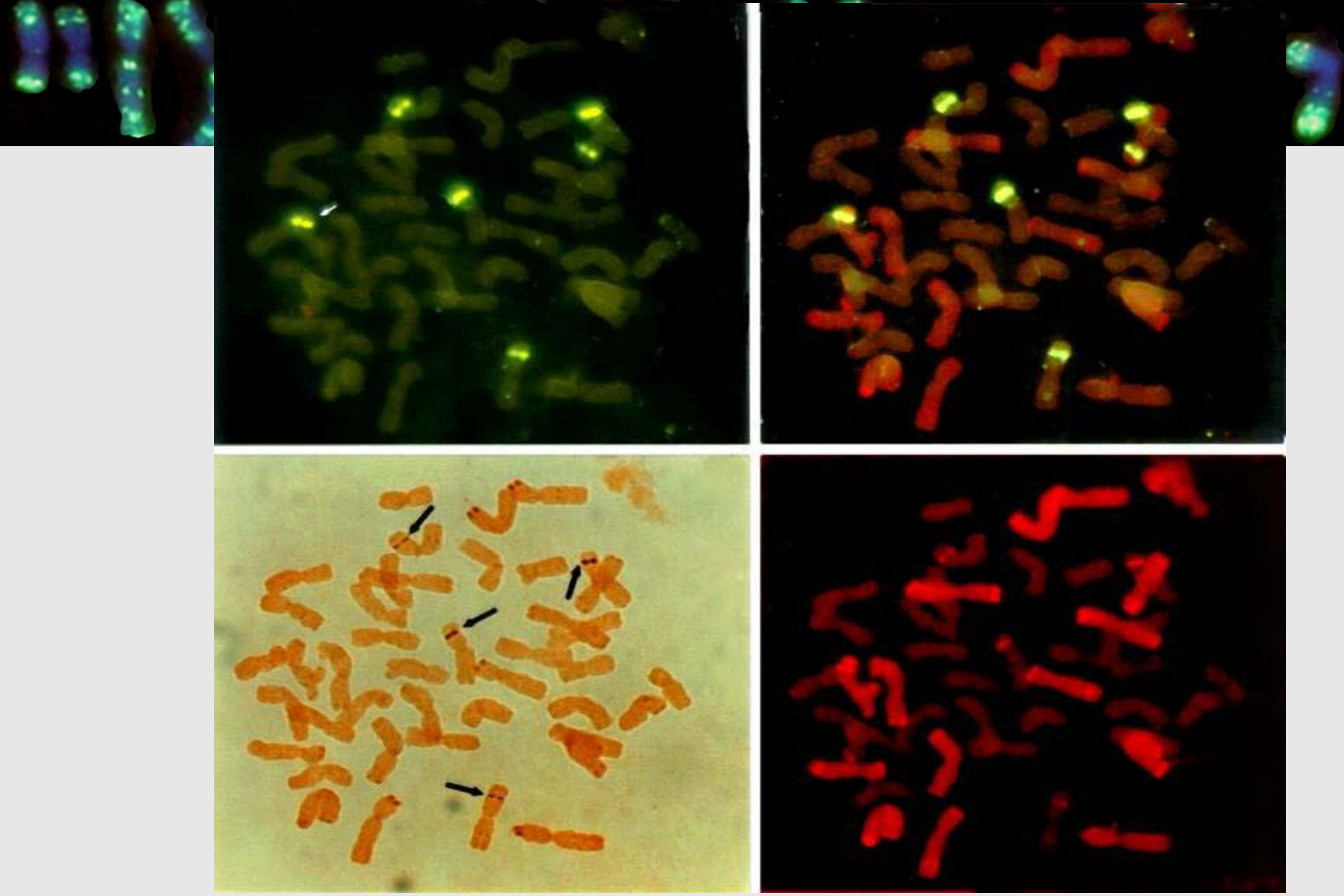
dpTa1

Correlation between genetic relationships and similarity of dpTa1 hybridization

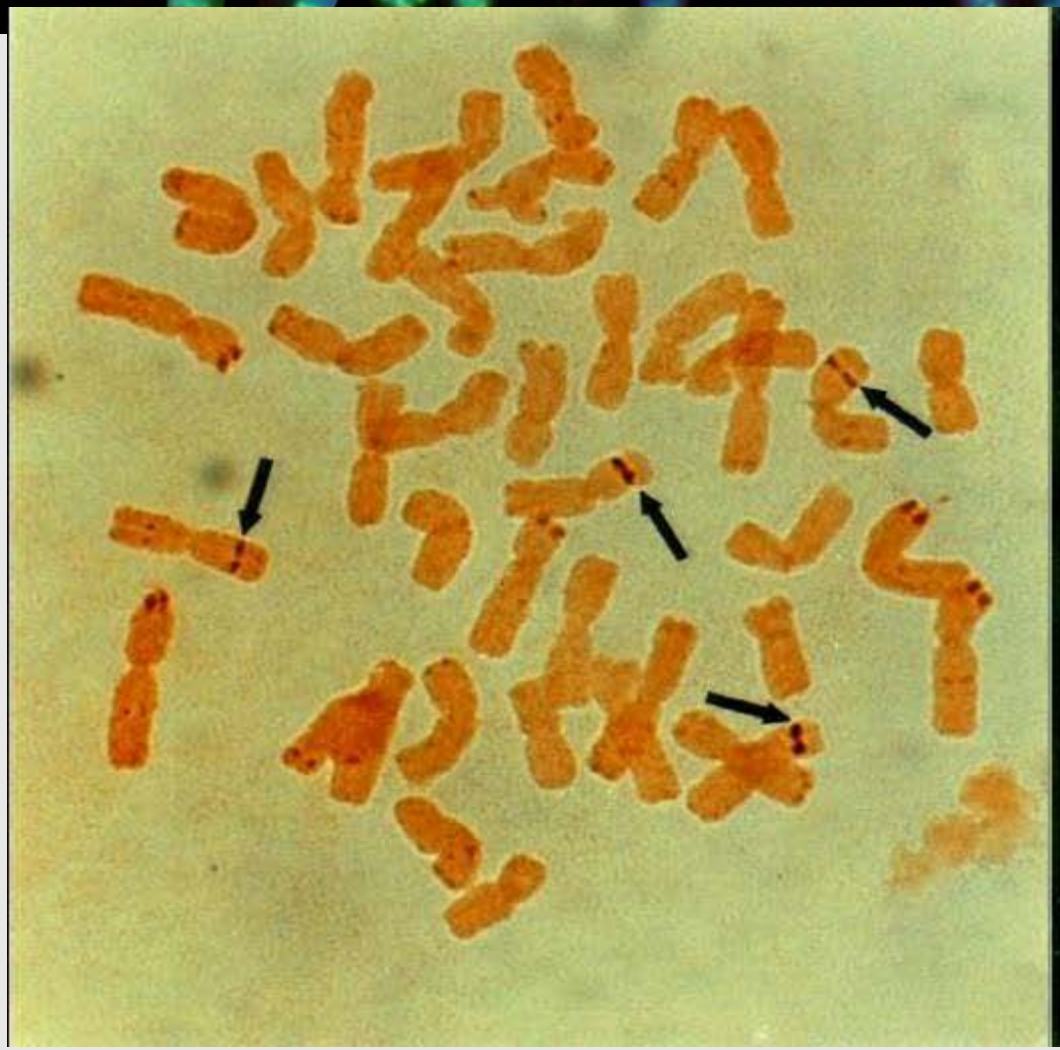


No correlation between genetic relationships and similarity of pSc119.2 hybridization

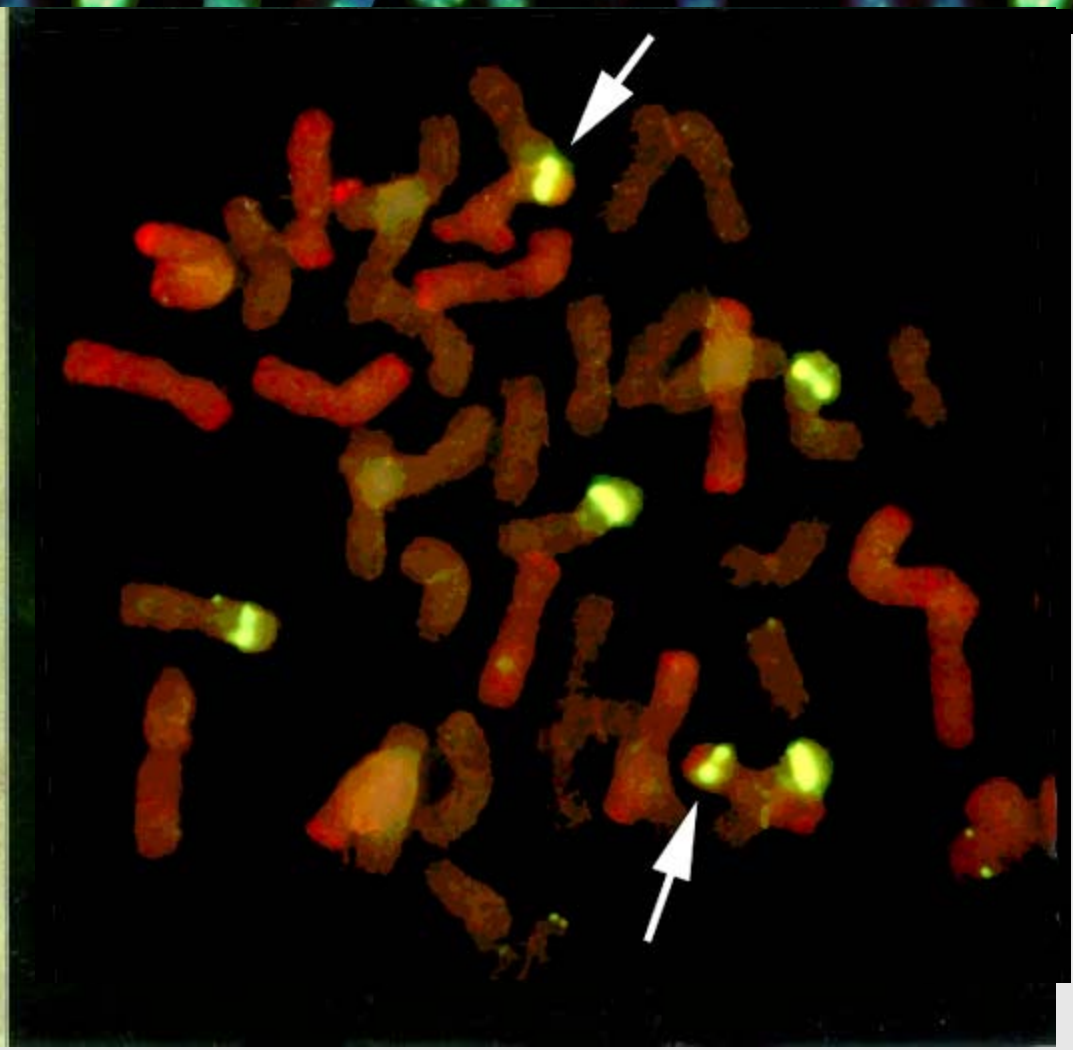




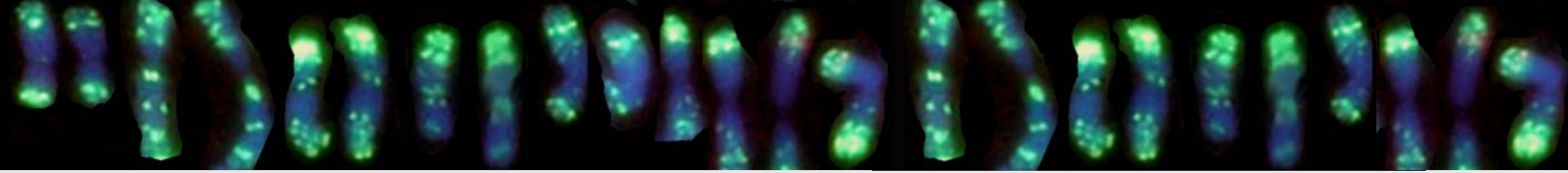
rRNA gene expression in Triticale



Four expression sites



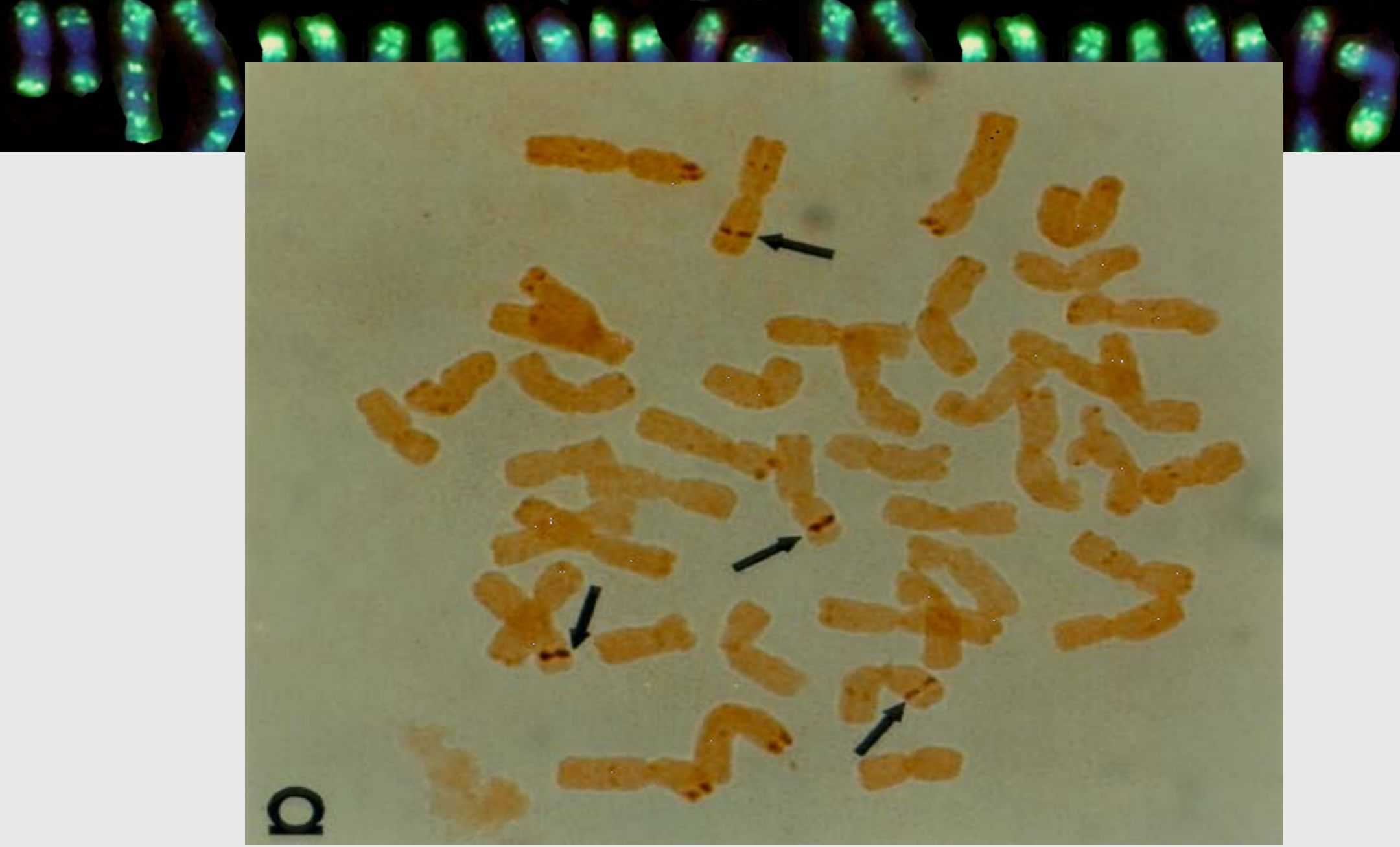
Six gene sites

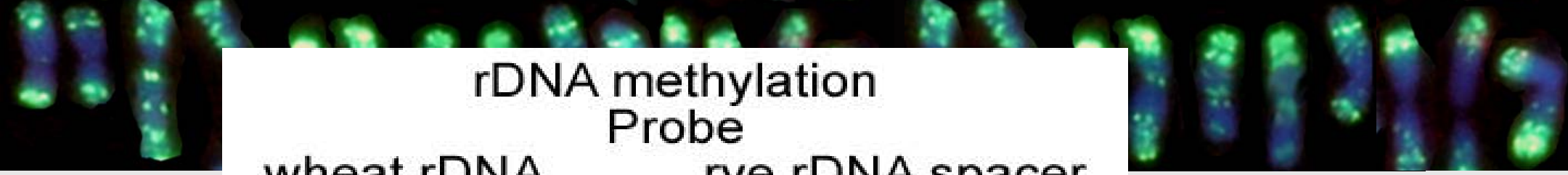


Modification of DNA Methylation

- Methylation widely implicated in gene expression control
- Treat with 5-azacytidine
  - N at carbon-5 position not C so $-CH_3$ cannot be added
- Effect of treatment on Triticale

- Ag-NOR method
  - see www.methods.molcyt.com methods page


Q



rDNA methylation

Probe

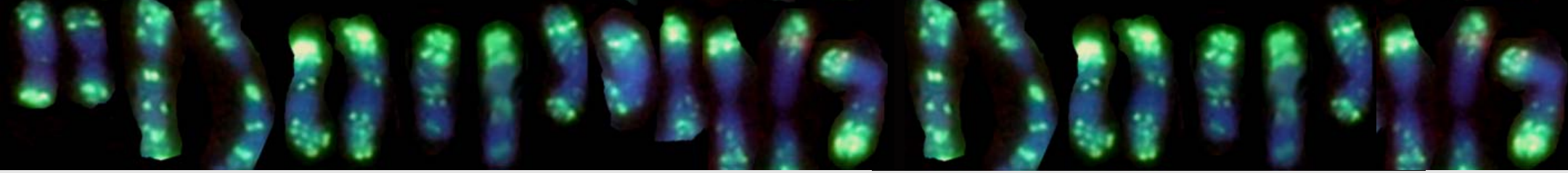
wheat rDNA rye rDNA spacer

Treatment

water AZC water AZC

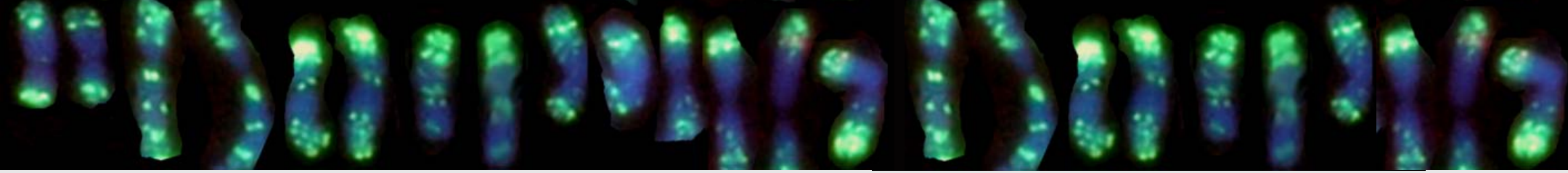
lambda *ApaI* *DraI* double *ApaI* *DraI* double

lambda *ApaI* *DraI* double *ApaI* *DraI* double



Modification of rDNA Methylation

- Stability of methylation
- Seedling treatment – all 6 active for life
- Embryo treatment:
- First 7 days – only wheat-origin active
- After 7 days – rye and wheat-origin active

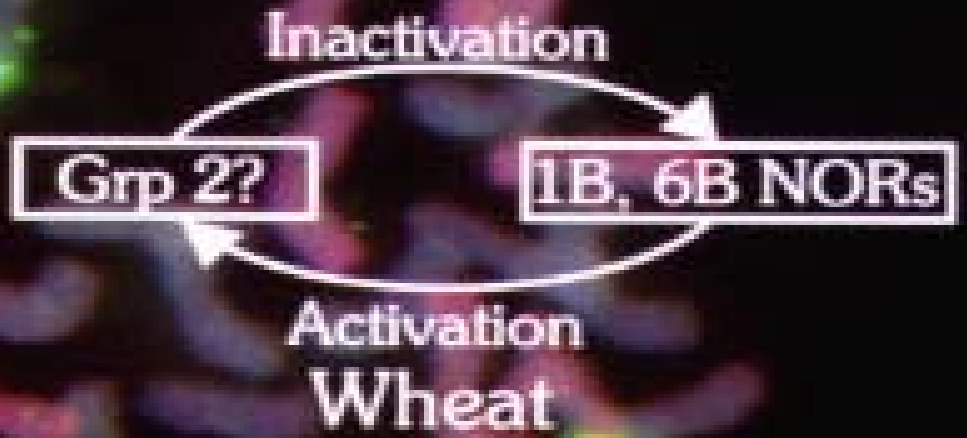


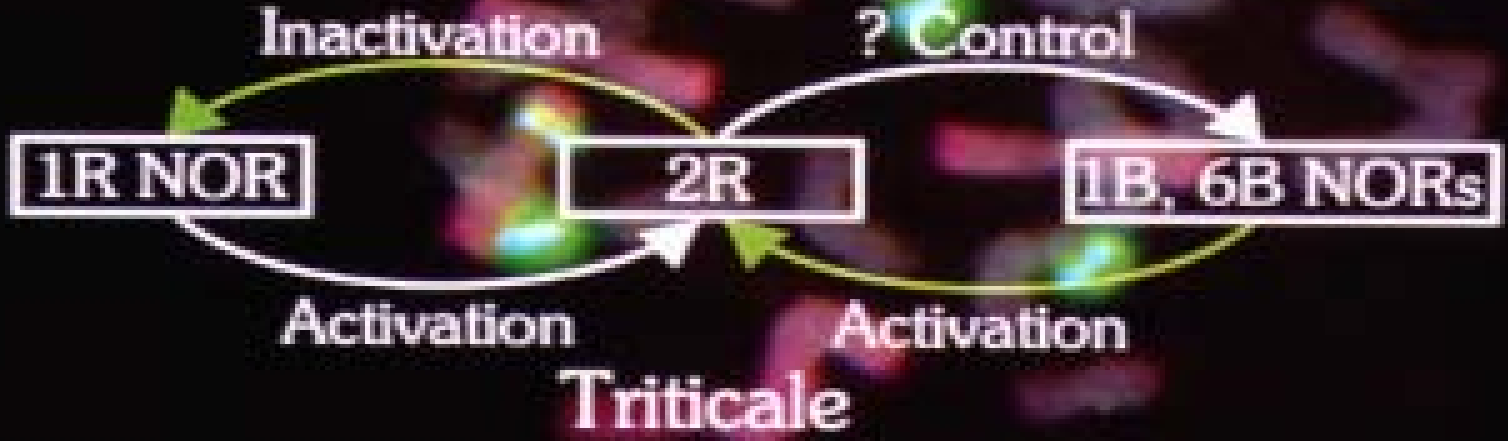
rDNA expression in Triticale

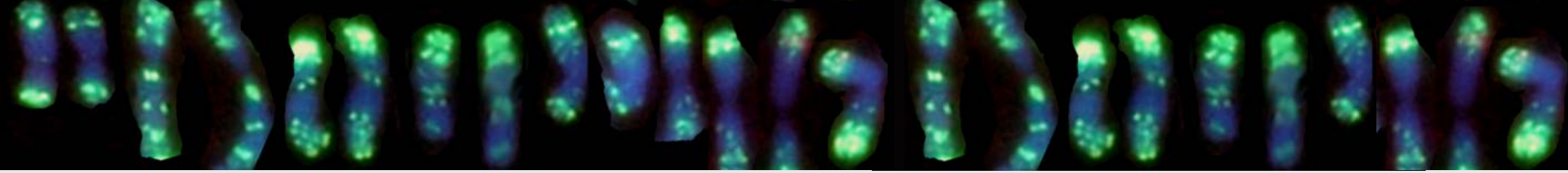
- Observation:
- Ag-staining showed 6 NORs sometimes

- These were in triticale with 12 rye chromosomes: 2D-2R substitution
- Found rather frequently so breeders must select it

Interactions between rDNA and control loci

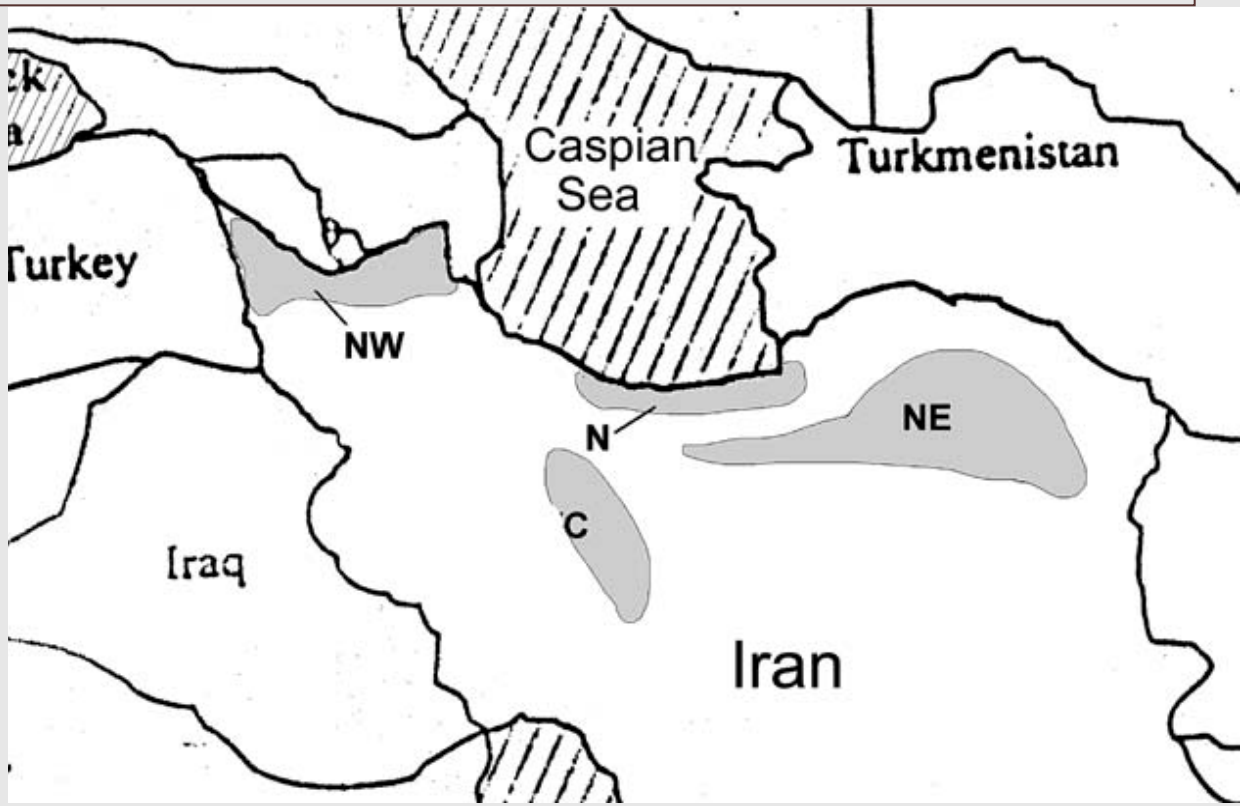






Aegilops tauschii (D genome donor) in Iran

- 57 accessions collected
  - ssp. *tauschii*
    - *var. meyeri (*18)
    - *var. tauschii* (22)
    - *var. anathera* (4)
    - *var. meyeri* (12)

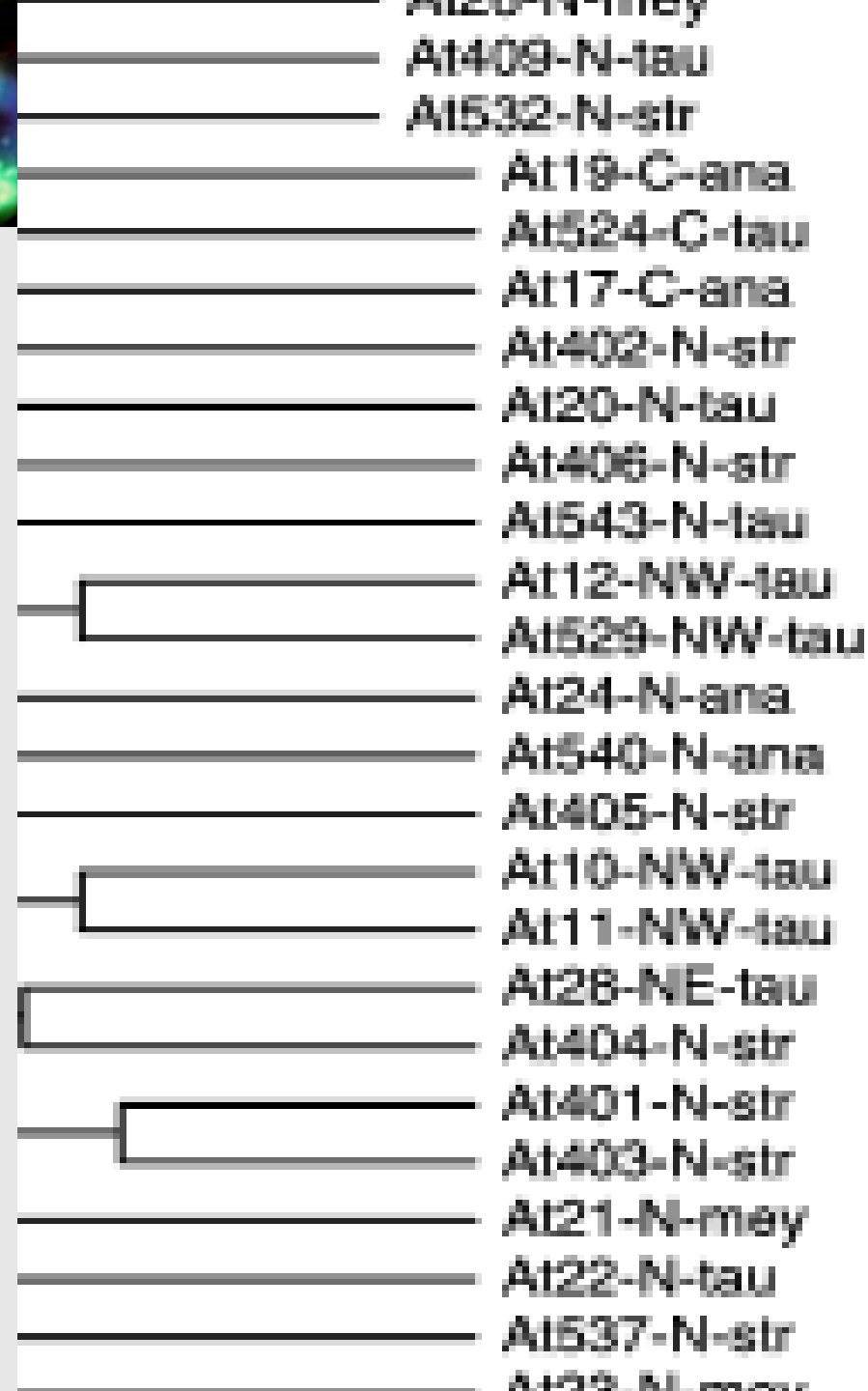


Hojjatollah Saeidi, Mohammad Reza Rahiminejad, Sadeq Vallian, HH
Genetic Resources & Crop Plant Evolution 2006

Diversity in D genome

- Microsatellite markers
- 57 accessions of wild *Aegilops tauschii* (2n = 2x = 14; D genome)
- No SSR markers were characteristic for taxa or geographical origin
- High diversity present

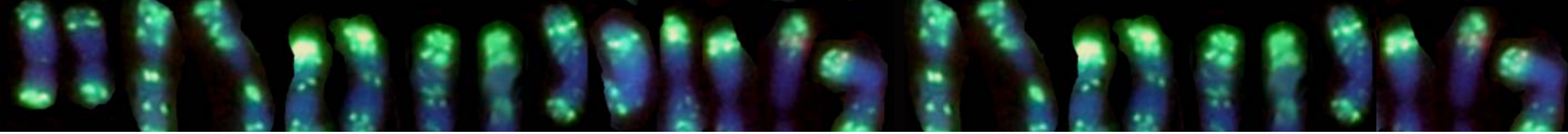
Saeidi, HH et al. Genet Resources & Crop Evolution 2005



Aegilops tauschii in Iran

dpTa1-Repetitive banding pattern does correlate with taxonomic grouping

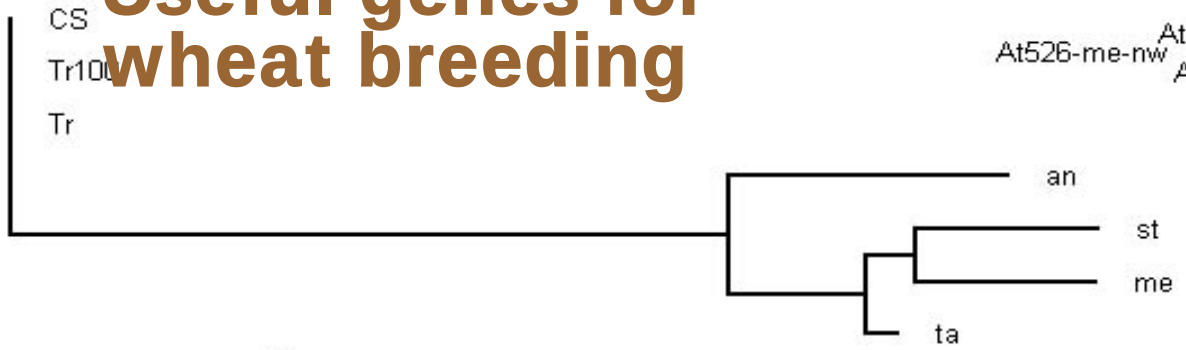
Hojjatollah Saeidi and Pat Heslop-Harrison

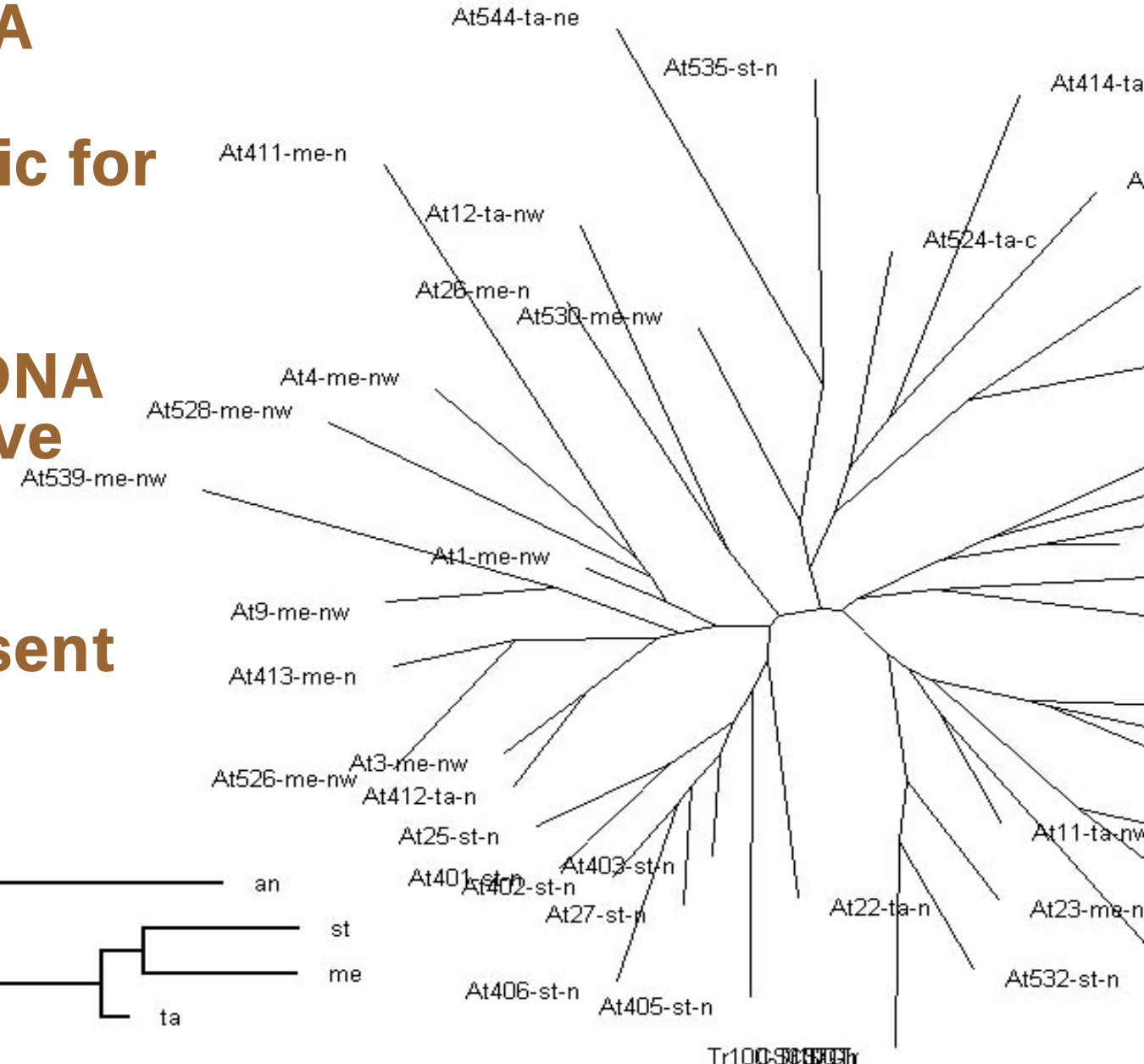


- ***In situ* repetitive DNA markers**
- **Markers characteristic for taxa**

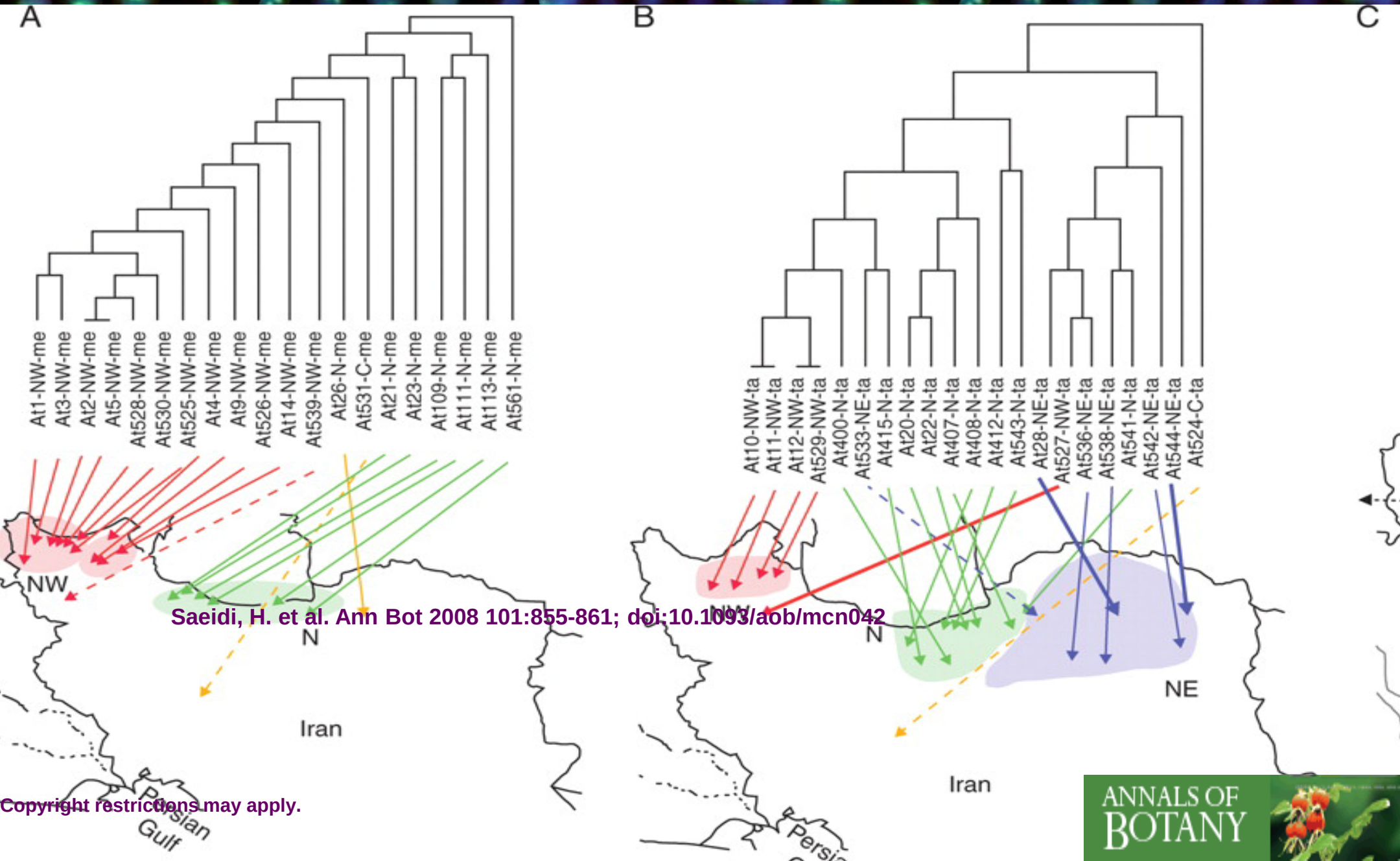
- **Evolution of genes/DNA markers and repetitive (SSR are different)**

- **High diversity present**
- **Useful genes for wheat breeding**





UPGMA dendrograms of the relationships based on IRAP analysis of (A) accessions of Ae. tauschii subsp



Saeidi, H. et al. Ann Bot 2008 101:855-861; doi:10.1093/aob/mcn042

ANNALS OF BOTANY

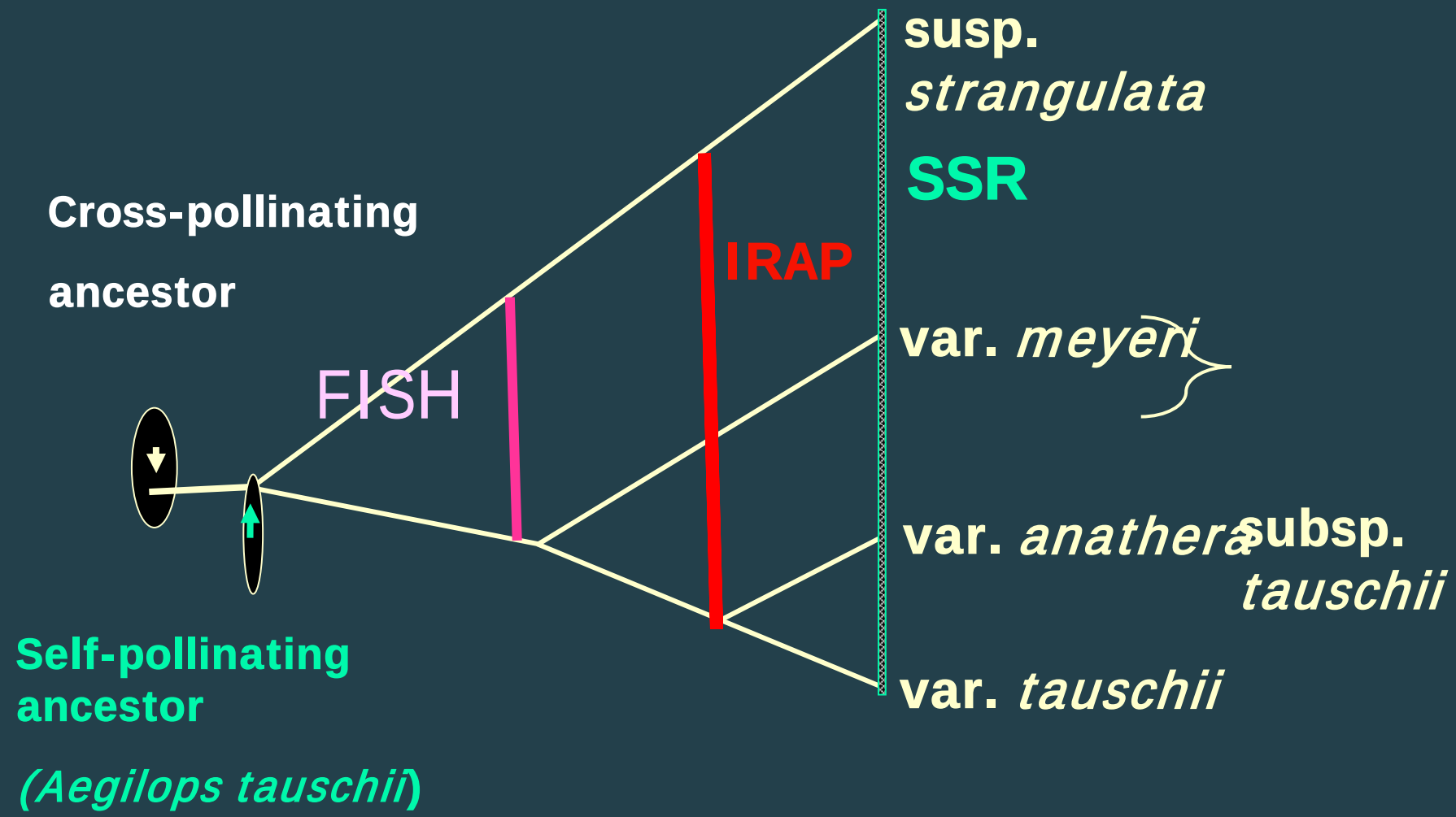
Demonstration of the direction of distribution (phylogeography) even over short geographic distances

Phylogeography of *Ae. tauschii*

Species originated from North of Iran and distributed in two directions.

tauschii genotype passes from middle parts of Alborz Mountains and the distributed eastward and westward (direction 1)

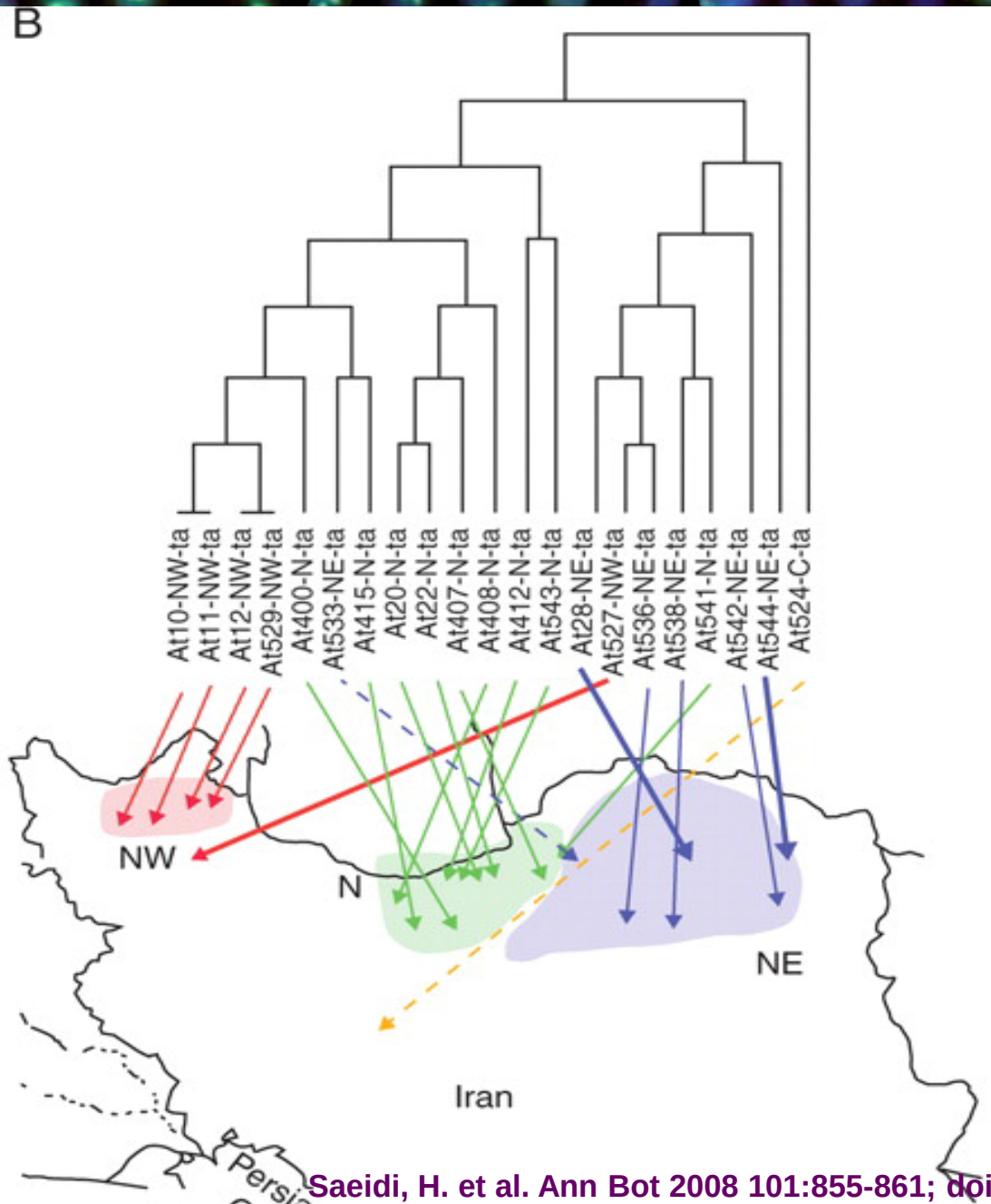
strangulata genotype are distributed along the Caspian Sea shore (direction 2)



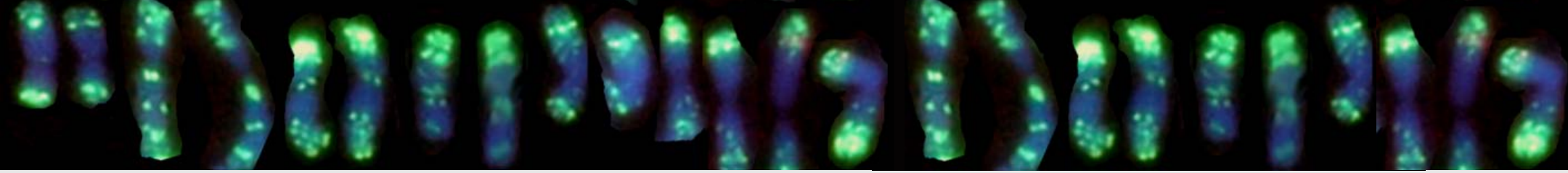
An evolutionary model supported by molecular analyses

Saeidi, HH et al. 2010

UPGMA dendrograms of the relationships based on IRAP analysis of (A) accessions of Ae. tauschii subsp



Saeidi, H. et al. Ann Bot 2008 101:855-861; doi:10.1093/aob/mcn042



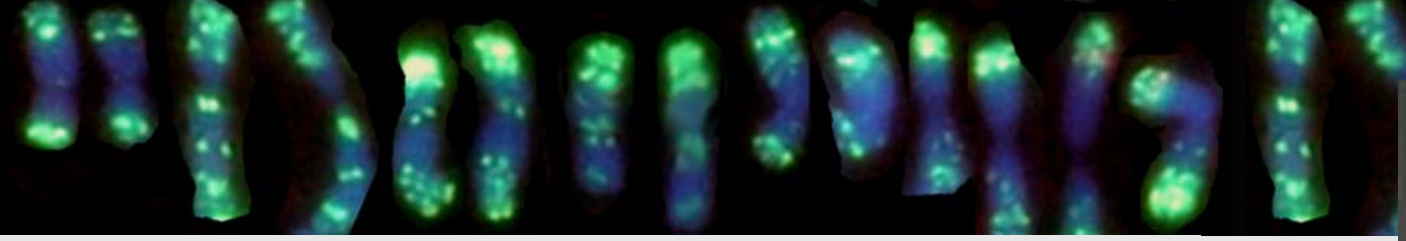
- Different DNA sequences evolve more-or-less independently
- There is no ‘molecular clock’ for many sequence types
- Multiple sequence types should be used to gain a full understanding of genome evolution

- Wild Wheat – Using Genes -

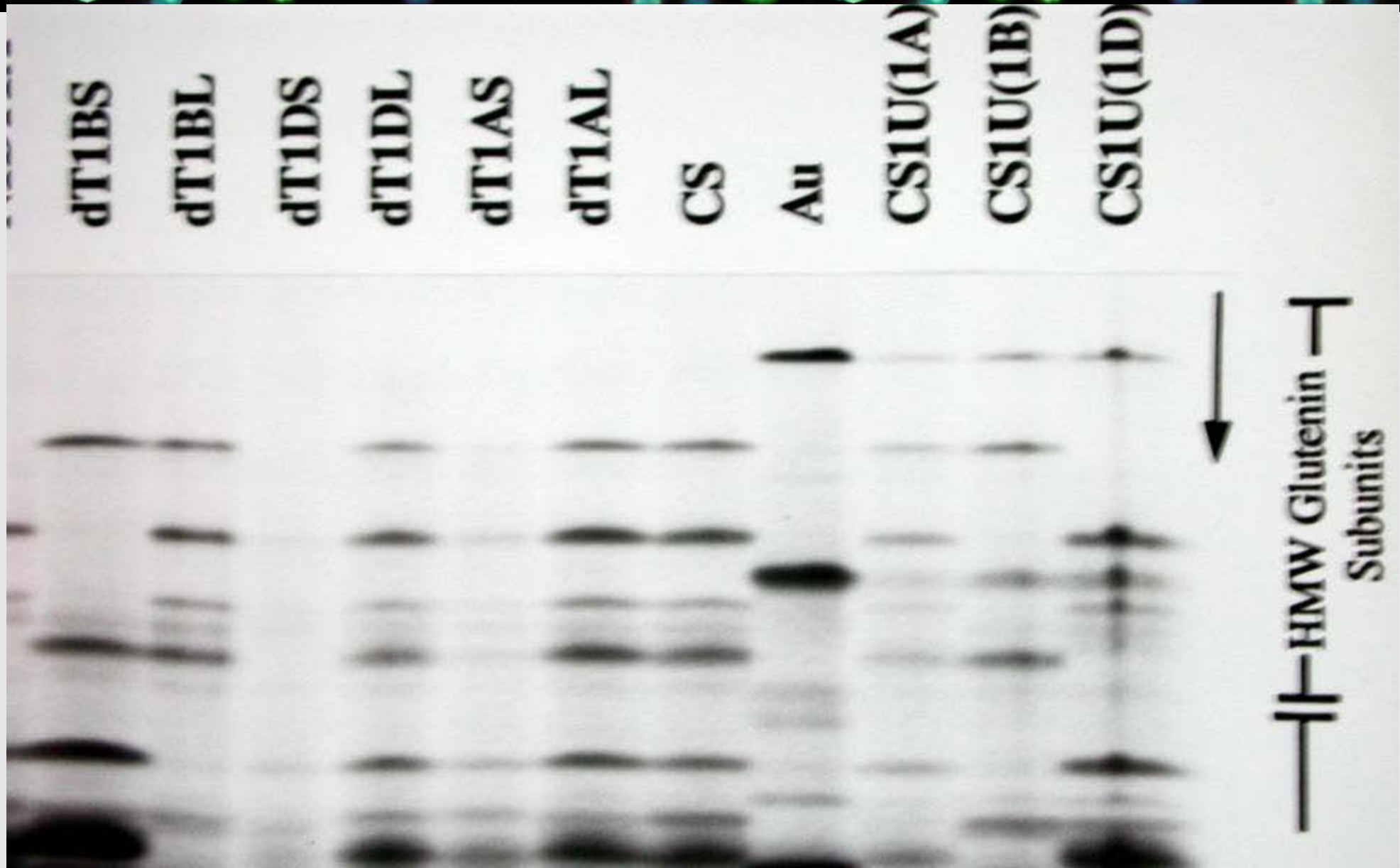
Aegilops

Triticum durum

Ae. umbellulata type × *T. durum*



Wheat proteins: High bands = good bread

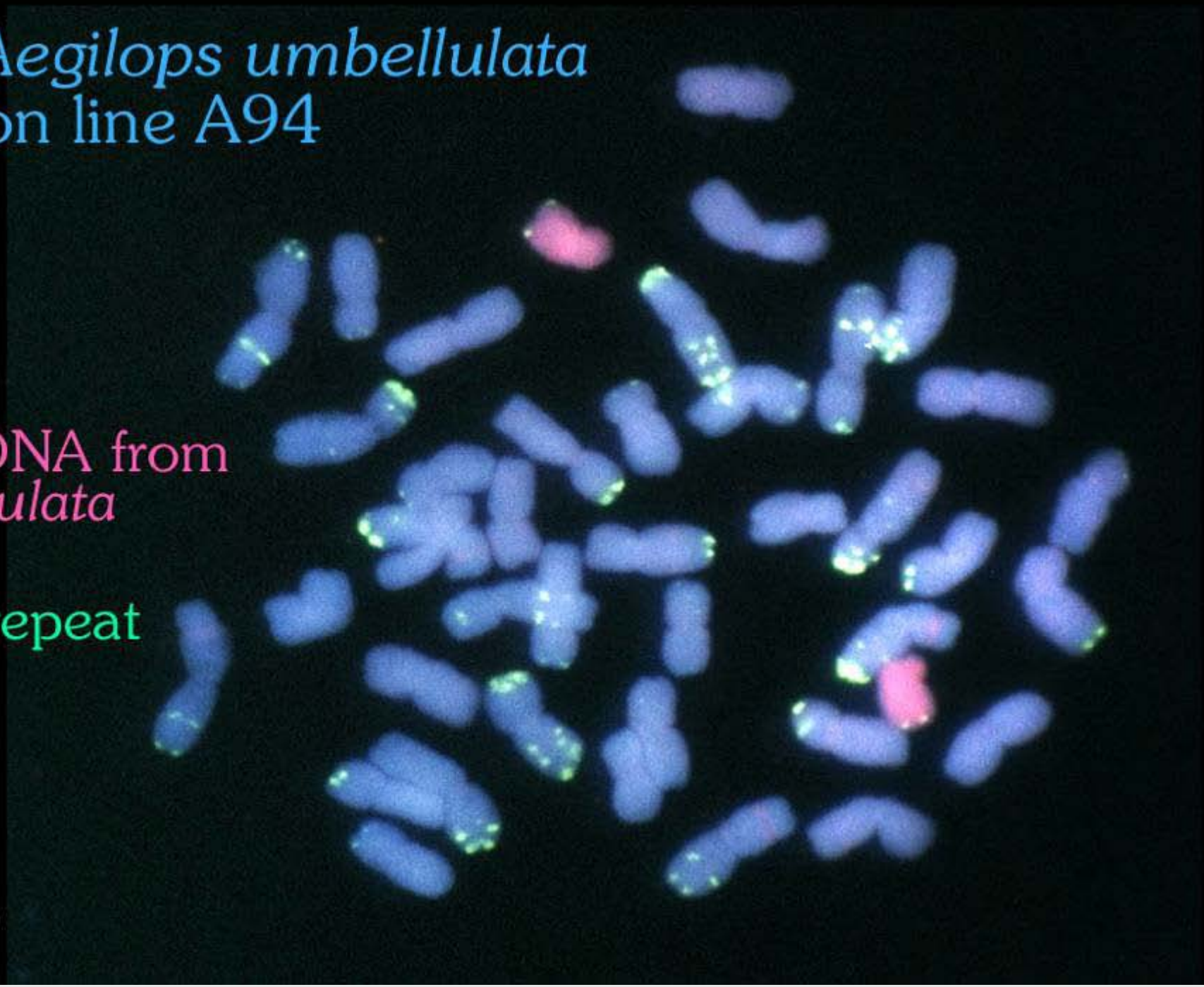


Wheat - *Aegilops umbellulata* substitution line A94

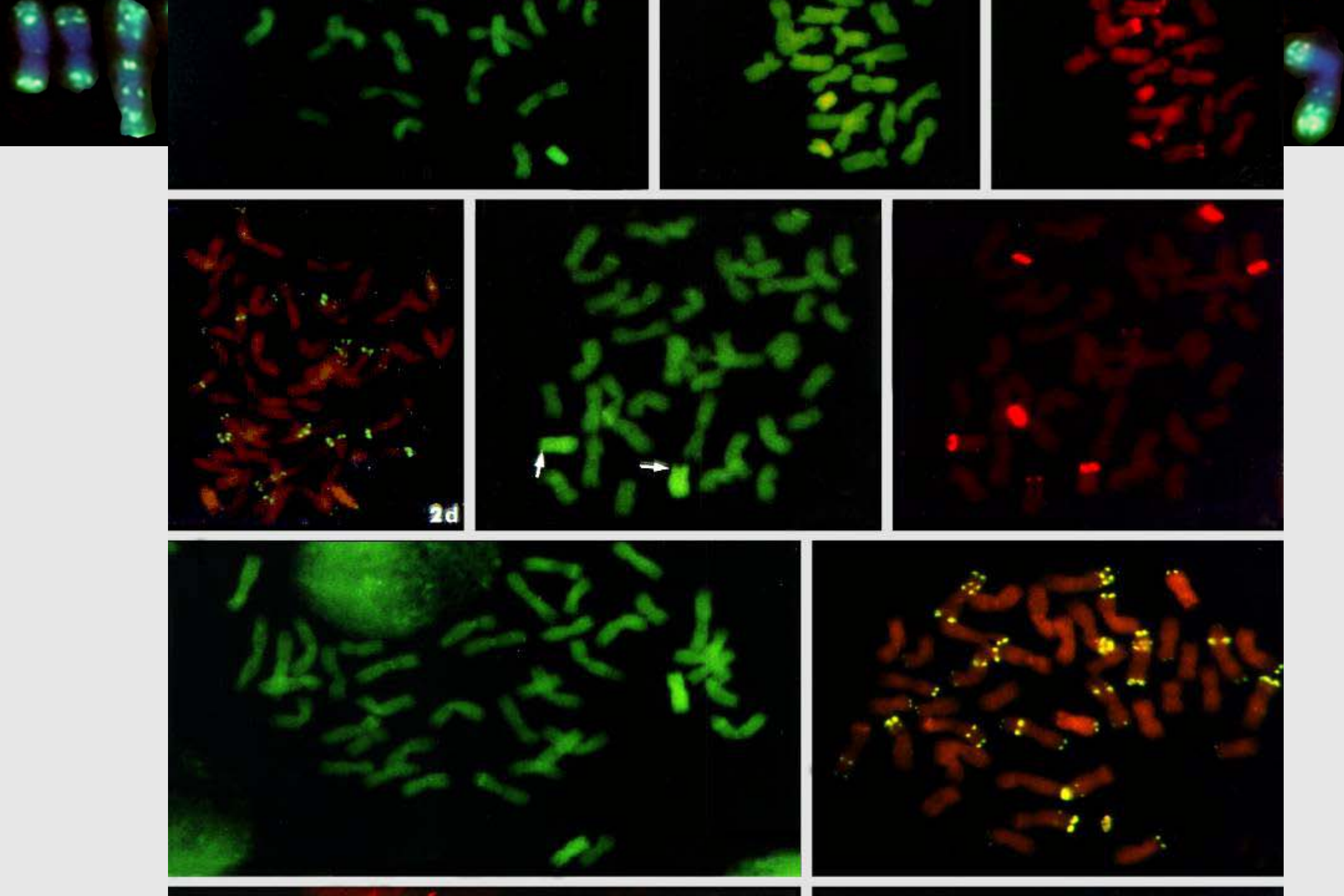
2n=6x=42

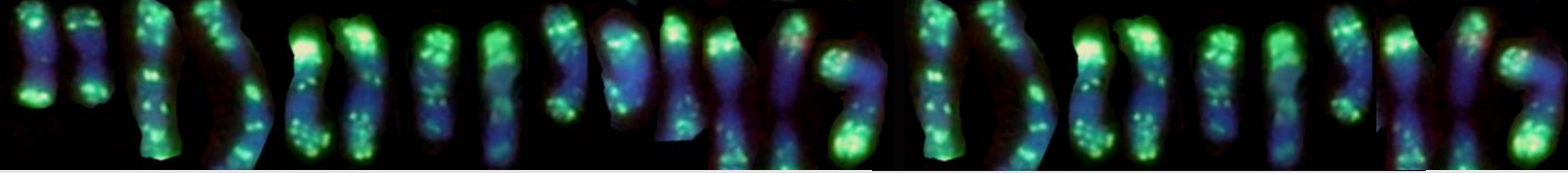
Genomic DNA from *Ae. umbellulata*

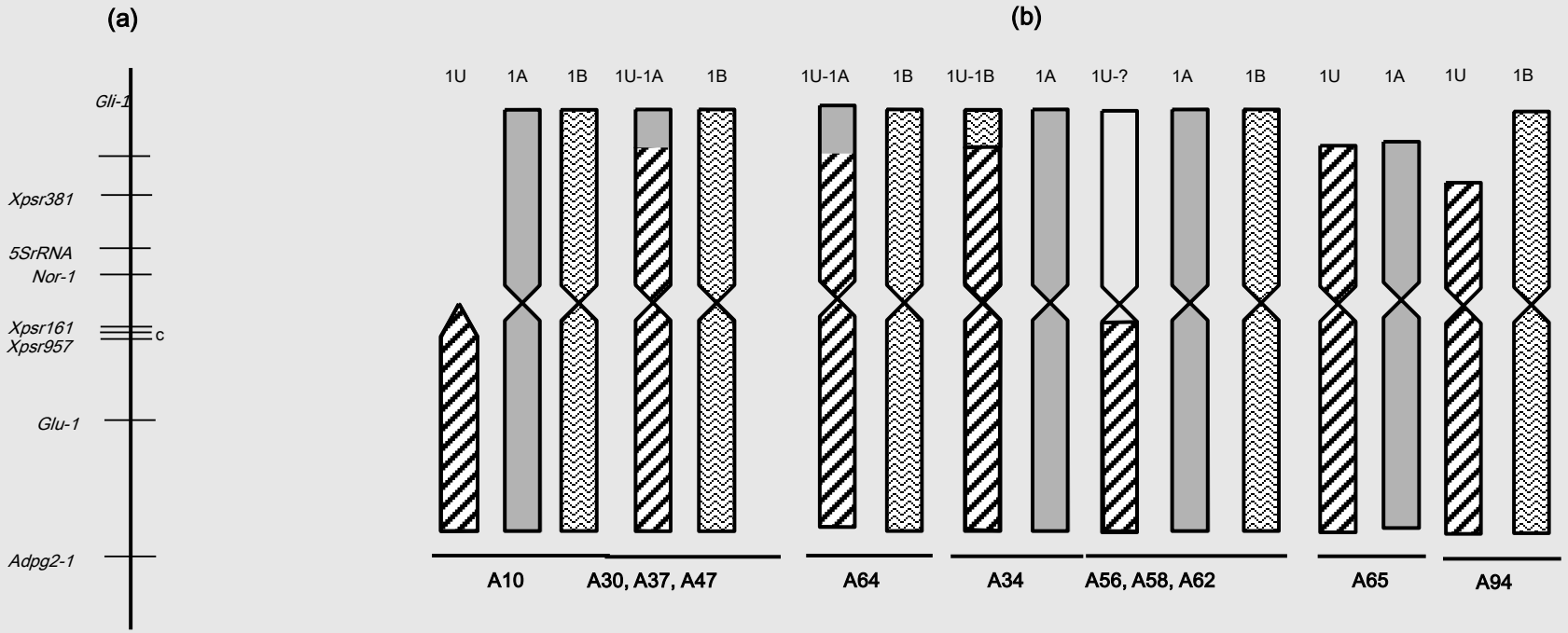
pSc119.2 repeat



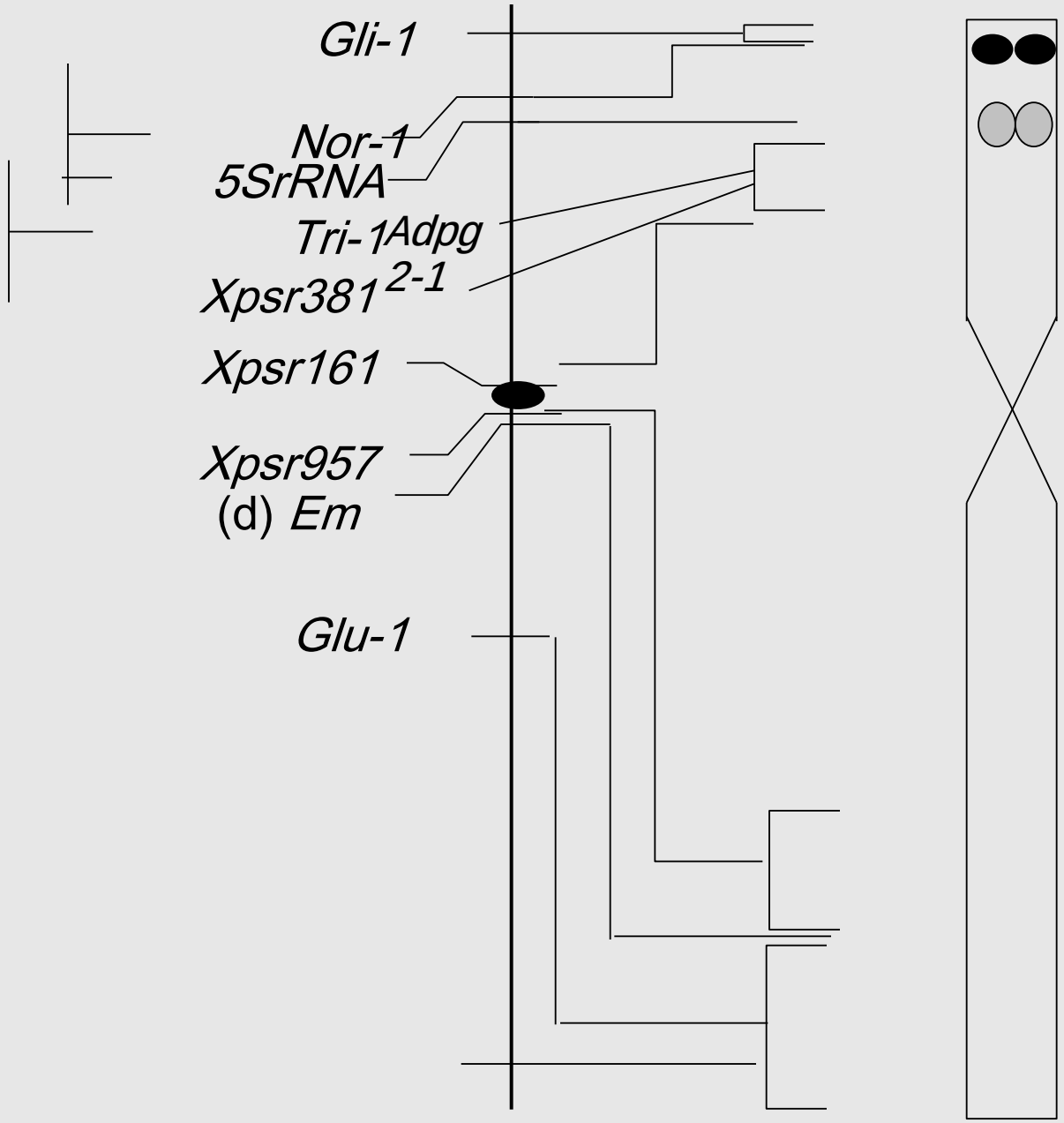
Xana Castilho


2d





(a) Genetical map of the RFLP probes used. Genetical distances are approximate and based on Gale *et al.*, 1995 for the wheat 1B chromosome.
The order of the *5S rRNA* and *Nor-1* markers is reversed on wheat chromosome 1A .
(b) Physical maps of the wheat-Ae. umbellulata lines assigning the RFLP probes on the recombinant chromosome and on the background wheat
group 1 chromosomes. all lines carry a pair of 1D chromosome.

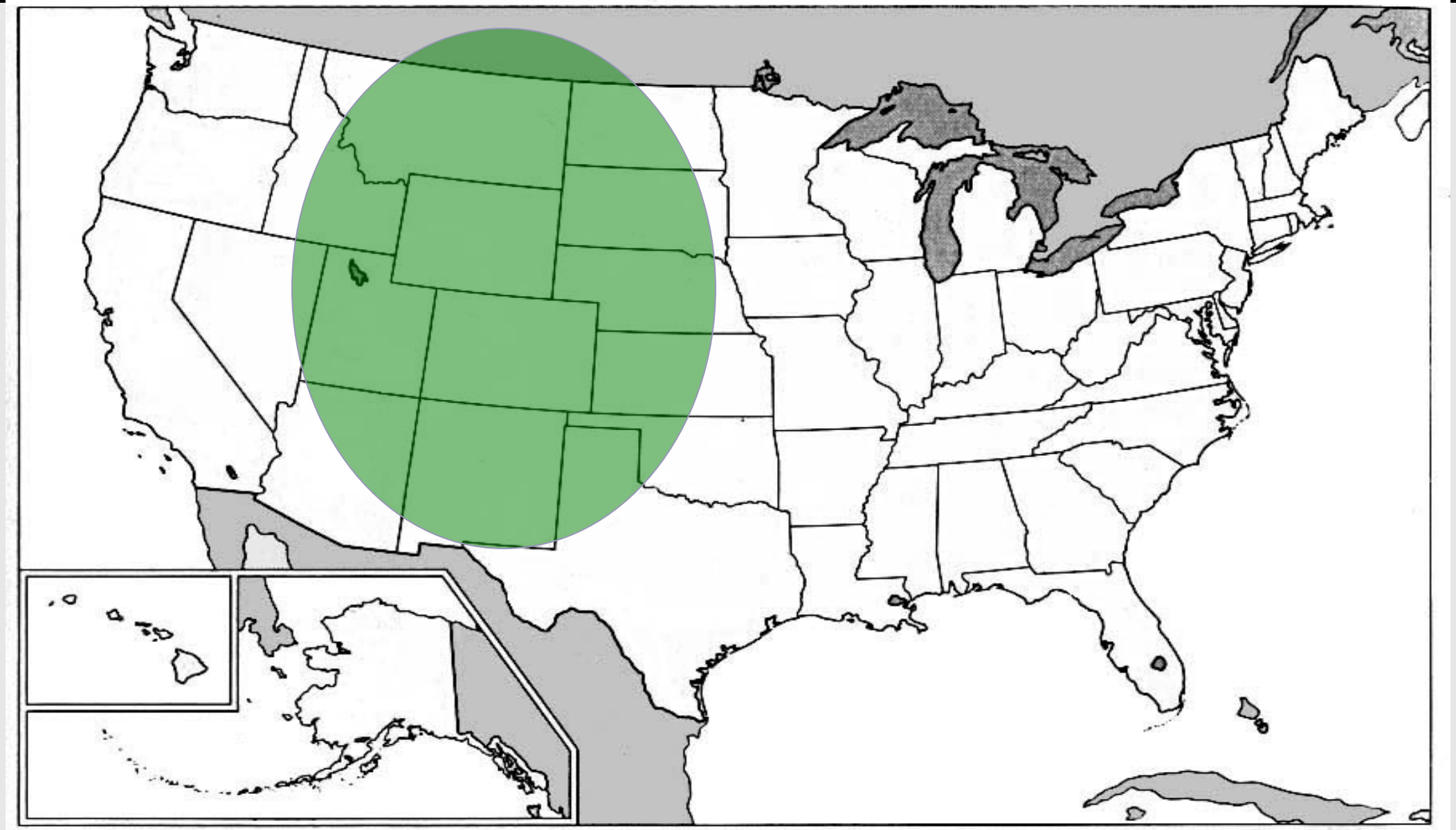


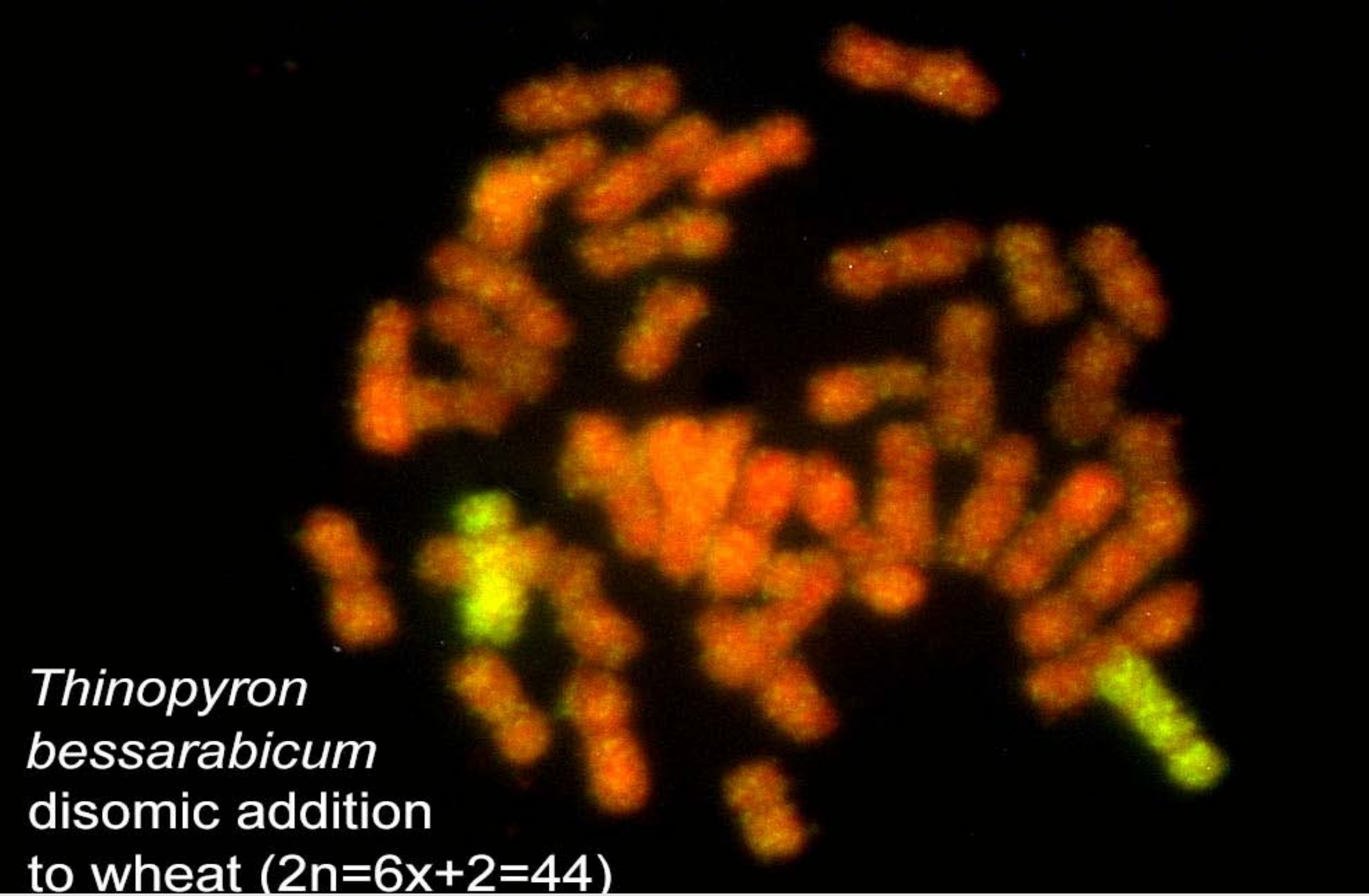
Physical map vs
Genetic map

Genes are often clustered
Genes (and recombination
are often distal

Wheat Streak Mosaic Virus in North America

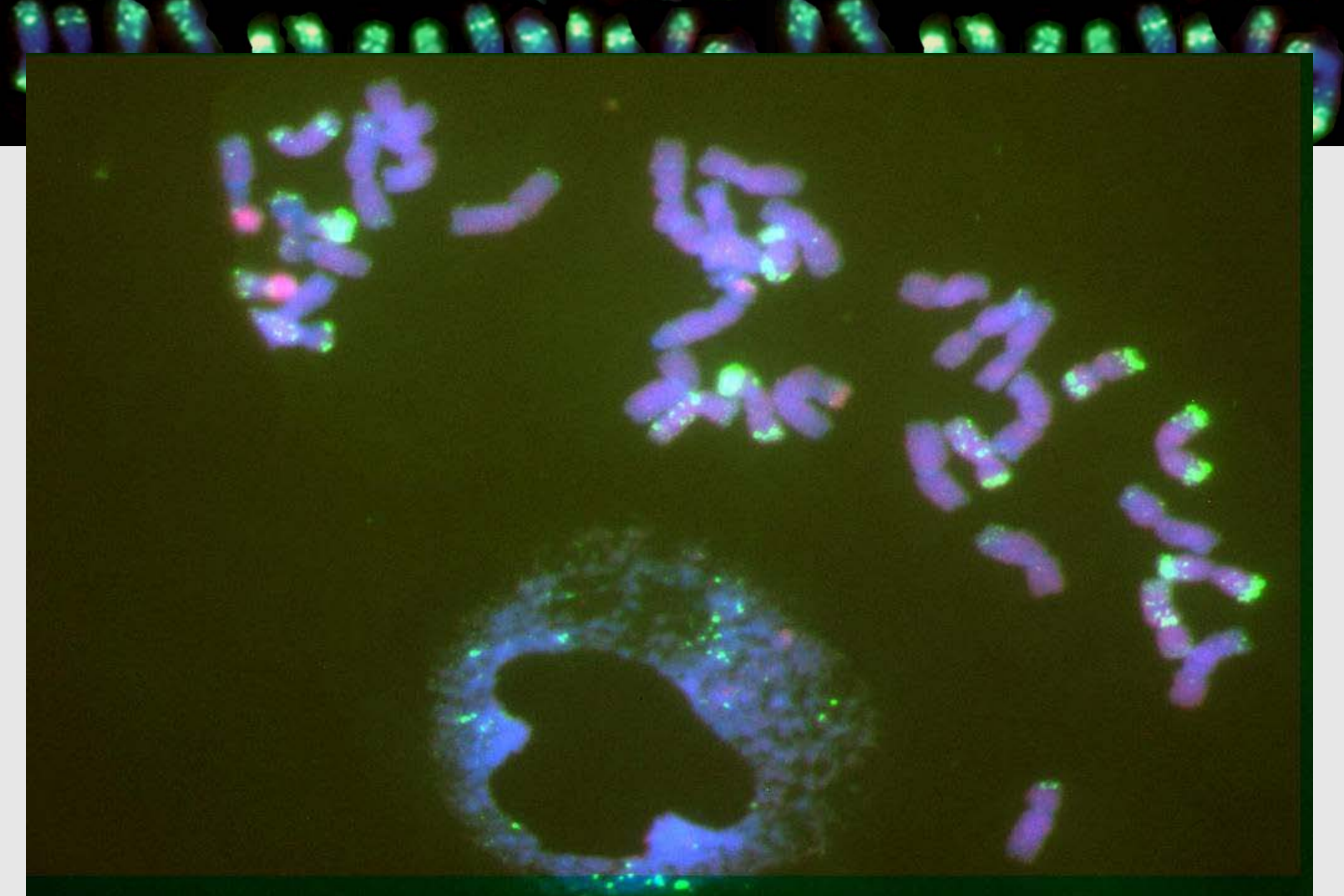
Bob Graybosch, USDA




Thinopyron
bessarabicum
disomic addition
to wheat (2n=6x+2=44)

Wsm-1: only highly effective source of resistance to WSMV

Intermediate wheat-grass, western Nebraska



Registration of 'Mace' Hard Red Winter Wheat

R. A. Graybosch,* C. J. Peterson, P. S. Baenziger, D. D. Baltensperger, L. A. Nelson, Y. Jin, J. Kolmer, B. Seabourn, R. French, G. Hein, T. J. Martin, B. Beecher, T. Schwarzacher, and P. Heslop-Harrison

ABSTRACT

'Mace' (Reg. No. CV-1027, PI 651043) hard red winter wheat (*Triticum aestivum* L.) was developed by the USDA-ARS and the Nebraska Agricultural Experiment Station and released in December 2007. Mace was selected from the cross Yuma//PI 372129/3/CO850034/4/4*Yuma/5/(KS91H184/Arlin S//KS91HW29/3/NE89526). Mace primarily was released for its resistance to *Wheat streak mosaic virus* (WSMV) and adaptation to rainfed and irrigated wheat production systems in Nebraska and adjacent areas in the northern Great Plains. Mace was derived from a head selection made from a heterogeneous, in terms of field resistance to WSMV, F_5 line. Resistance to WSMV is conditioned by the *Wsm-1* gene, located on an introgressed chromosome arm from *Thinopyrum intermedium* (Host) Barkworth & D.R. Dewey [*Agropyron intermedium* (Horst.) Beauv.] present as a 4DL.4AgS chromosomal translocation. Mace was tested under the experimental designation N02Y5117.

Abbreviations: NRPN, Northern Regional Performance Nursery; PCR, polymerase chain reaction; WSBMV, *Wheat soilborne mosaic virus*; WSMV, *Wheat streak mosaic virus*.

Published in the Journal of Plant Registrations 3:51–56 (2009).
doi: 10.3198/jpr2008.06.0345crc

677 S. Segoe Rd., Madison, WI 53711 USA

such line, subsequently named 'Mace' (Reg. No. CV-1027, PI 651043), was deemed suitable for cultivar release. Mace is a hard red winter wheat cultivar developed cooperatively by the USDA-ARS and the Nebraska Agricultural Experiment Station and released in 2007 by the developing institutions. Mace was released primarily for its field resistance to *Wheat streak mosaic virus* (WSMV) and adaptation to rainfed and irrigated wheat production systems in Nebraska and adjacent areas in the northern Great Plains. Resistance to WSMV is conditioned by the *Wsm-1* gene (Seifers et al., 1995), situated on an introgressed chromosome arm from


NSK
NSK

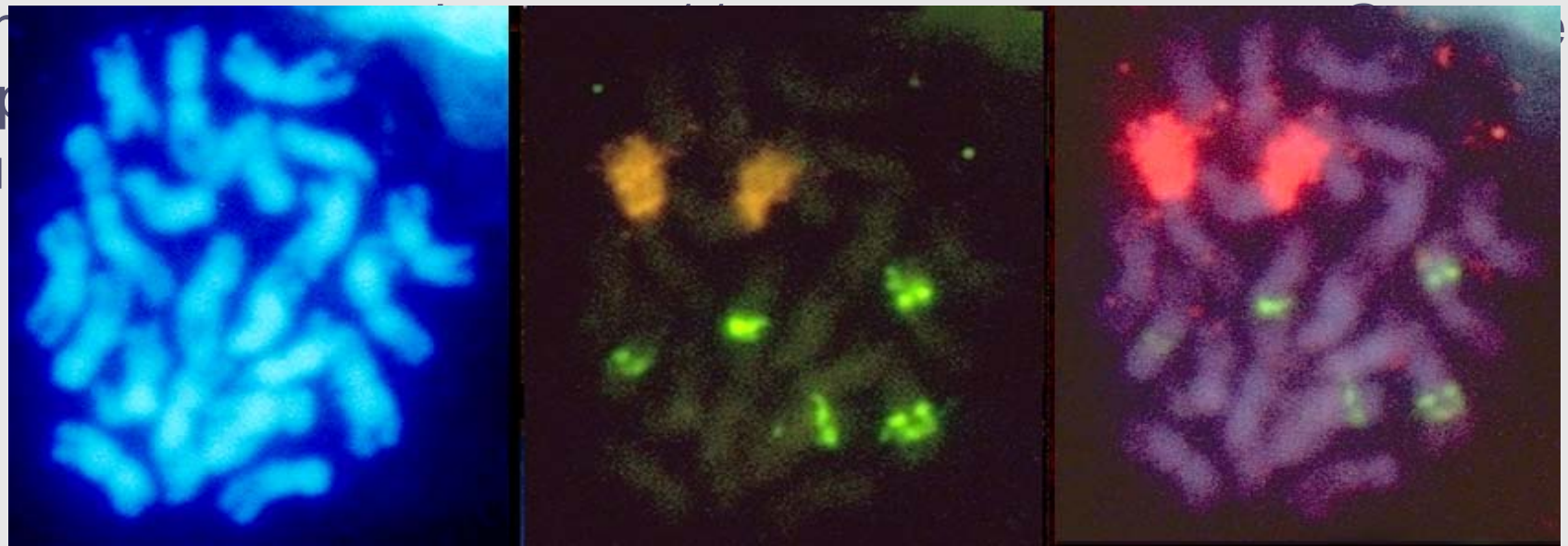
Wild banana species:

Musa acuminata – A genome

Musa balbisiana – B genome

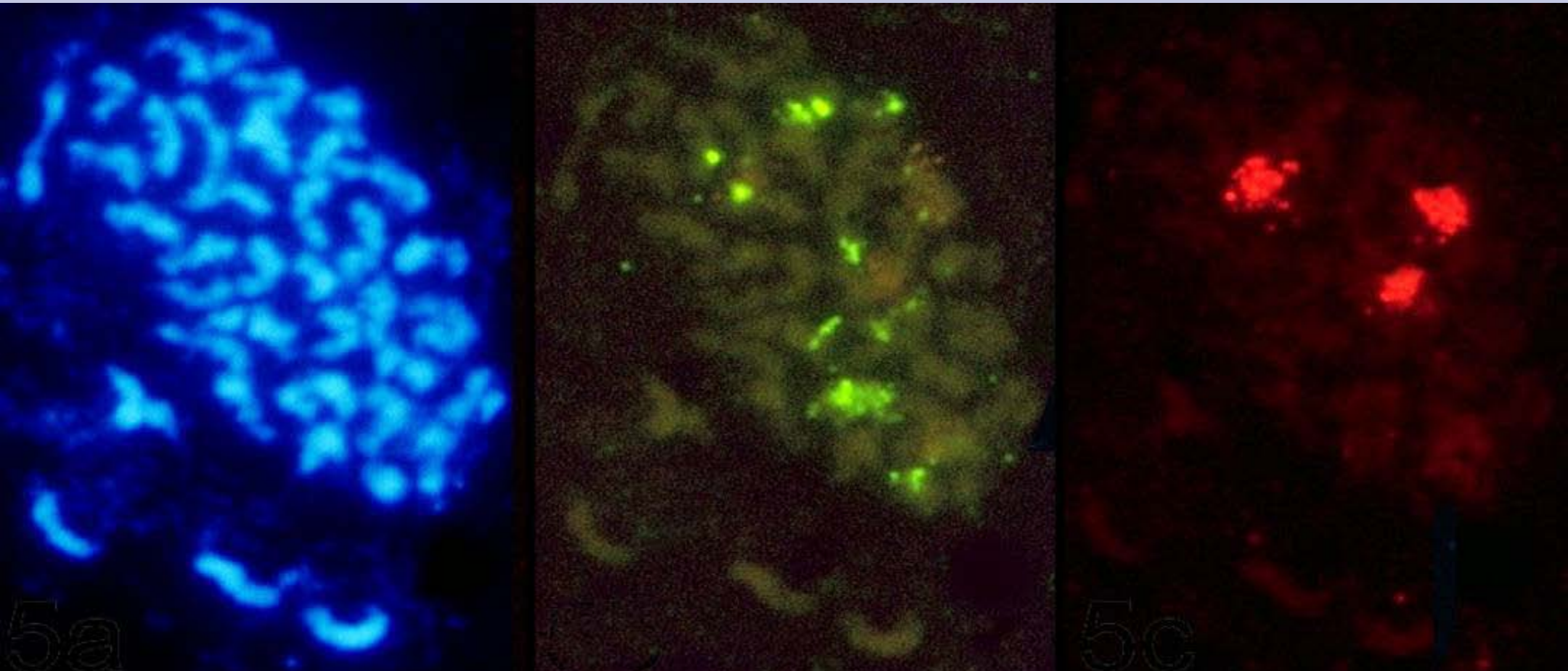
Basic ch… size c. 550 Mbp

Most cu…



Cavendish : the most common dessert banana cultivar

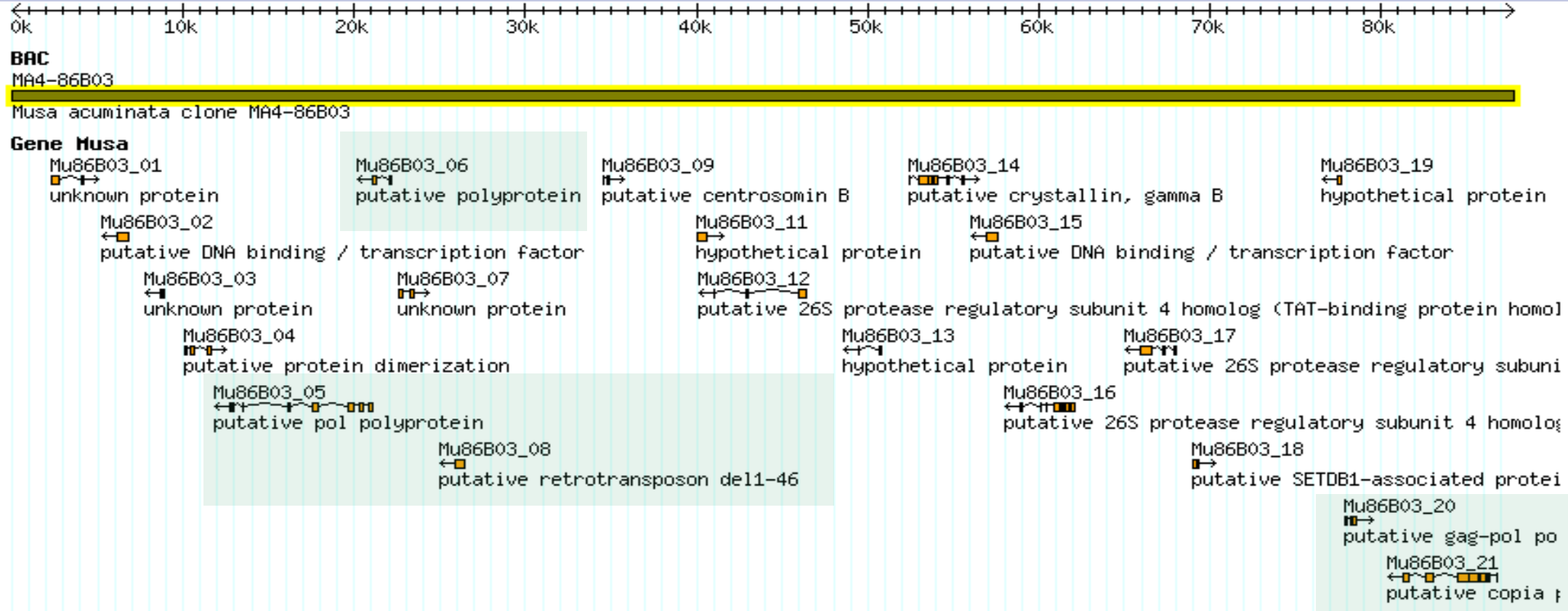
2n=3x=33; AAA genomes

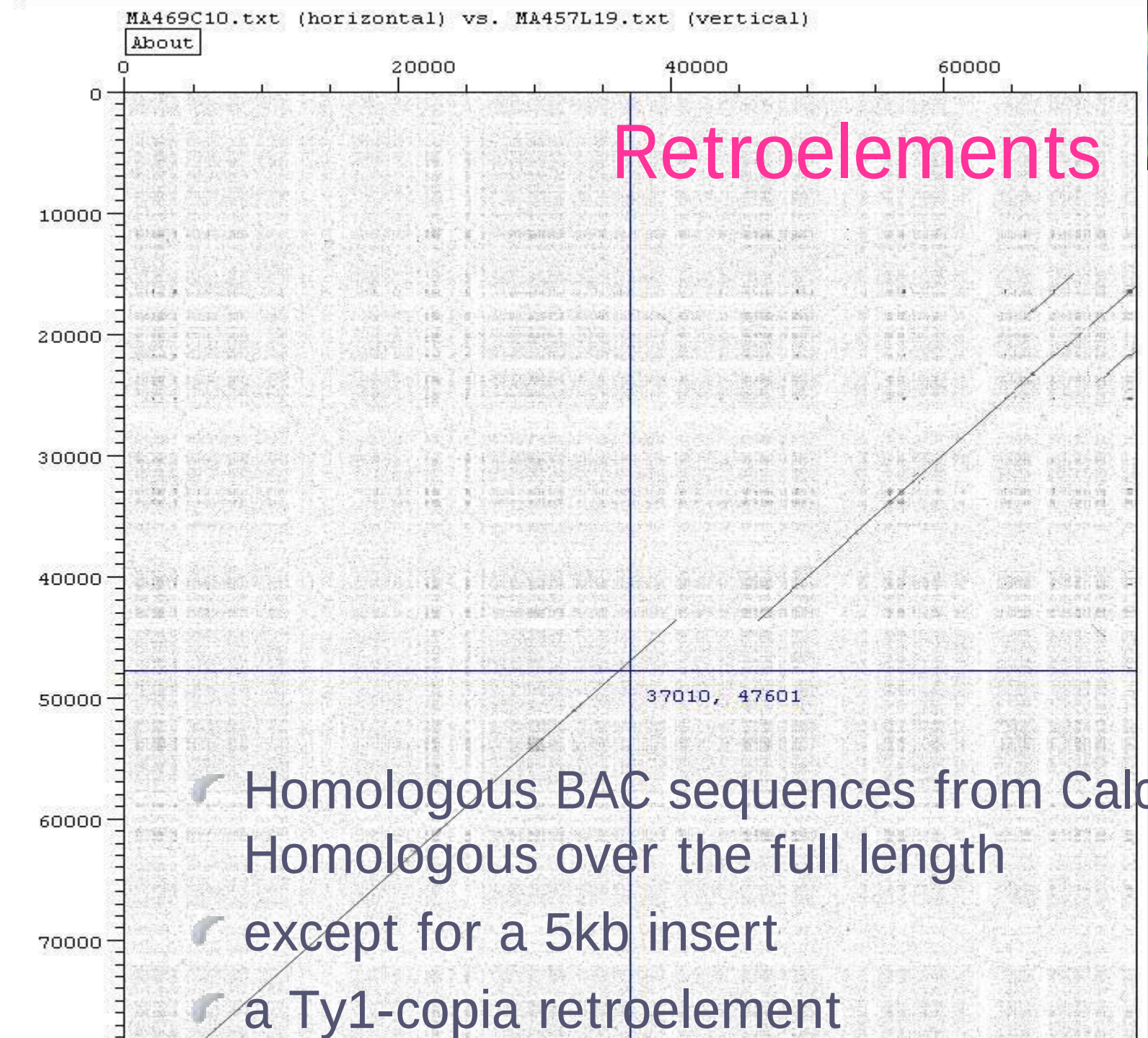


Retroelements

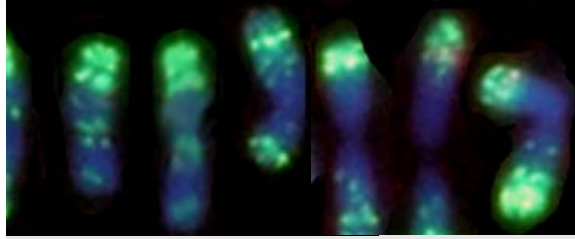
Sequences which amplify through an RNA intermediate

30% to 50% of all the DNA!





Retroelements

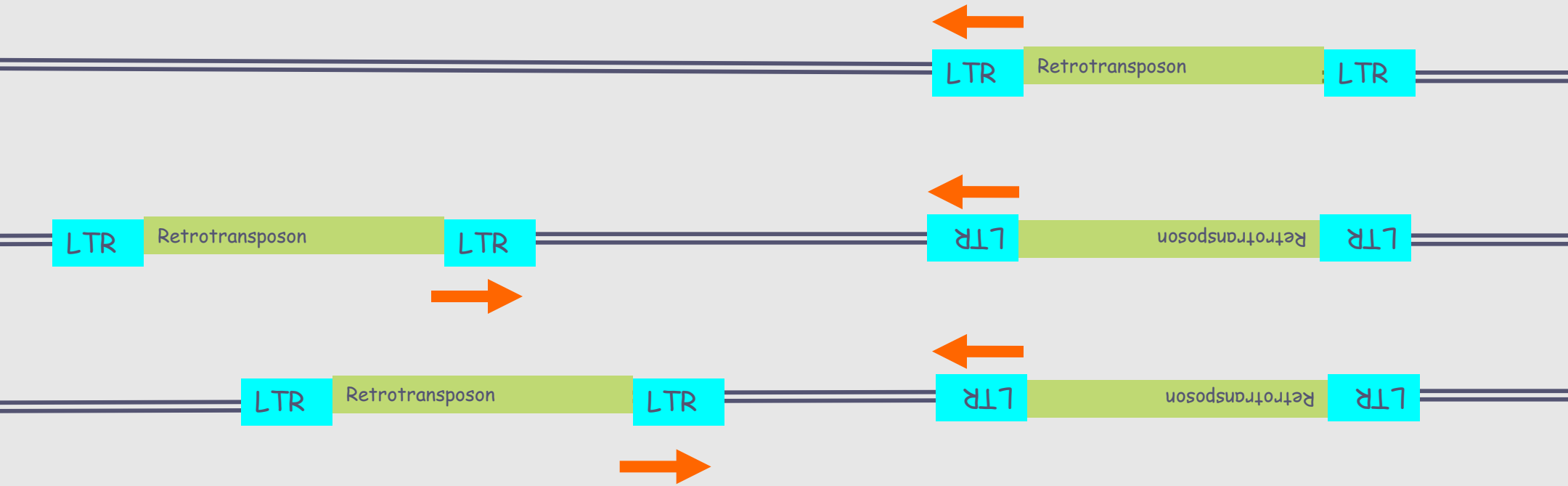


- Homologous BAC sequences from Calcutta 4 Homologous over the full length
- except for a 5kb insert
- a Ty1-copia retroelement

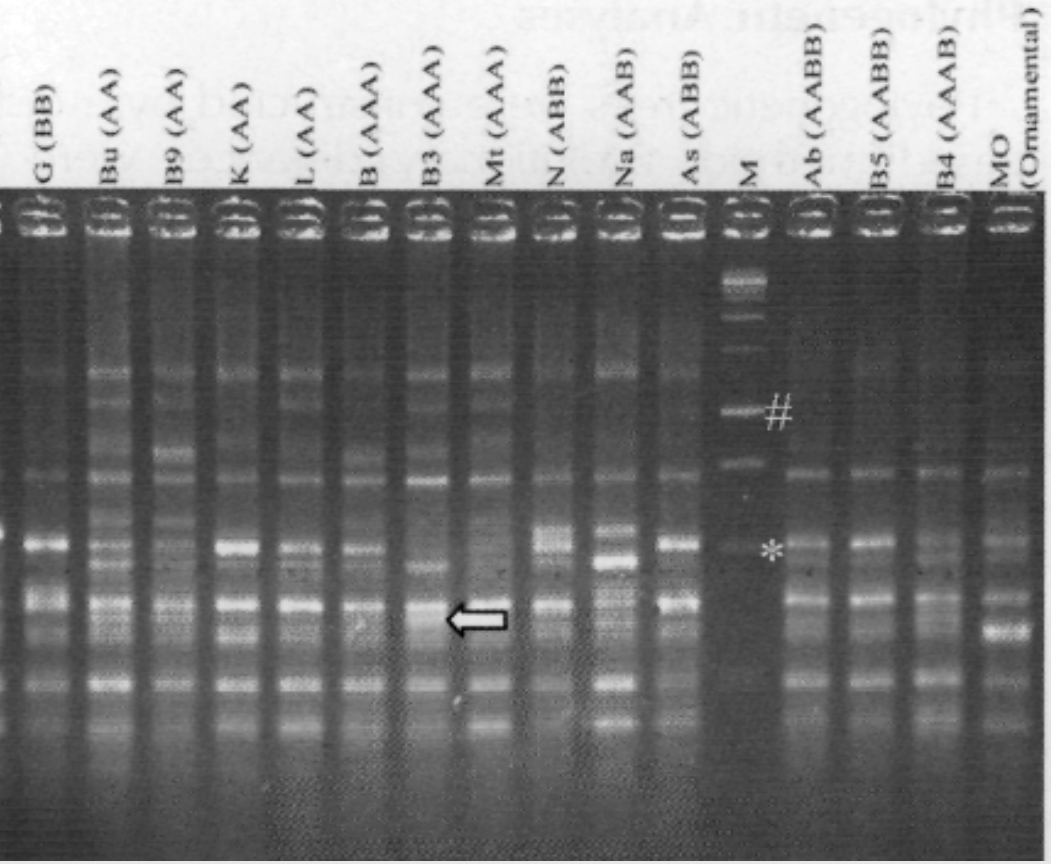
Retroelement Markers

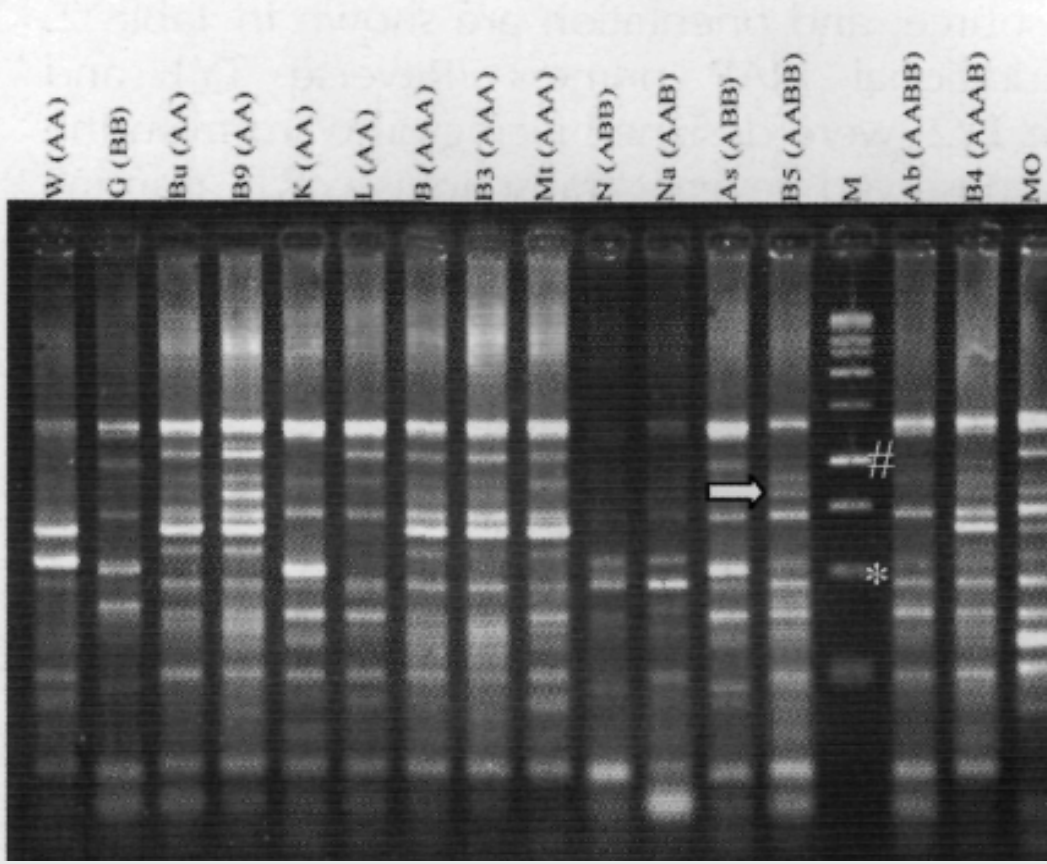
Insertion

IRAP – InterRetroelement PCR



IRAP diversity in Musa



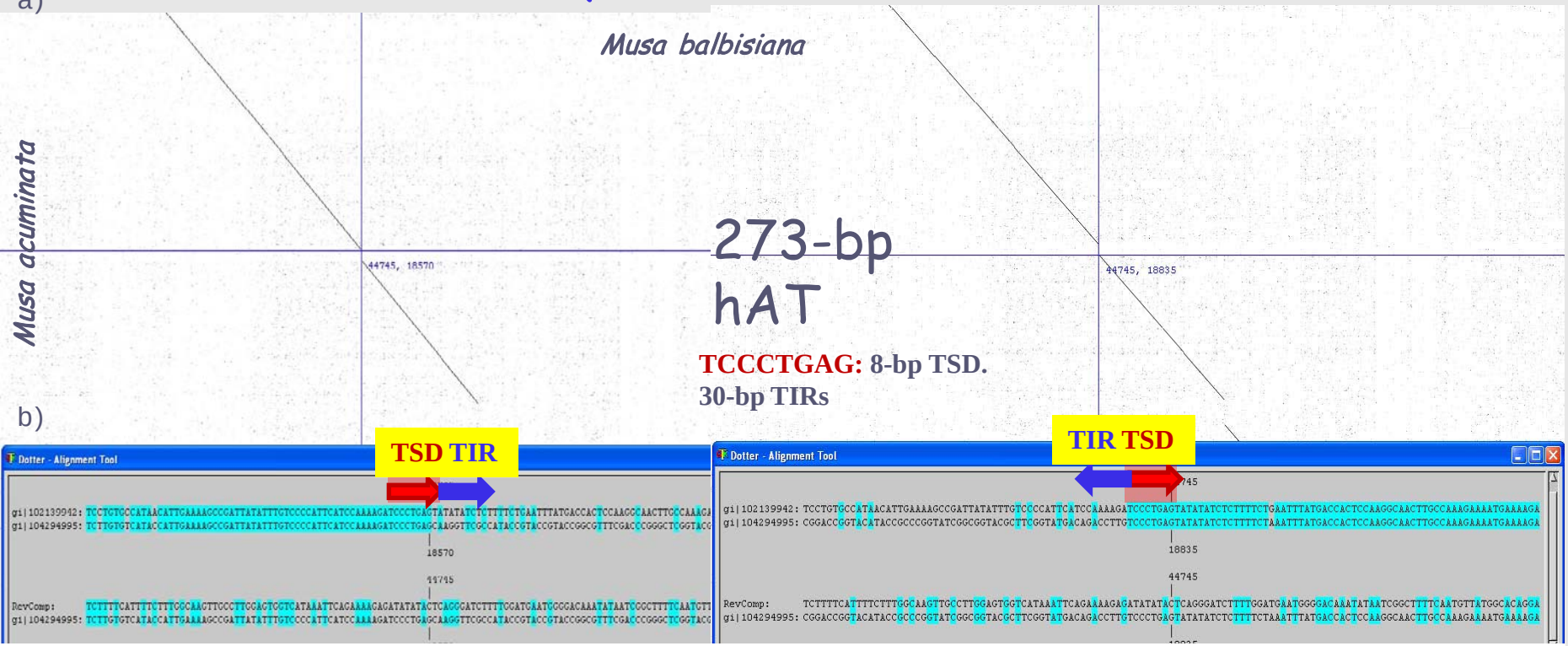


Teo, Tan, Ho, Faridah, Othman, HH, Kalendar, Schulman 2005 *J Plant Biol*

Nair, Teo, Schwarzacher, HH 2006 Euphytica

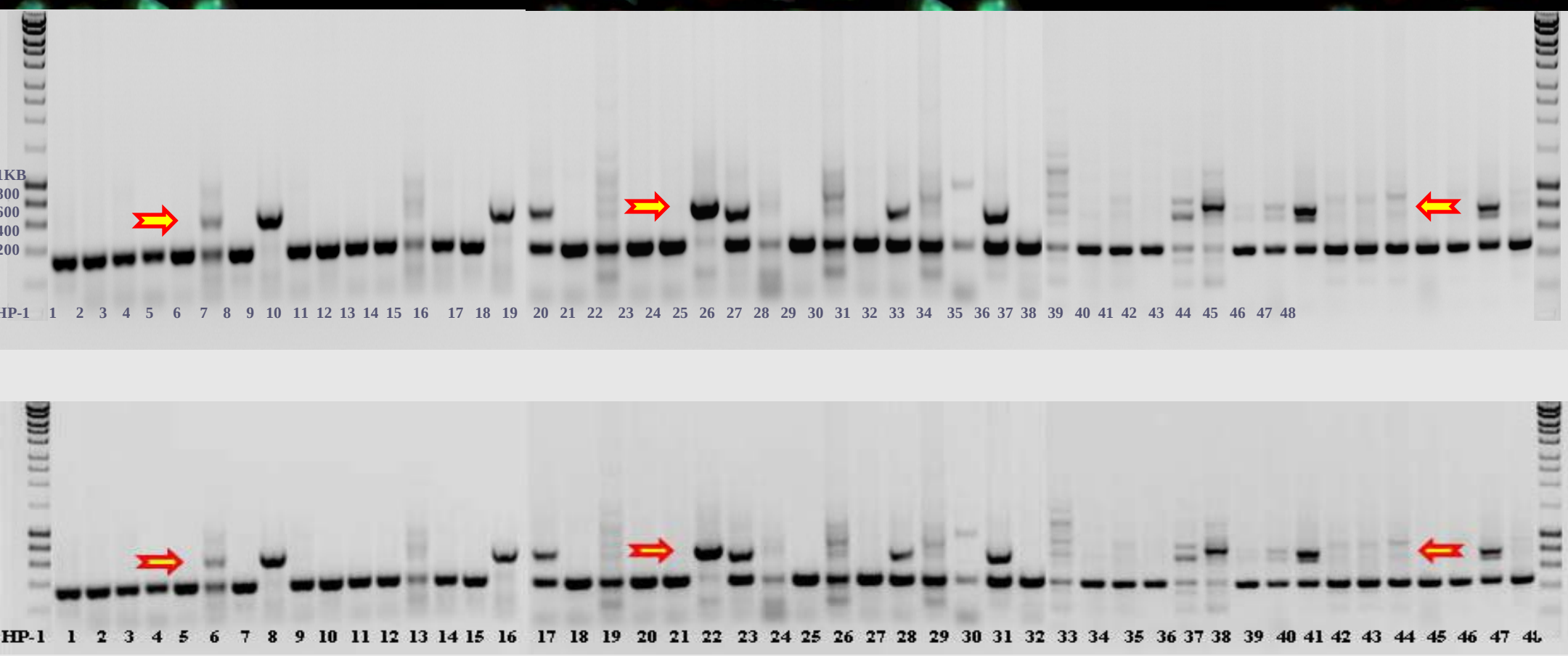
ACCCACCTGGCTCTTGTGTCATACCATTGAAAAGCCGATTATATTTGTCCCCATTCATCCAAAAGA**TCCCTGA**
GCAAGGTCTG*C****CATACCG***TA**CCGTACCG**G**CG**TTTCGACCCGGGGCTCGGTACGGTACCGGTGTACCGGGCAG
TACATCAGGGTGTACCGAATGGTACACCCTGATGTACCGAACAATTTTATACTTTTTCATACTGTAGCAGTGCT
ACAGTATAATACTGTAGCACTGTAGCGGTATCGGGCGGTCCGCGTACCGGTAACCTGTCGGACCGGTACATAC
CGCCCGGTAT**CGG****CGGTACG**CTT***CGGTATG***A***CAGACCTTG*****TCCCTGAG**TATATATCTCTTTTCTAAATTTATG
ACCACTCCAAGGCAACTTGCCAAAGAAAATGAAAAGAAGAAAAAAATTAGGGGAATGAAGATTCTCCACA
ATTCCTTATTCTTTGATTTGAGATAAATAATGTCCATAGTAAAACATATCTTATGATCATCATTGCTGATTAATCA
AAATACCTGATTCTATAGTCTCAAGCTTTAGTGGTCAAAACACATTCGC

a)



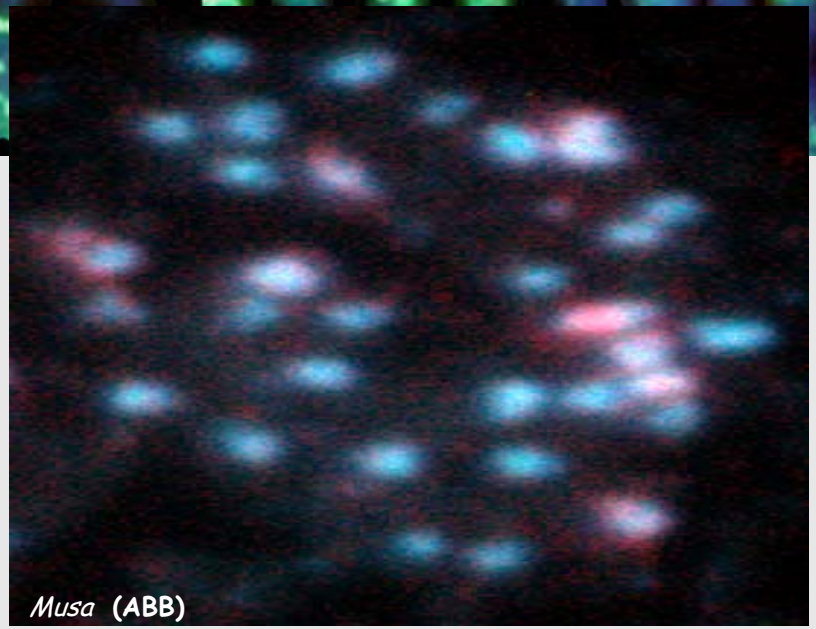
hAT1 in *Musa acuminata*

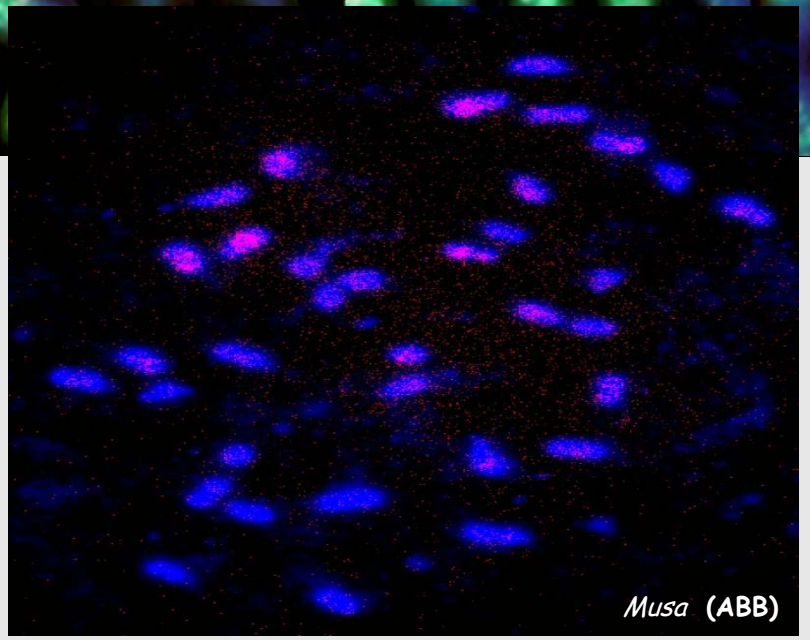
F and R primers indicated by blue arrows in sequence

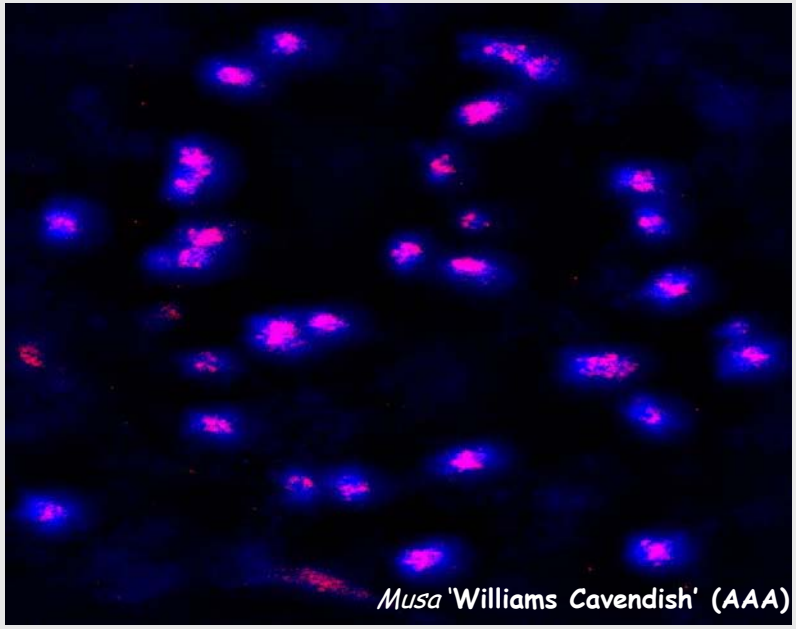


***hAT1* insertion sites in *Musa* diversity collection**
hAT486F and hAT037R
Top bands (560-bp) amplified hAT element and lower bands amplifying the

The hAT1 **insertion sites in** ***Musa with*** **hAT486F and hAT037R in: 6)** ***acuminata,*** **8)** ***acuminata,*** **16)** ***acuminata,*** **17) AAB, 22)** ***acuminata,*** **23) AB cv.**





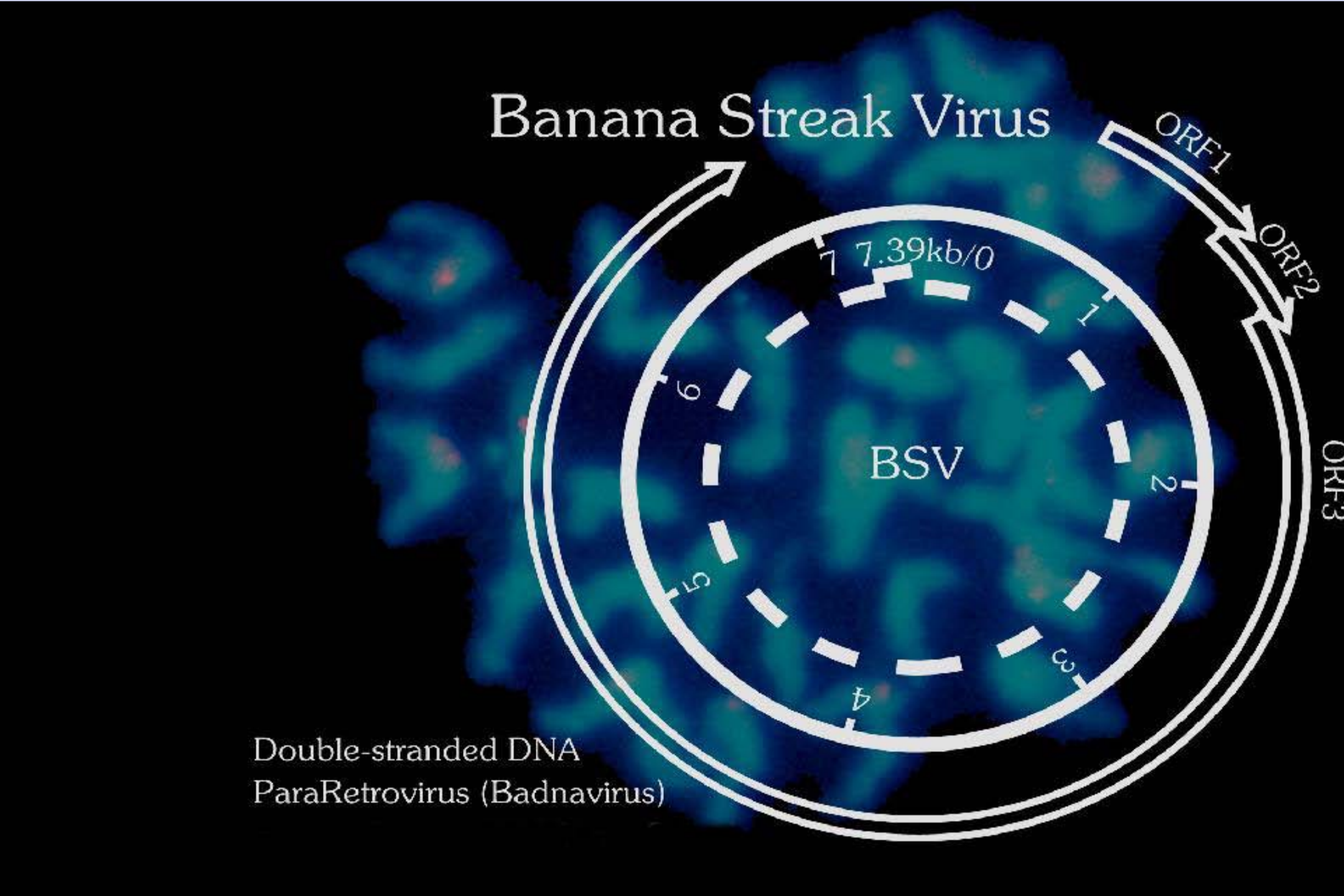


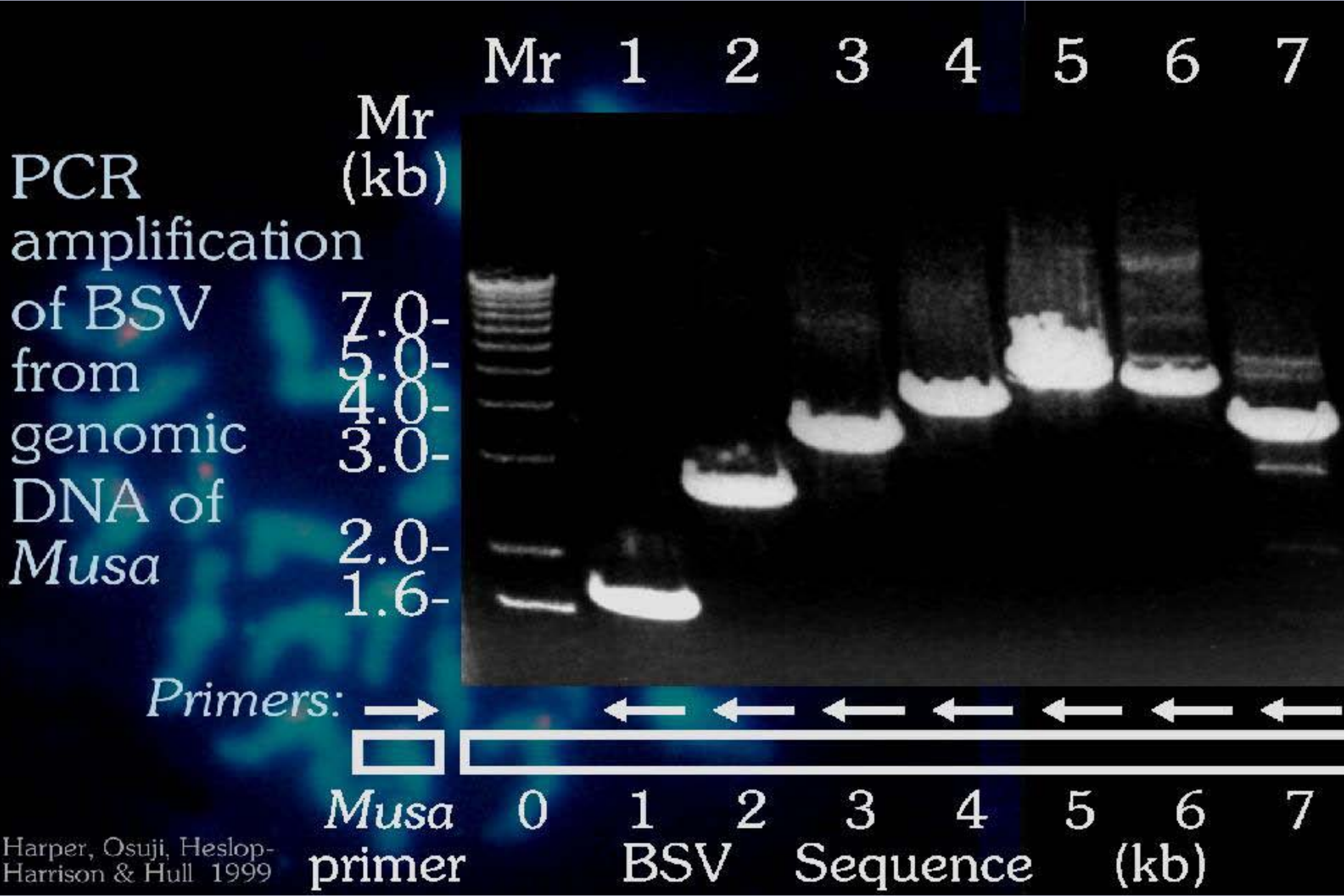
A-genome specific hAT in three *Musa* hybrids (2n=3x=33)

Banana Streak ParaRetrovirus (BSV)

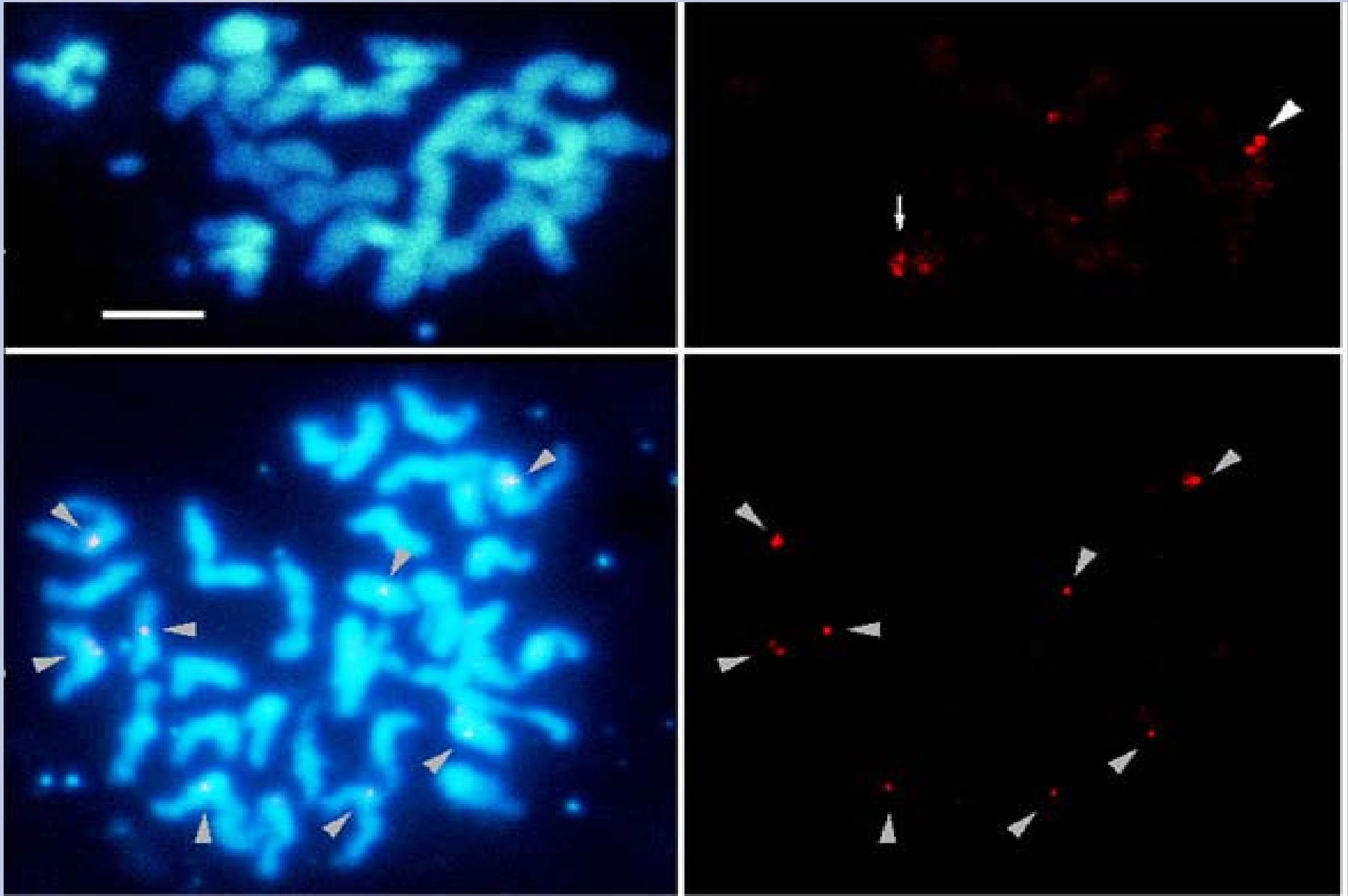
- Double stranded DNA is infective
- Insect vector
- Unexpected epidemiology
  - Appearance after cold or tissue culture

Glyn Harper & Roger Hull

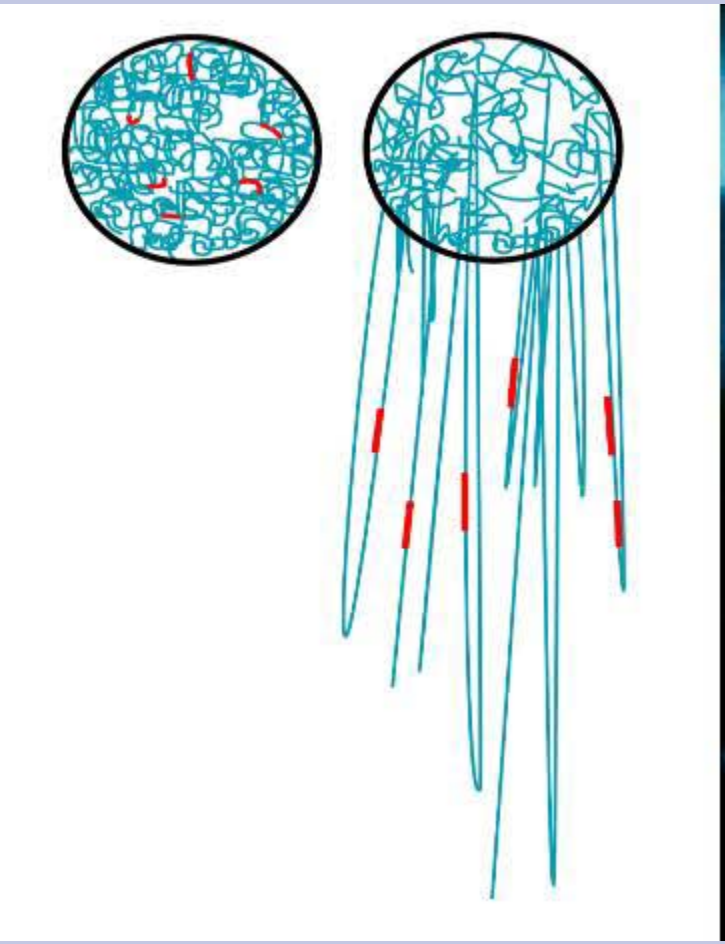

Banana Streak Virus
ORF1
ORF2
ORF3
7.39kb/0
1
2
3
4
5
6
7
BSV
Double-stranded DNA
ParaRetrovirus (Badnavirus)

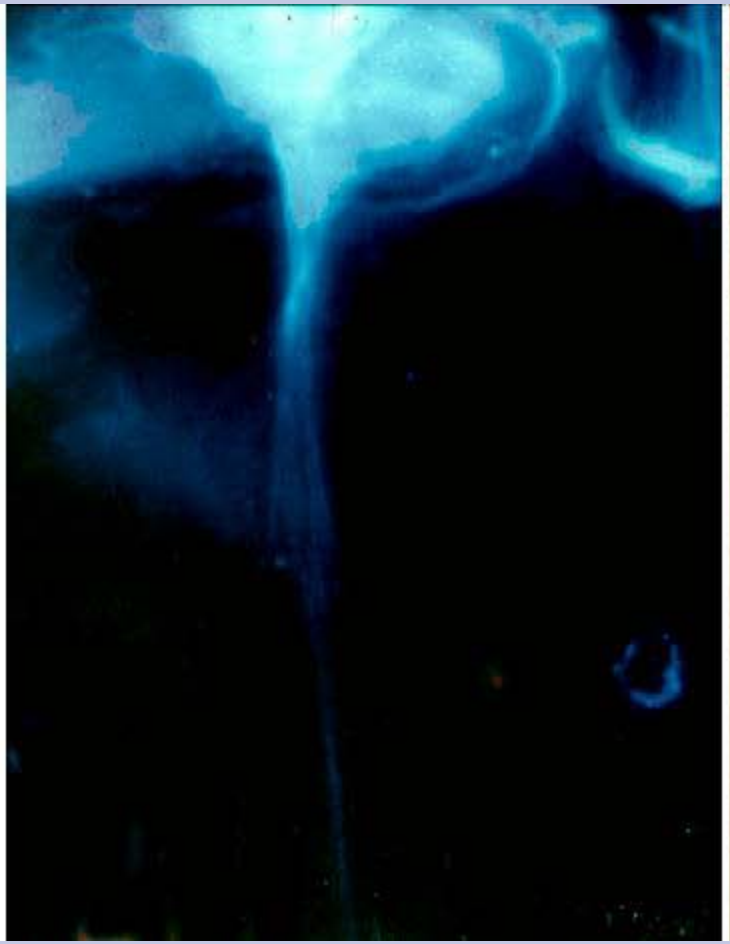

Mr 1 2 3 4 5 6 7
Mr (kb)
PCR amplification of BSV from genomic DNA of Musa
7.0-
5.0-
4.0-
3.0-
2.0-
1.6-
Primers:
Musa primer
0 1 2 3 4 5 6 7
BSV Sequence (kb)
Harper, Osuji, Heslop-Harrison & Hull 1999

Nuclear Copies of BSV in Banana

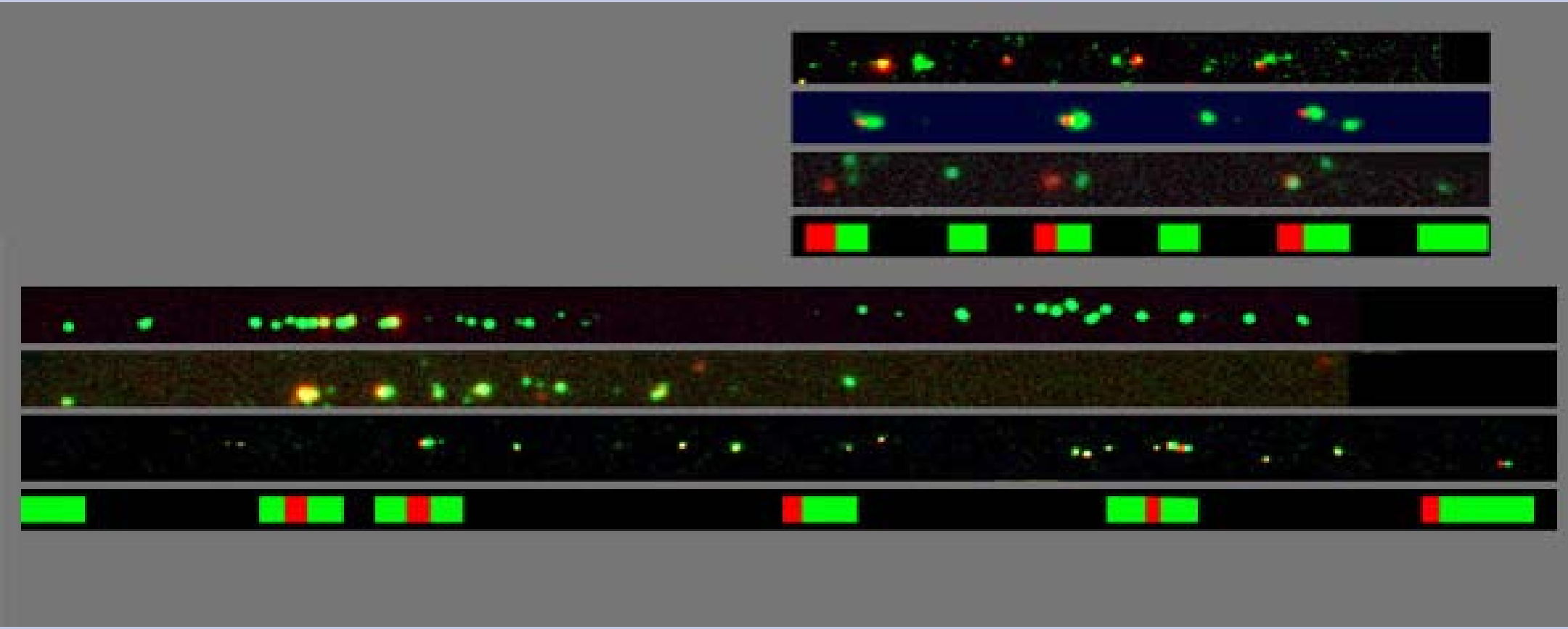


DNA Fibre Hybridization





Nuclear Copies of BSV in Banana



Oil palm: *Elaeis guineensis*

Malaysian Palm Oil Board
Alex Vershinin, Sybille Kubis,
Maria Madon, Xana Castilho,
Trude Schwarzacher

MPOB


Deli Dura (D)
DxP
Pisifera (P)

Epigenetics

Phenotype appears 5 years after tissue culture

Modulation of Methylation

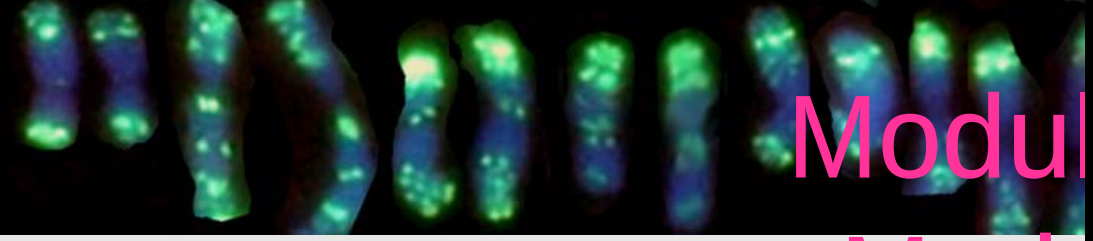
McrBC

unusual restriction enzyme cutting between methylated cytosine (^{m}C) sites

Cuts ^{m}C *NNNNNNNNNNN* ^{m}C

Leaves *C NNNNNNNNNN C*

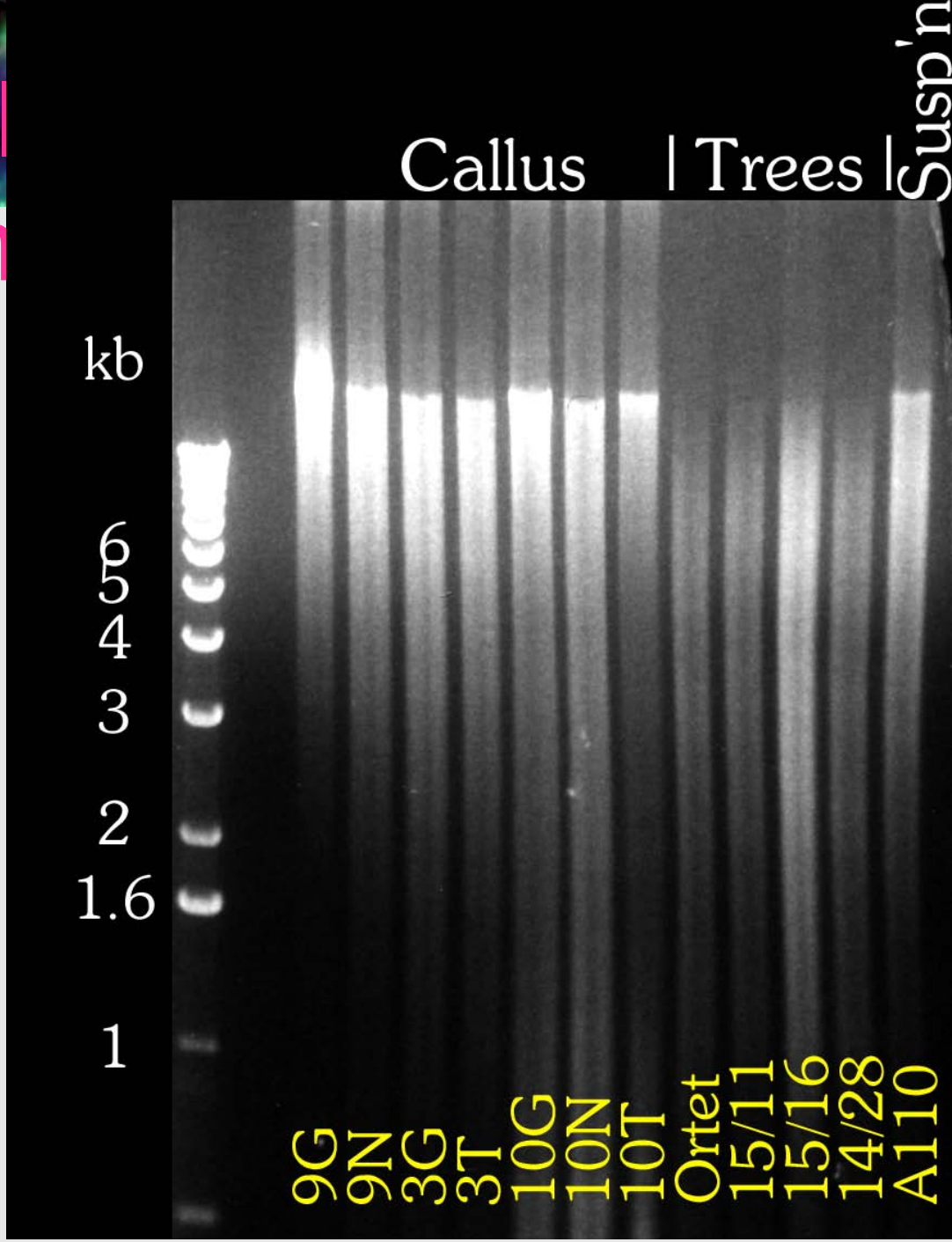
N typically 20 to 40 bases

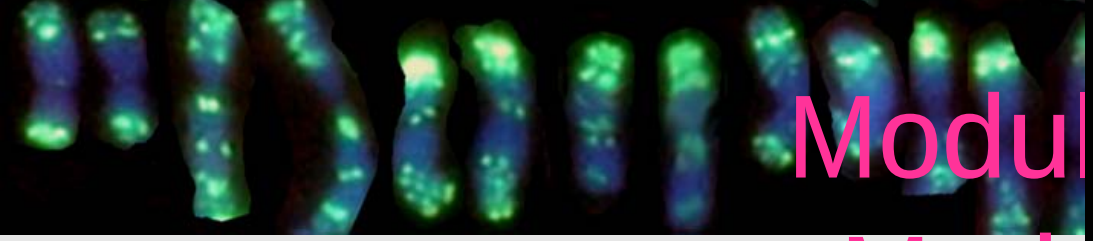


Modul
Meth

- McrBC - shows substantial reduction in methylation in tissue culture lines
- Cuts methylated DNA

Kubis, Castilho, Vershinin, HH 2003



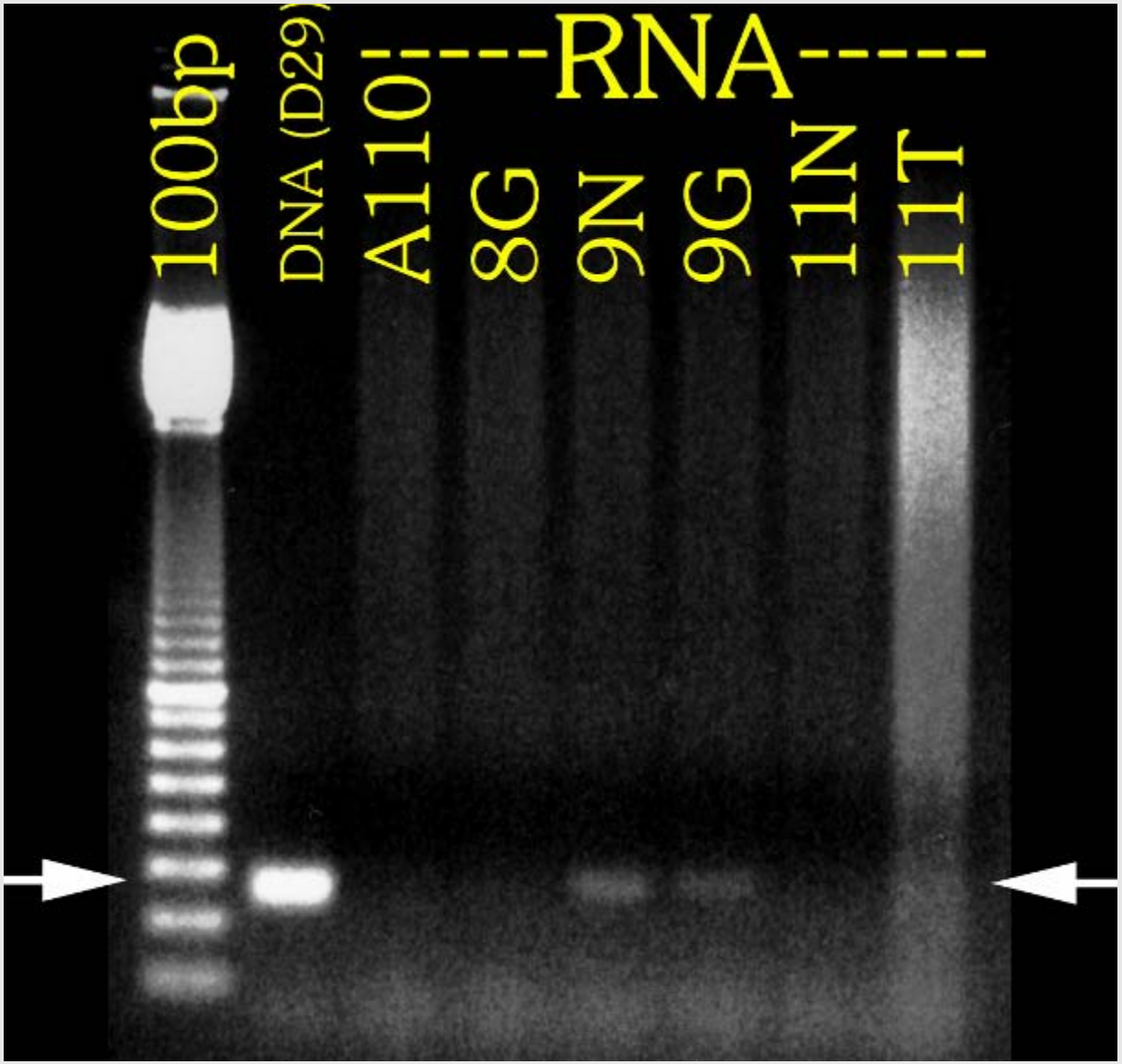


Modul
Meth

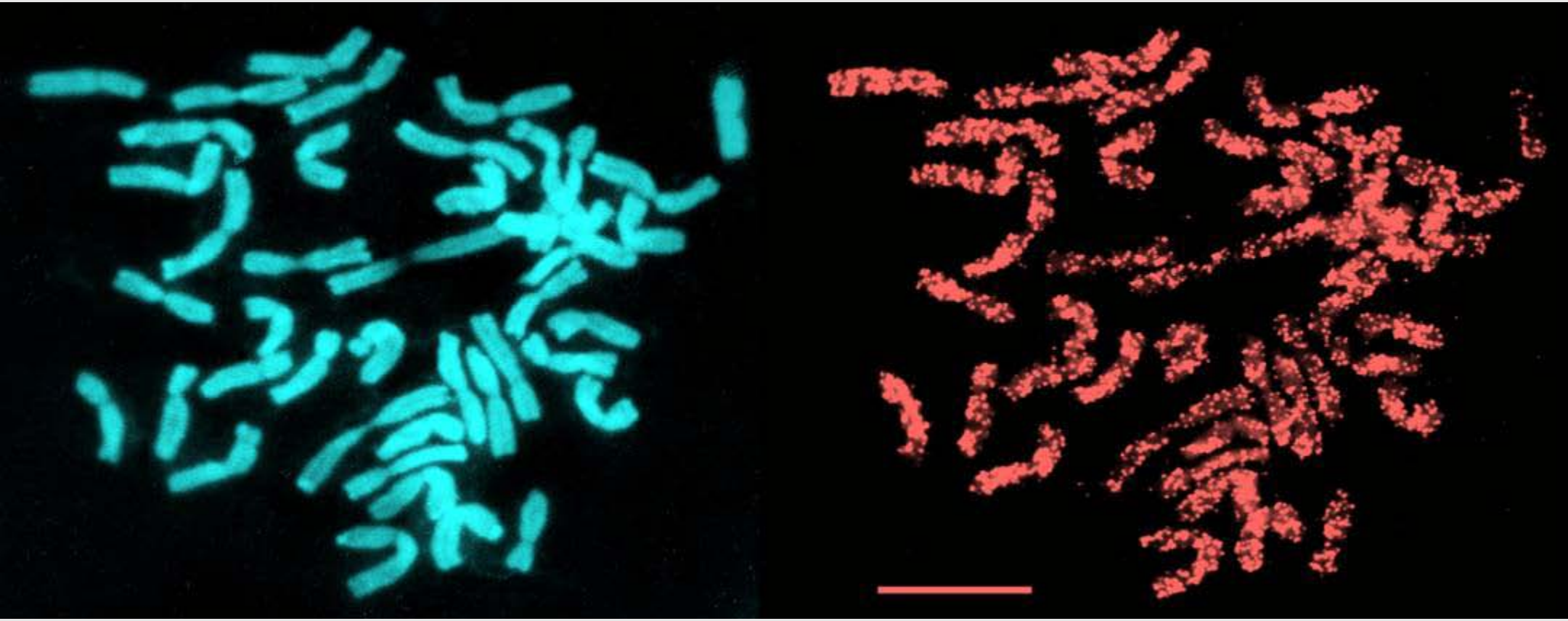
- McrBC digests probed with *gypsy* clones
- present only in N and T lines
- Similar with *copia* probe

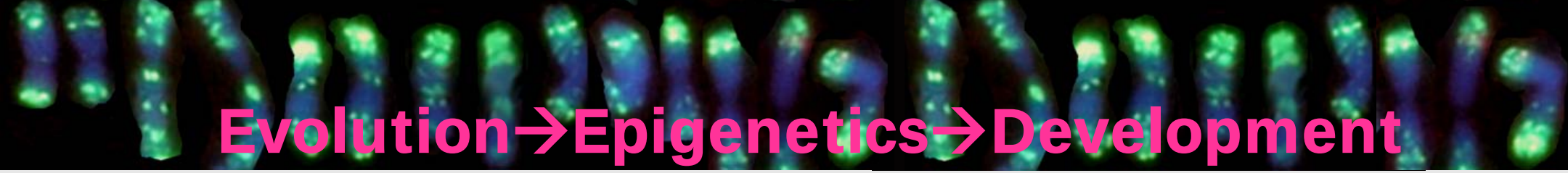
Transcriptional Activity

- *Copia* mRNA is present tissue culture
- Analysis by RT-PCR
- 260bp product in some lines



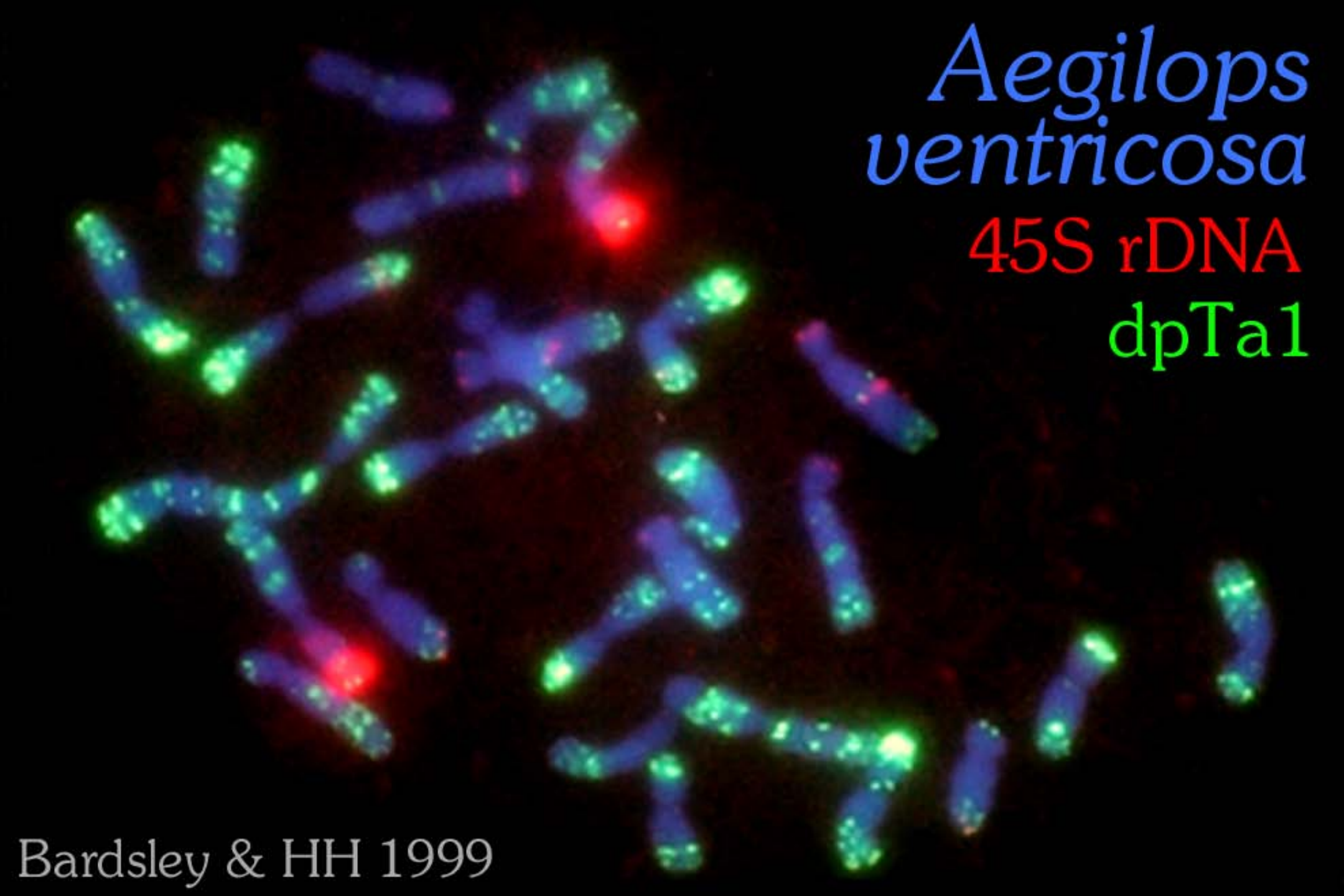
Modulation of Methylation
Anti-methylcytosine antibody

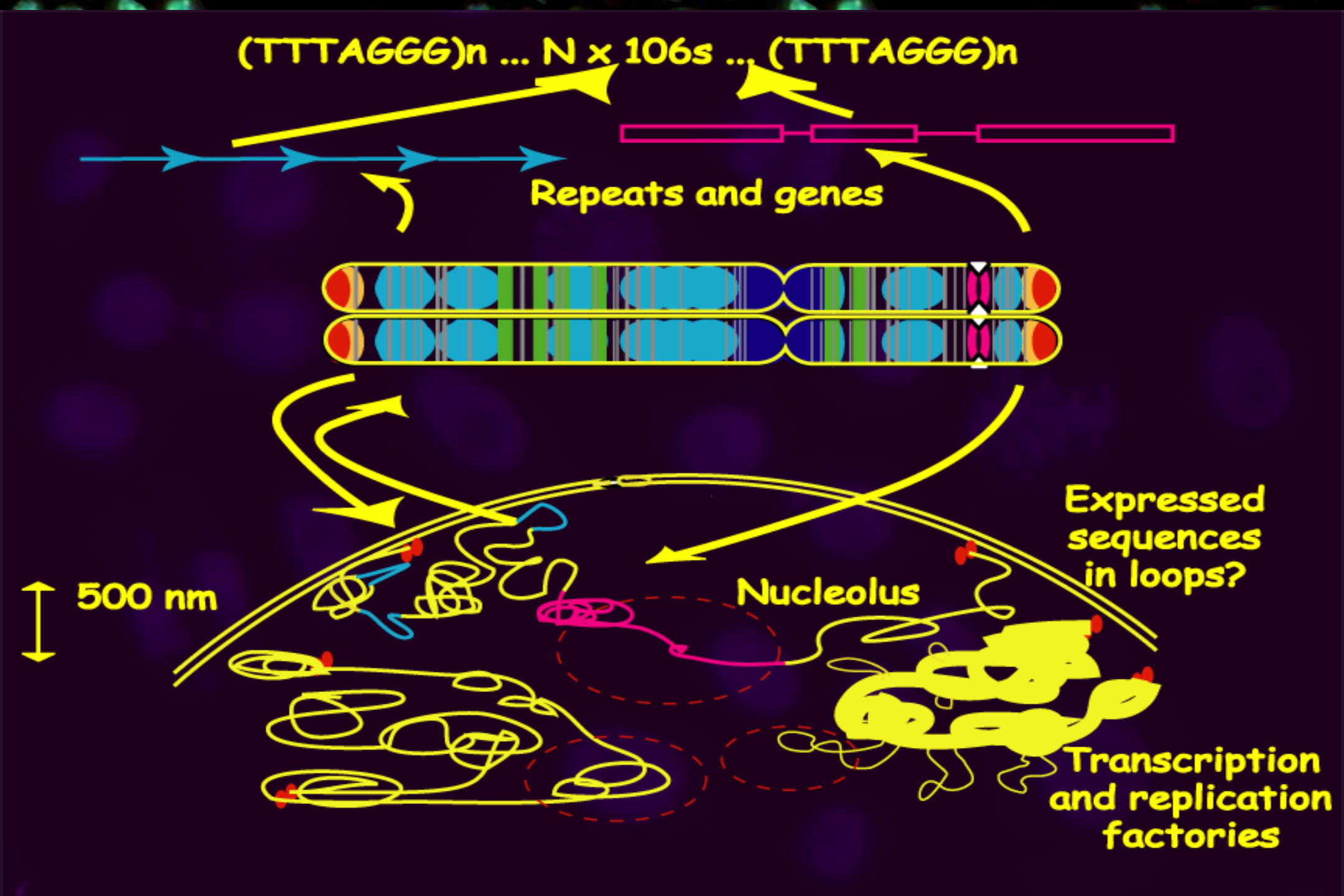




Evolution→Epigenetics→Development

Phenotype	Cause
Multiple abnormalities	Chromosomal loss, deletion or translocation
Genetic changes non-reverting	Gene mutation / base pair changes
	Telomere shortening
	Retro)transposon insertion
Changes seen, some reverting	Retrotransposon activation
	SSR expansion
	Methylation
(Male/Female) Normal Differentiation	Heterochromatinization
	Chromatin remodelling
	Histone modification


Aegilops
ventricosa
45S rDNA
dpTa1
Bardsley & HH 1999


(TTTAGGG)n ... N x 106s ... (TTTAGGG)n
Repeats and genes
Expressed sequences in loops?
500 nm
Nucleolus
Transcription and replication factories

Super-Domestication: United Nations Millennium Development Goals

- **Goal 1 – Eradicate extreme poverty and hunger**
- **Goal 2 – Achieve universal primary education**
- **Goal 3 – Promote gender equity and empower women**
- **Goal 4 – Reduce child mortality**
- **Goal 5 – Improve maternal health**
- **Goal 6- Combat HIV/AIDS, malaria and other diseases**
- **Goal 7 - Ensure environmental sustainability**
- **Goal 8 - Develop a global partnership for development**

Convention on Biodiversity ("Rio Convention"): inventory the worlds diversity

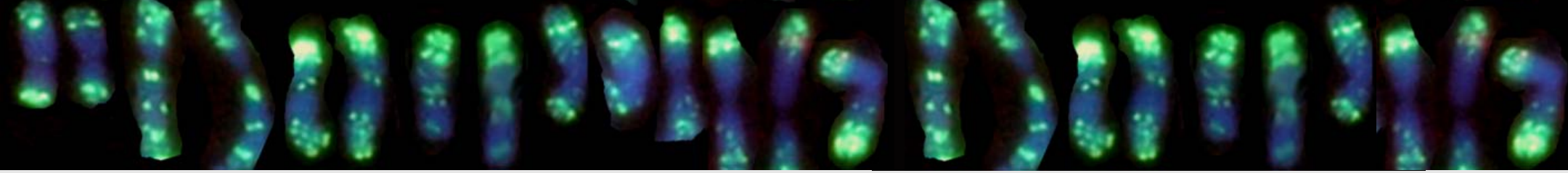
… needs for agriculture: not the only reasons for genomics

Moral imperative not to destroy that we have in the world


Thank You For
Shopping

researchers have been working with. One banana genotype was rather flavourless and starchy (Prata Ana), but two others emphasized what we in the temperate countries miss: Garantida II with citrus flavours overlaying a sweet smooth texture, while Caipira had a more savoury and vanilla custard taste. But the

Banana genotypes



Conventional Breeding

- Cross the best with the best and hope for something better

Superdomestication

- Decide what is wanted and then plan how to get it
- - variety crosses
- - mutations
- - genepool
- - genes

FINANCIAL TIMES

From Prof Donald Braben and others.

Sir, We the undersigned scientists write to draw attention to a neglected aspect of the current economic crisis. Robert Solow won the Nobel Prize in economics in 1987 for his 1950s discovery that *technical change* was the biggest source of growth, a discovery that seems to have been forgotten.

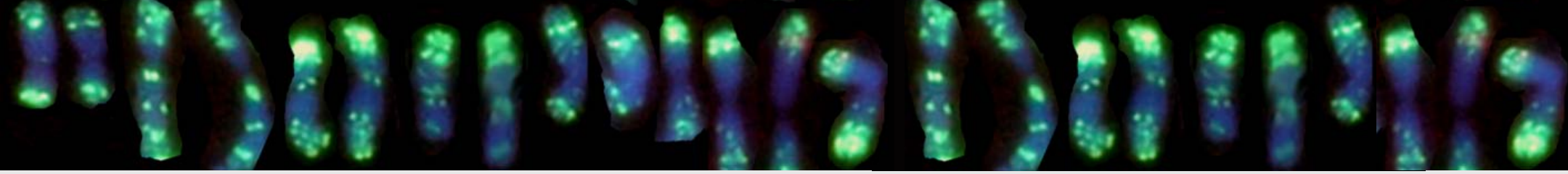
Scientific advances are not predictable.

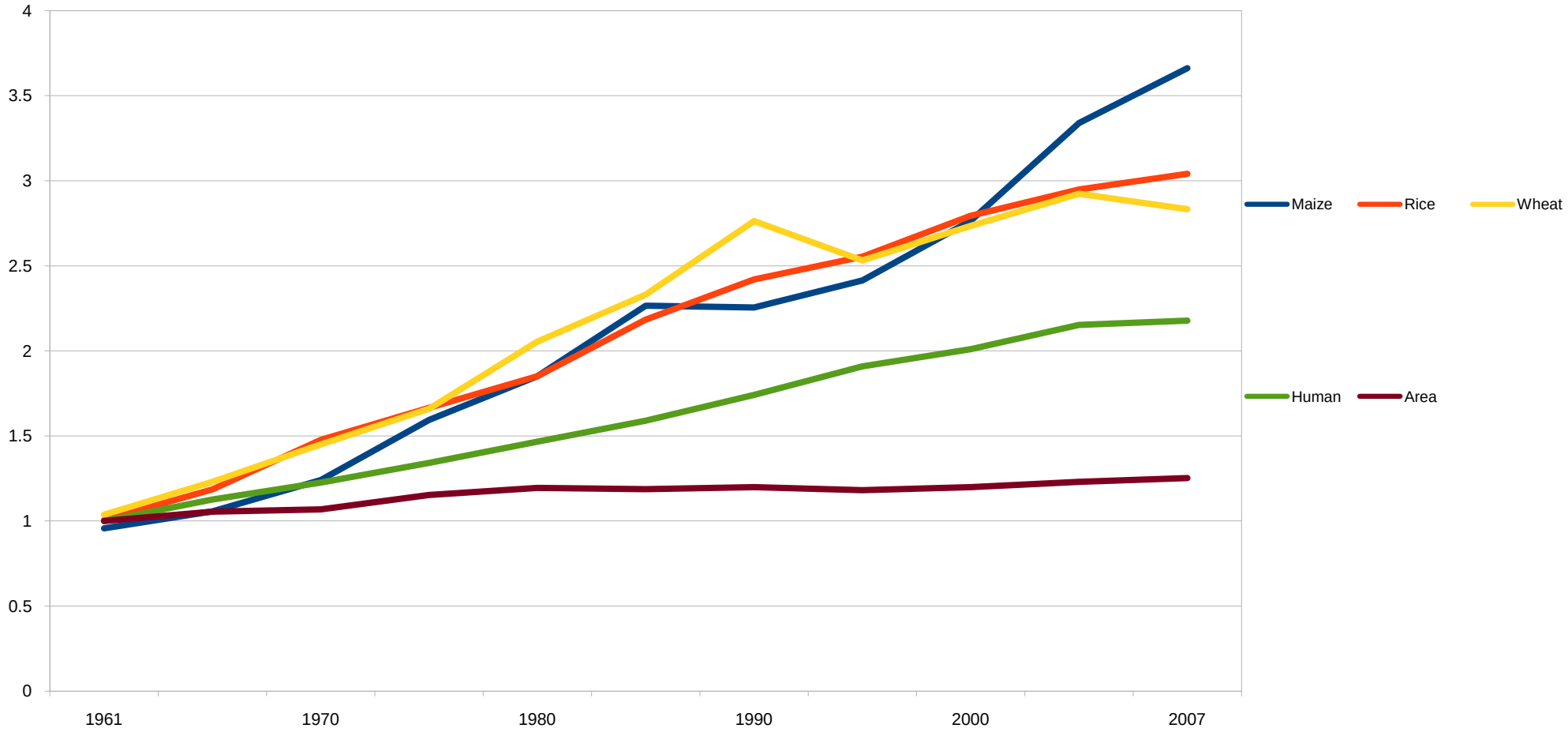
University, Nobel laureate
Pat Heslop-Harrison, University of Leicester
Steve Howdle, University of

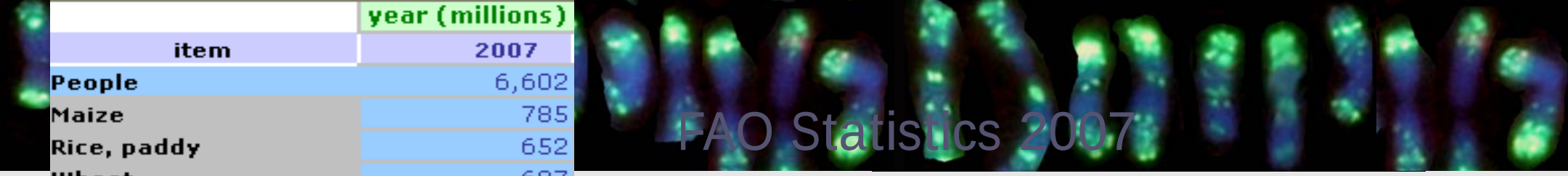
Future – Pollution and land use

Threats to sustainability: no different for 10,000 years

- Habitat destruction
- Climate change (abiotic stresses)
- Diseases (biotic stresses)
- Changes in what people want
- Blindness to what is happening
- Unwillingness to change




4
3.5
3
2.5
2
1.5
1
0.5
0
1961
1970
1980
1990
2000
2007
Maize
Rice
Wheat
Human
Area



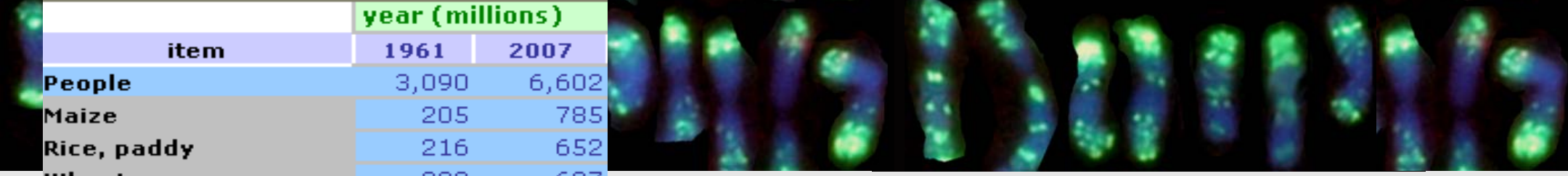
item	year (millions) 2007
People	6,602
Maize	785
Rice, paddy	652
Wheat	607
Potatoes	322
Sugar beet	248
Cassava	228
Soybeans	216
Oil palm fruit	192
Barley	136
Sweet potatoes	126
Tomatoes	126
Watermelons	93
Bananas	81
Seed cotton	73
Cabbages and other bra	69
Grapes	66
Sorghum	65
Onions, dry	64
Apples	64
Oranges	64
Coconuts	55
Yams	52
Rapeseed	49
Cucumbers and gherkin	45
Groundnuts, with shell	35
Plantains	34
Mangoes, mangosteens	33
Eggplants (aubergines)	32
Millet	32

All plant crops with >30M tons annual production

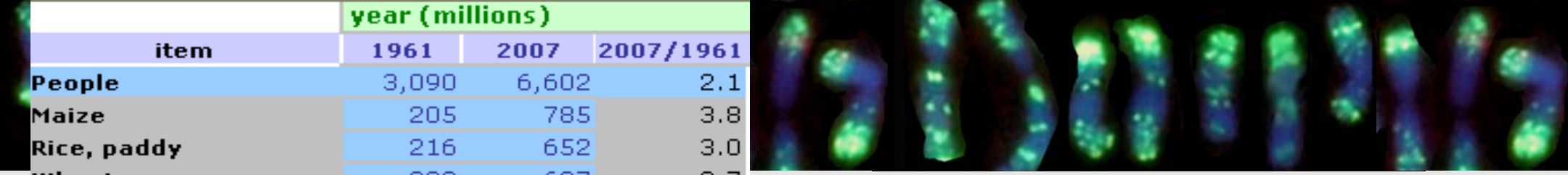
excluding sugar cane and ‘other vegetables’

People: WHO

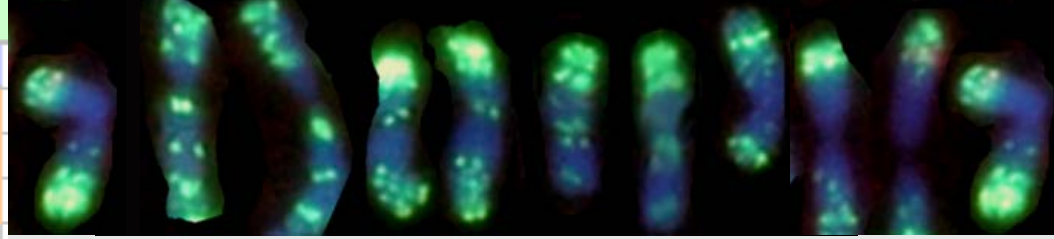
Calories are pretty important – ‘let them eat micronutrients’ is



	year (millions)	
item	1961	2007
People	3,090	6,602
Maize	205	785
Rice, paddy	216	652
Wheat	222	607
Potatoes	271	322
Sugar beet	161	248
Cassava	71	228
Soybeans	27	216
Oil palm fruit	14	192
Barley	72	136
Sweet potatoes	98	126
Tomatoes	28	126
Watermelons	18	93
Bananas	21	81
Seed cotton	27	73
Cabbages and other bra	23	69
Grapes	43	66
Sorghum	41	65
Onions, dry	14	64
Apples	17	64
Oranges	16	64
Coconuts	24	55
Yams	8	52
Rapeseed	4	49
Cucumbers and gherkin	10	45
Groundnuts, with shell	14	35
Plantains	13	34
Mangoes, mangosteens	11	33
Eggplants (aubergines)	7	32
Millet	26	32



item	year (millions)		
	1961	2007	2007/1961
People	3,090	6,602	2.1
Maize	205	785	3.8
Rice, paddy	216	652	3.0
Wheat	222	607	2.7
Potatoes	271	322	1.2
Sugar beet	161	248	1.5
Cassava	71	228	3.2
Soybeans	27	216	8.0
Oil palm fruit	14	192	13.7
Barley	72	136	1.9
Sweet potatoes	98	126	1.3
Tomatoes	28	126	4.5
Watermelons	18	93	5.2
Bananas	21	81	3.9
Seed cotton	27	73	2.7
Cabbages and other bra	23	69	3.0
Grapes	43	66	1.5
Sorghum	41	65	1.6
Onions, dry	14	64	4.6
Apples	17	64	3.8
Oranges	16	64	4.0
Coconuts	24	55	2.3
Yams	8	52	6.5
Rapeseed	4	49	12.3
Cucumbers and gherkin	10	45	4.5
Groundnuts, with shell	14	35	2.5
Plantains	13	34	2.6
Mangoes, mangosteens	11	33	3.0
Eggplants (aubergines)	7	32	4.6
Millet	26	32	1.2



	year (millions)		
item	1961	2007	2007/1961
Oil palm fruit	14	192	13.7
Rapeseed	4	49	12.3
Soybeans	27	216	8.0
Yams	8	52	6.5
Watermelons	18	93	5.2
Onions, dry	14	64	4.6
Eggplants (aubergines)	7	32	4.6
Tomatoes	28	126	4.5
Cucumbers and gherkin	10	45	4.5
Oranges	16	64	4.0
Bananas	21	81	3.9
Maize	205	785	3.8
Apples	17	64	3.8
Cassava	71	228	3.2
Rice, paddy	216	652	3.0
Cabbages and other bra	23	69	3.0
Mangoes, mangosteens	11	33	3.0
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Seed cotton	27	73	2.7
Plantains	13	34	2.6
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Coconuts	24	55	2.3
People	3,090	6,602	2.1
Barley	72	136	1.9
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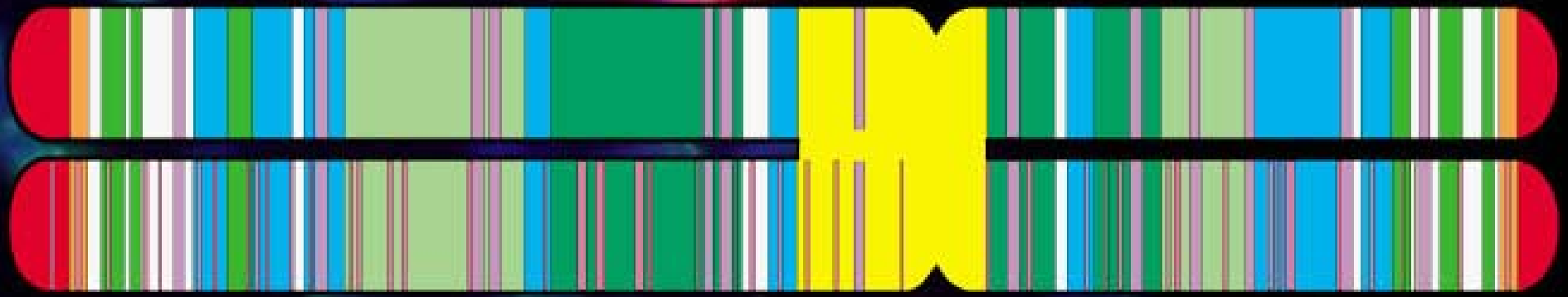
Grapes	43	66	1.5
Sweet potatoes	98	126	1.3
Millet	26	32	1.2
Potatoes	271	322	1.2

Plant Genome
Evolution and Diversity

1. Genomes and genomics
2. Markers from DNA
3. Diversity and its use
4. Challenges and breeding

The Linear Chromosome

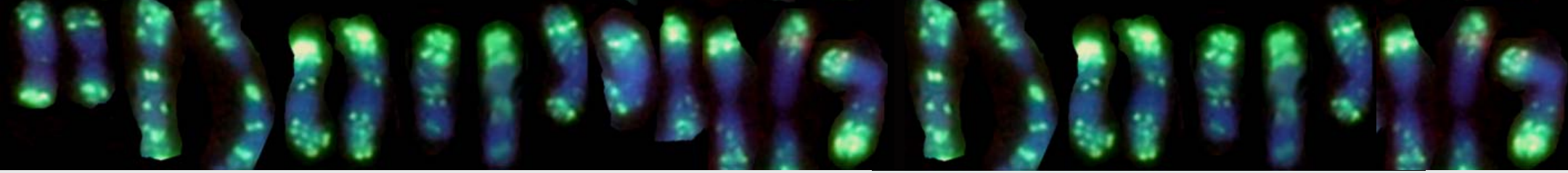


Tandem repeats

Retroelements
Simple sequence repeats

Terminal repeats

Genes



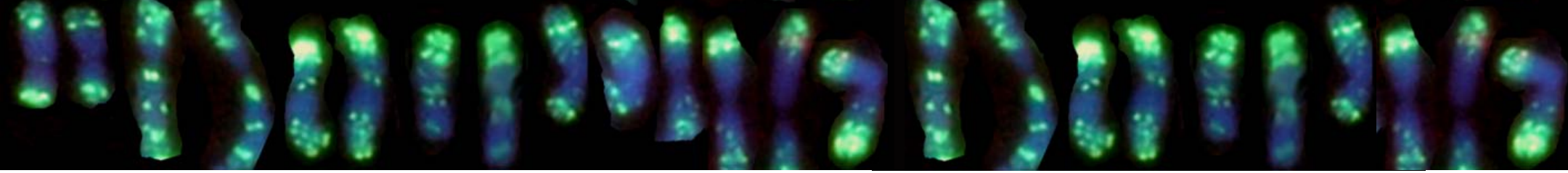
CytoGenomics ...

- The genepool has the diversity to address these challenges ...
- New methods to exploit and characterize germplasm let use make better and sustainable use of the genepool

Diversity, Genes and Genomics: From Models to Application

Species evolution
Polyploidy
Sequence evolution
Chromosome evolution
Genome diversity
Centromeres/mitosis
Nuclear architecture
Epigenetics
Chromatin
Meiosis/recombination

Origins
Phylogeny
Diversity
Introgression
Selection
Pre-Breeding
Propagation
Varieties



Plant Molecular Cytogenetics

Pat Heslop-Harrison

phh4@le.ac.uk

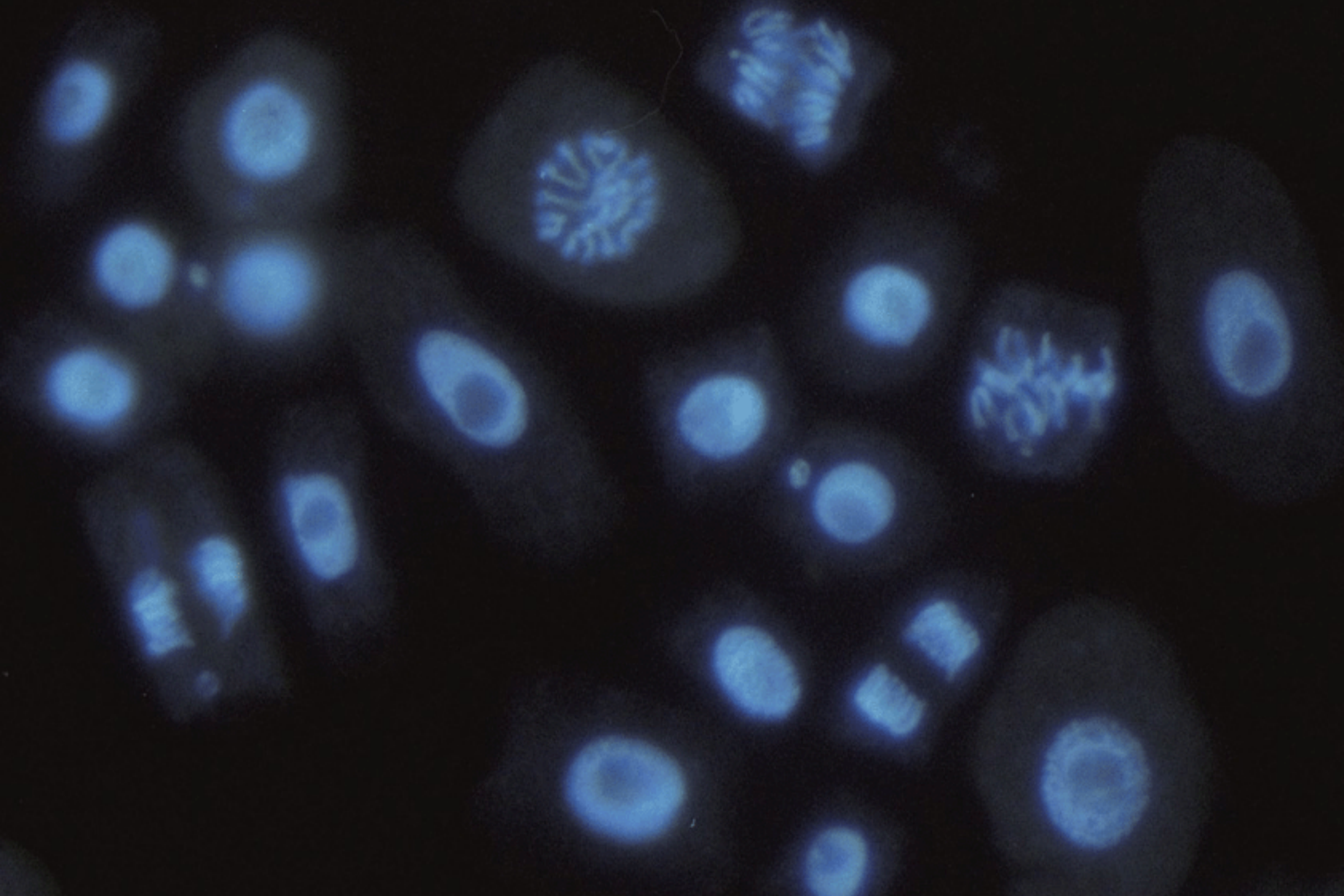
www.molcyt.com User&PW = ‘visitor’

This talk will be linked from homepage

Also: www.sblab.org www.crocusbank.org

www.biobanana.com www.musagenomics.org

- Weed control
- Monocultures
- Suitable inputs (nitrogen)
- Diseases – co-evolution
- Post-harvest losses
- Alien species



Do we need change?
Do we need faster change?

Crop varieties
-High yield
-High quality and safe
-Easy to grow agronomically
-Disease resistant
-Insect/nematode resistant
-Efficient water use
-Secure, stable production
-Environmentally friendly
    -Not invasive


Triticale:
a wheat x rye
hybrid