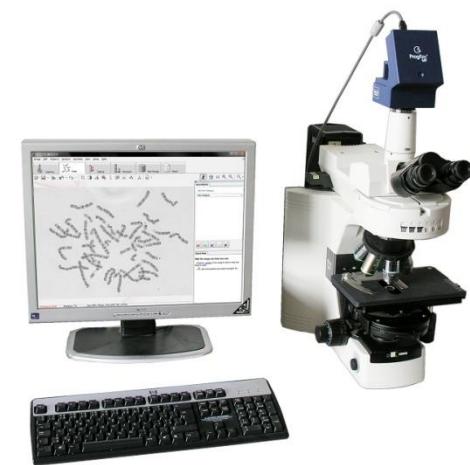
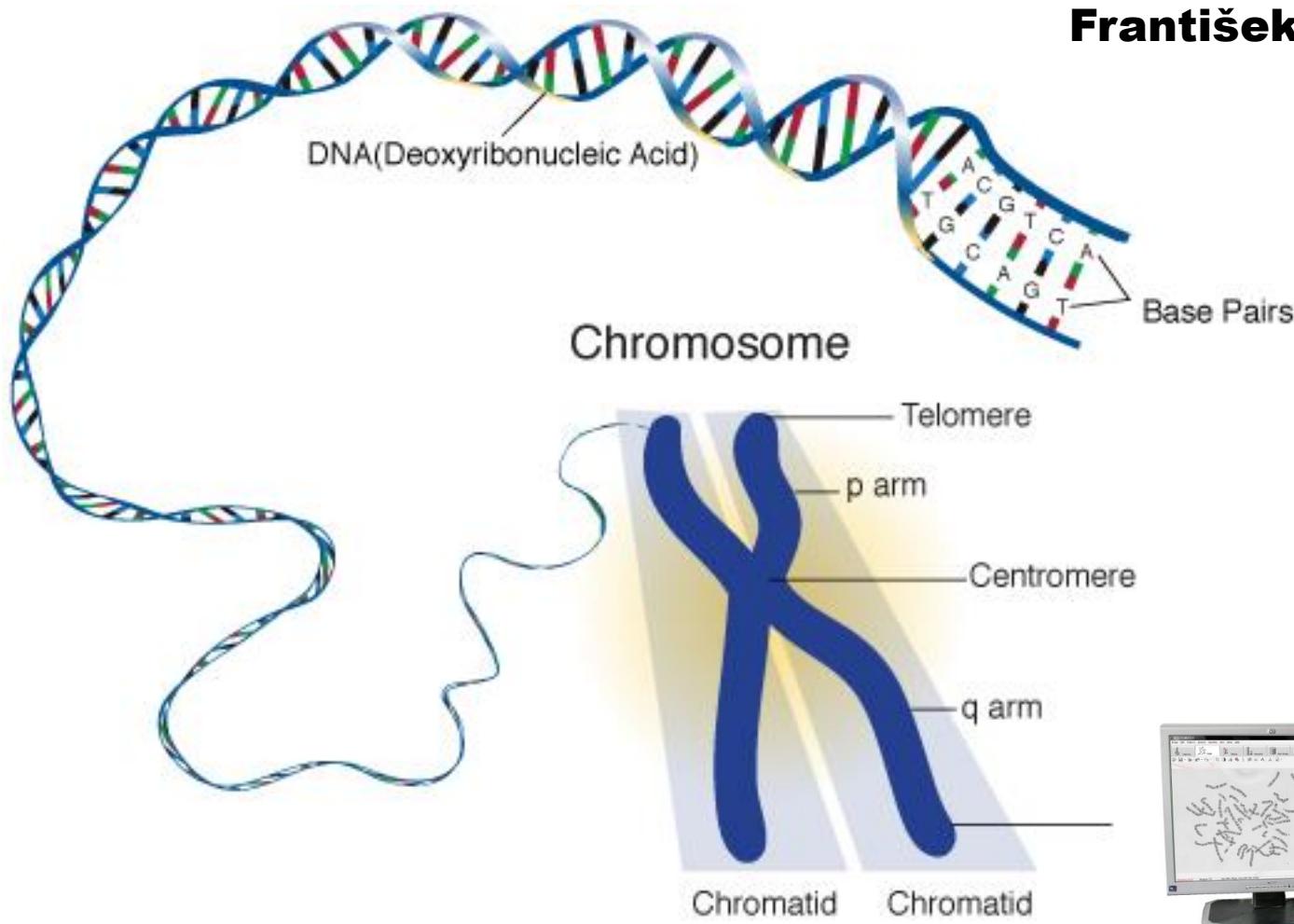


# Cytogenetic methods

František Štáhlavský



# Cytogenetic

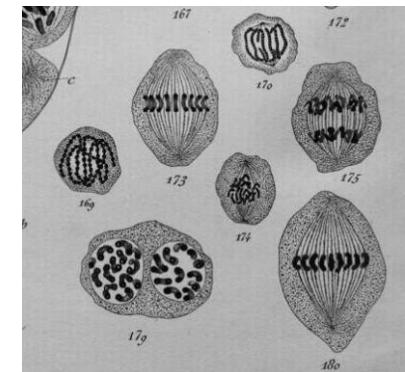
is a branch of genetics that is concerned with the study of the structure and function of the cell, especially the chromosomes.

1842 – first observations of chromosomes

1888 – used term ***chromosome***

(*chroma*=colour , *soma*=body )

1902-04 – chromosomal inheritance theory

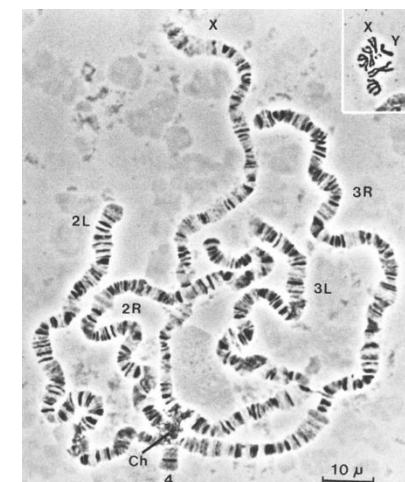
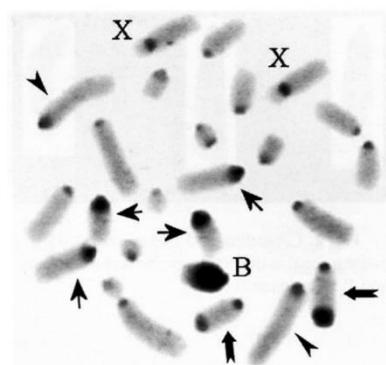
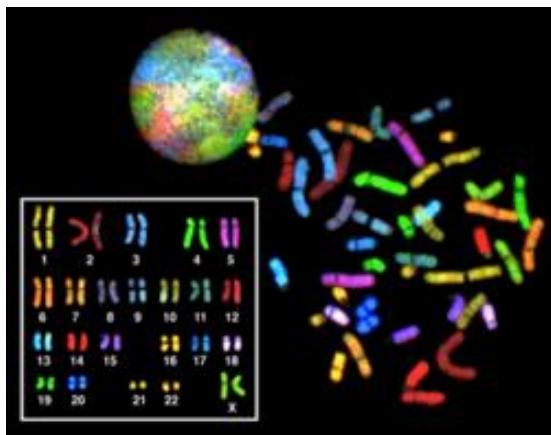


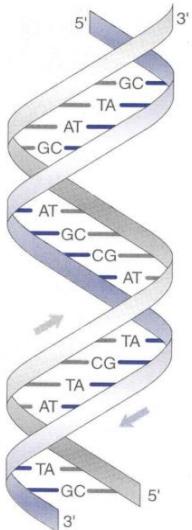
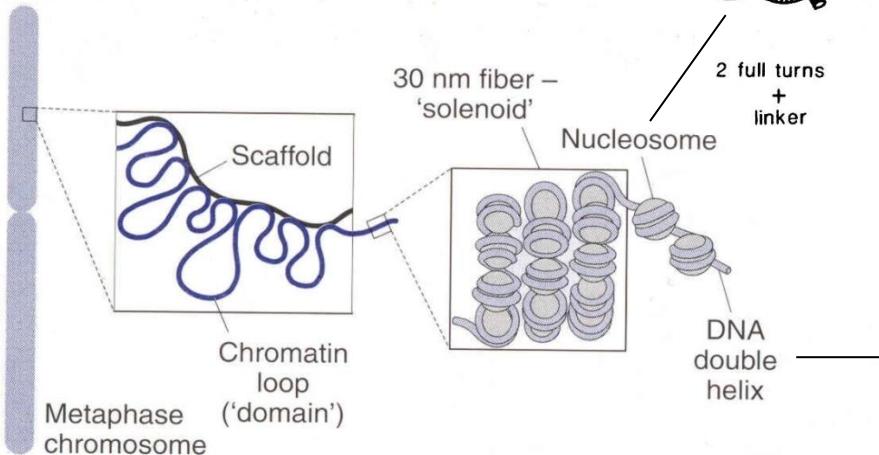
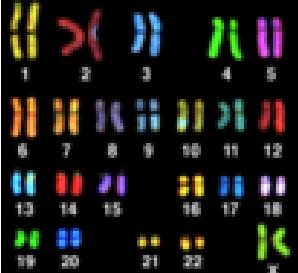
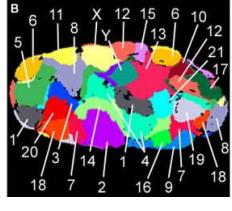
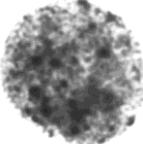
1950s – progress in methods (hypotonization,...)

1956 – final determination of  $2n$  in human

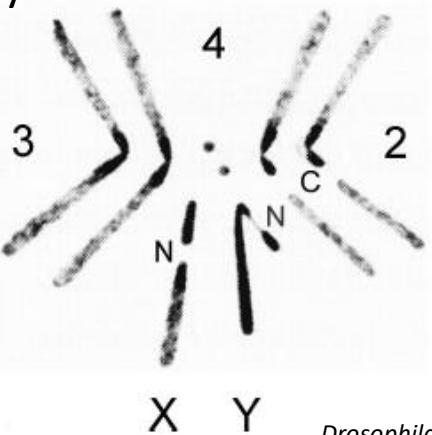
1968 – banding techniques

1990s – FISH techniques





**EUCHROMATIN x HETEROCHROMATIN**  
genetic activity      no genetic activity

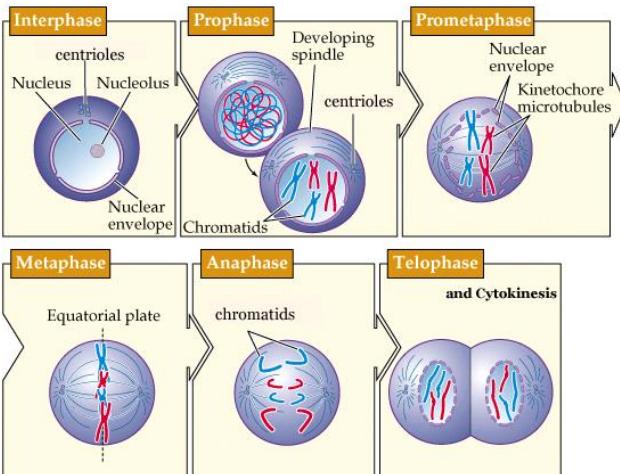


*Drosophila melanogaster* ( $2n = 8$ )

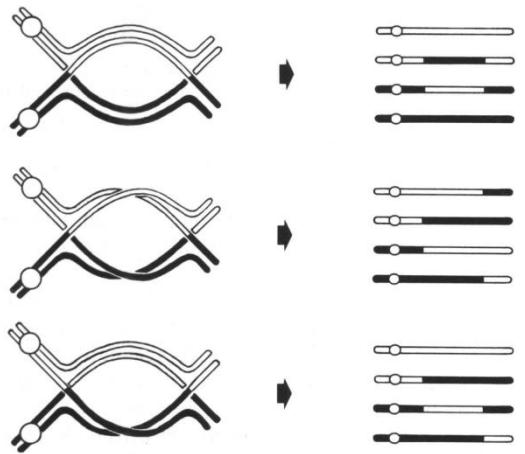
## Functions of chromosomes

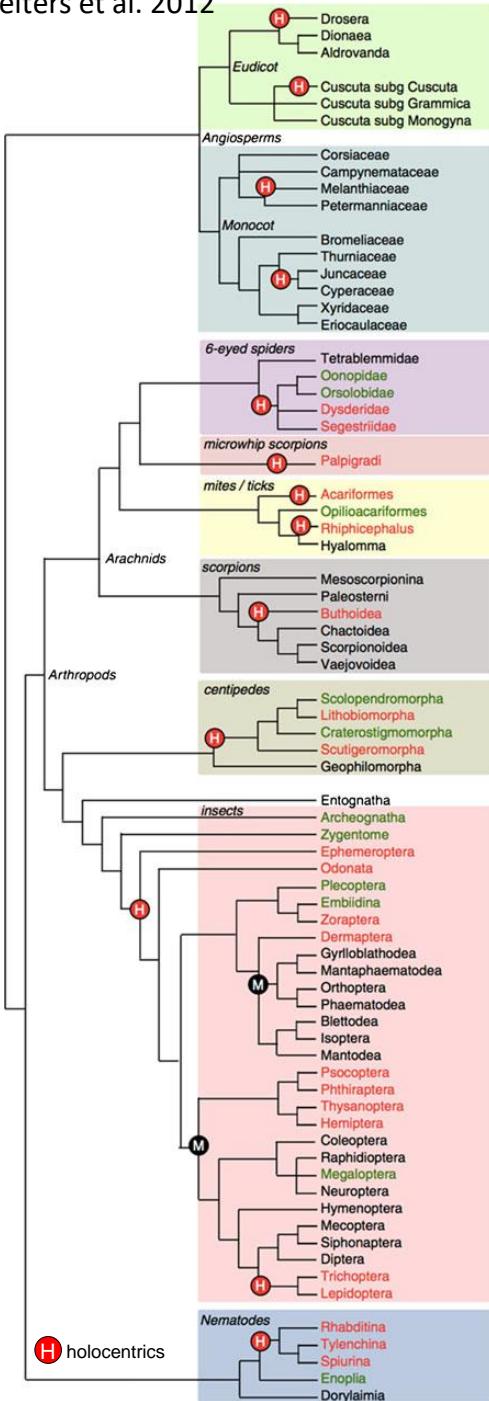
- spatial distribution of genes

- equal transport of genetic information during cell division



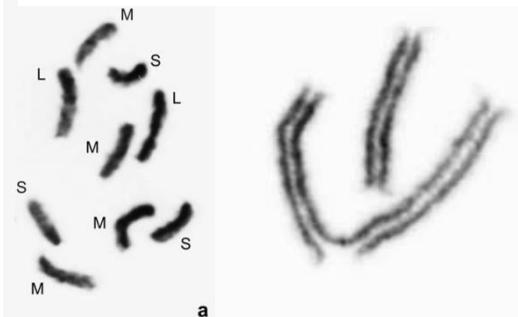
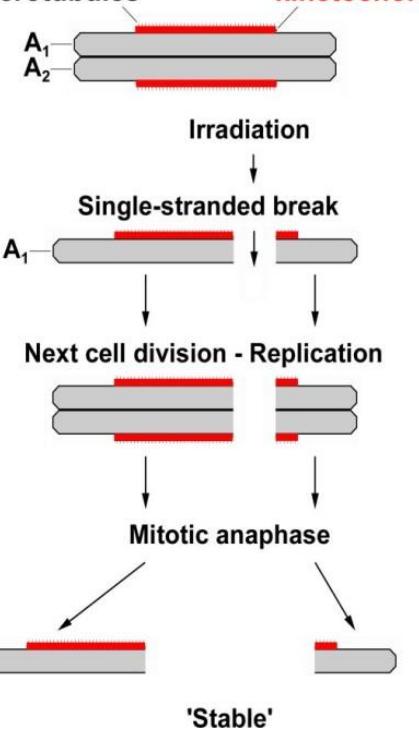
- crossing-over during meiosis,  
new genetic combinations





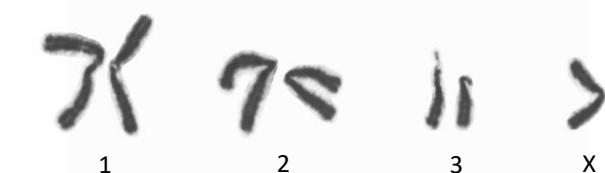
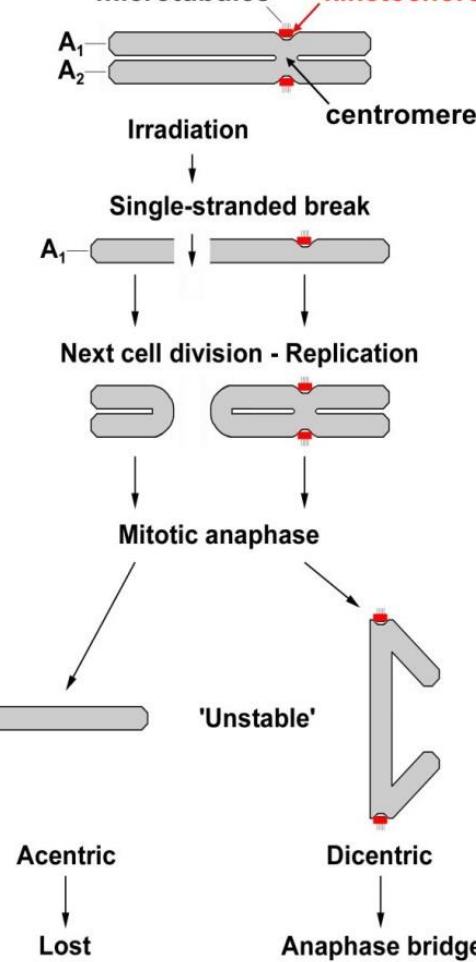
## Holocentric chromosomes

microtubules      kinetochore

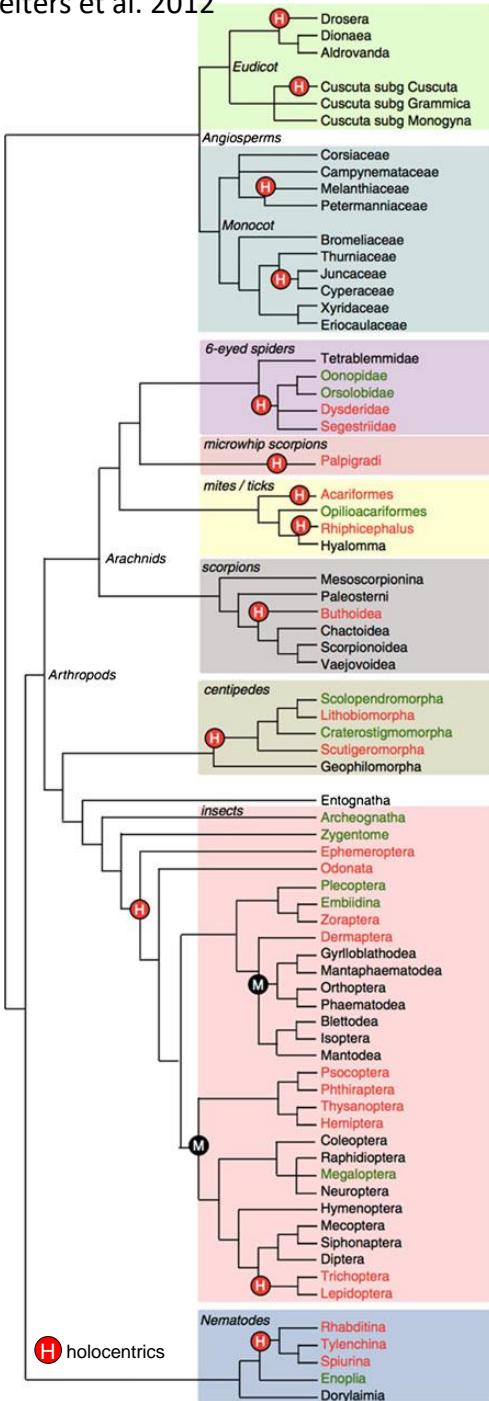


## Typical monocentric chromosomes

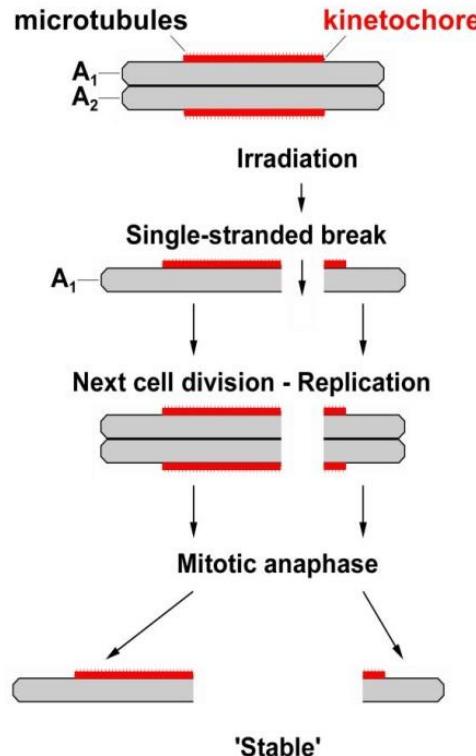
microtubules      kinetochore



Pseudoscorpion: *Olpium turcicum*: 2n = 7, X0



## Holocentric chromosomes

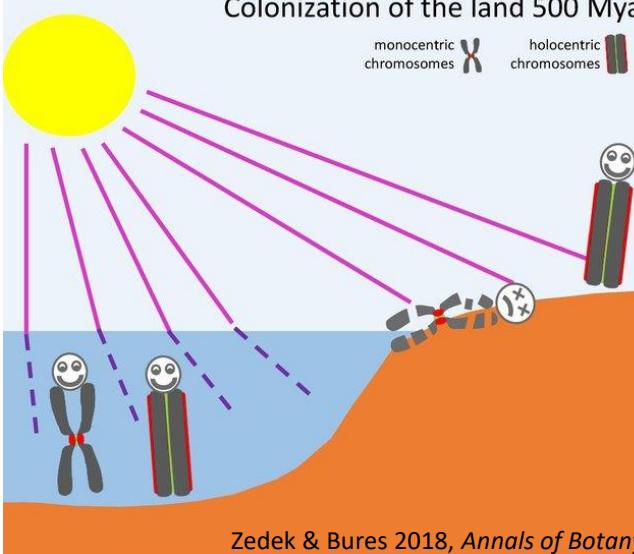


'Stable'

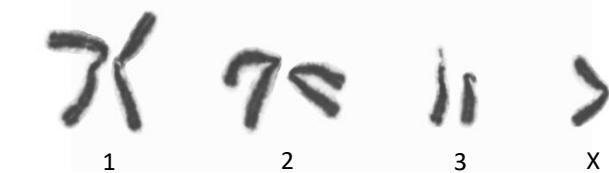
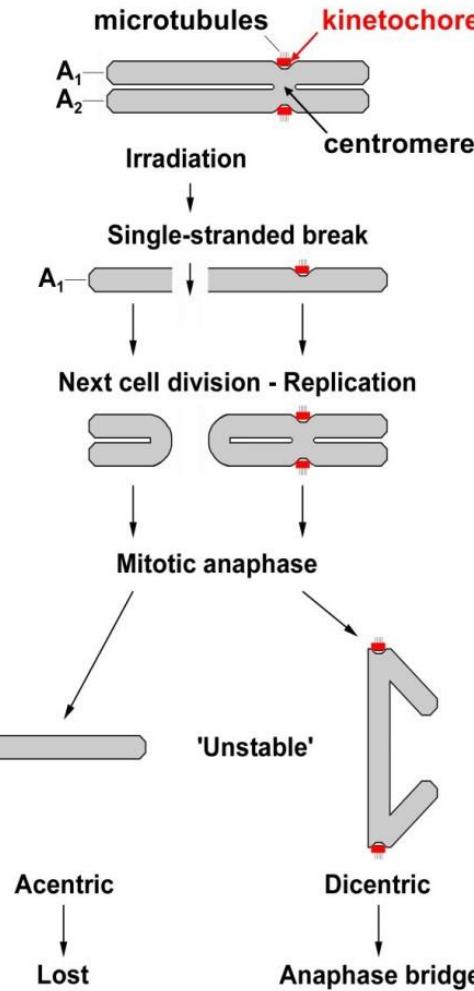
Colonization of the land 500 Mya

monocentric chromosomes

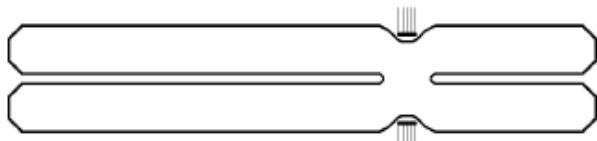
holocentric chromosomes



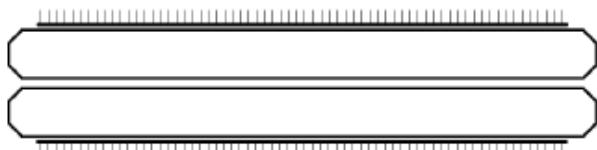
## Typical monocentric chromosomes



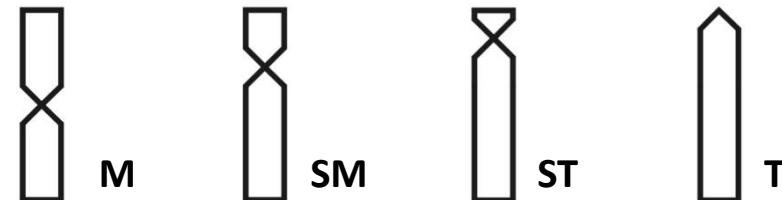
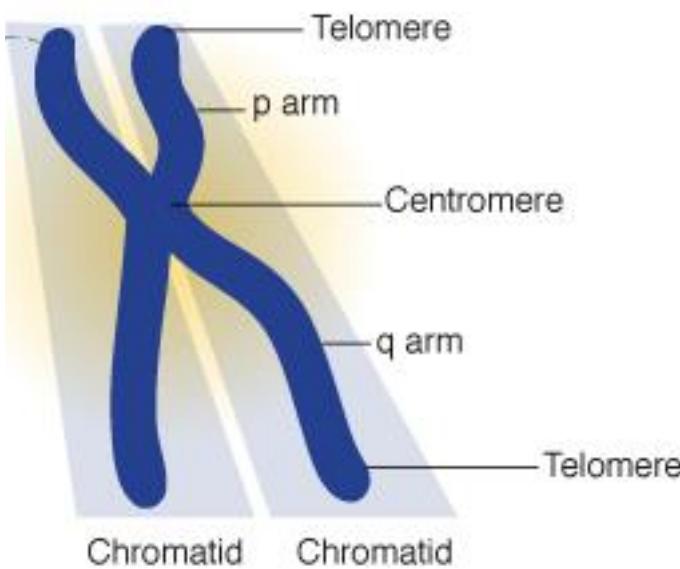
# Monocentric chromosomes



# Holocentric (holokinetic) chromosomes

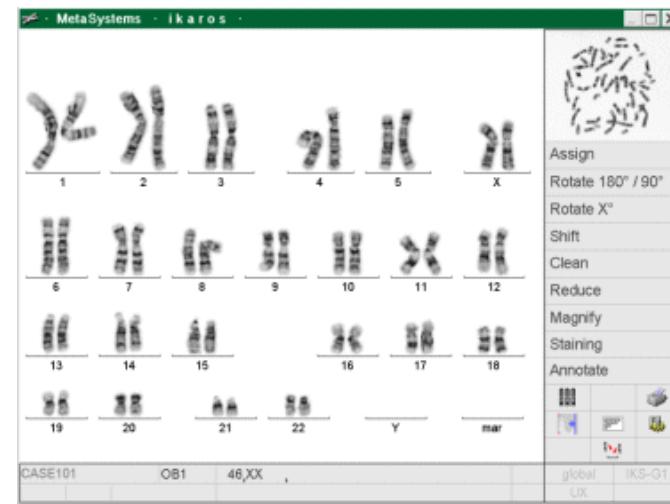


# Chromosome

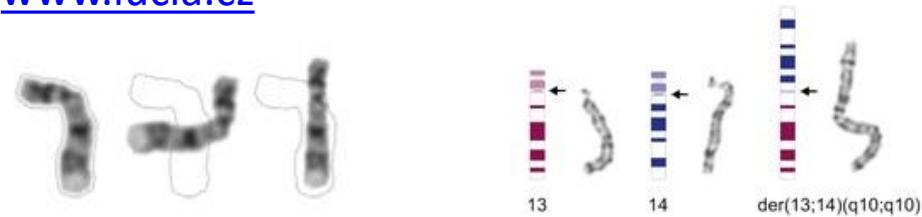


Arm Ratio	Levan et al. (1964)	Green & Sessions (1991)
1.0	<b>M (Metacentric)</b>	
$1.0 \leq x < 1.7$	<b>m (Metacentric)</b>	
$1.7 \leq x < 3.0$	<b>sm (Submetacentric)</b>	<b>sm (Submetacentric)</b>
$3.0 \leq x < 7.0$	<b>st (Subtelocentric)</b>	<b>st (Subtelocentric)</b>
$7.0 \leq x < \infty$	<b>t (Acrocentric)</b>	
$\infty$	<b>T (Telocentric)</b>	<b>t (Telocentric)</b>

[www.metasystems-international.com/ikaros](http://www.metasystems-international.com/ikaros)

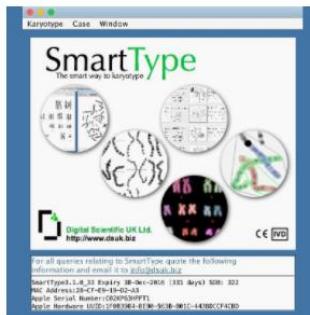


[www.lucia.cz](http://www.lucia.cz)



<https://karyotyper.com/>

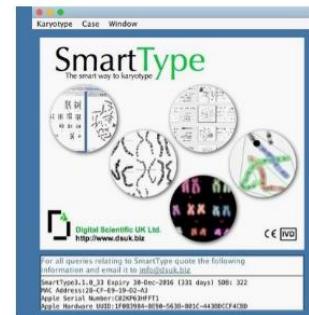
SERADIT PODLE ▾



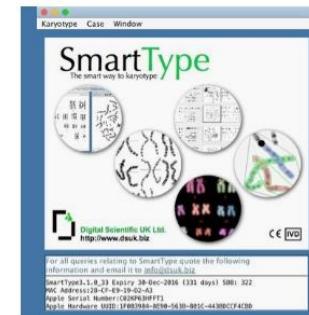
SmartType Single Seat 30 Day Licence  
£75.00



SmartType Single Seat Annual Licence  
£900.00



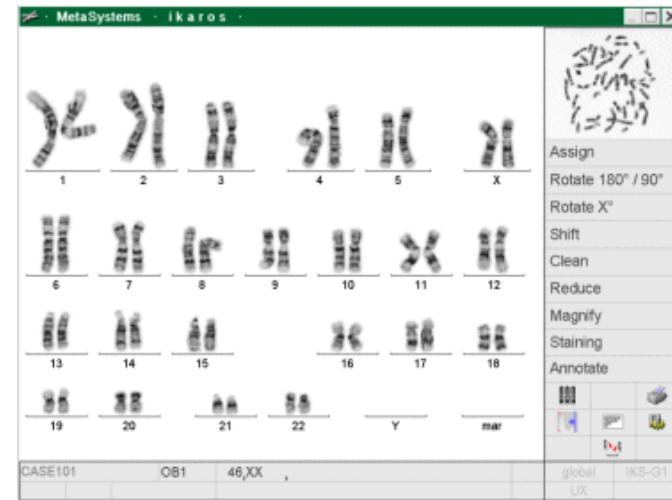
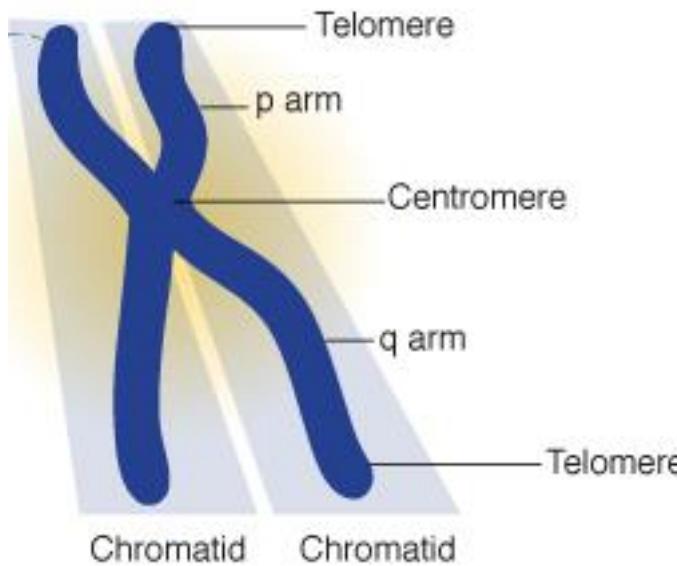
SmartType Classroom Annual Site  
Licence  
£500.00



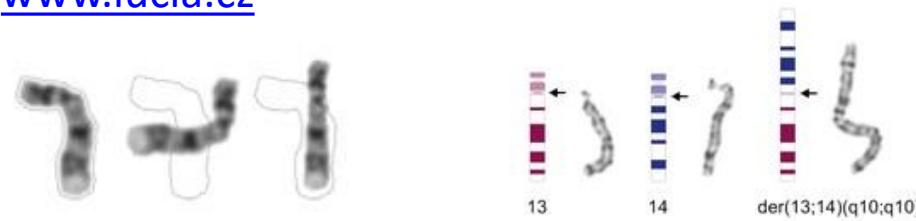
SmartType Single Seat Unlimited  
Licence  
£6,000.00

[www.metasystems-international.com/ikaros](http://www.metasystems-international.com/ikaros)

## Chromosome



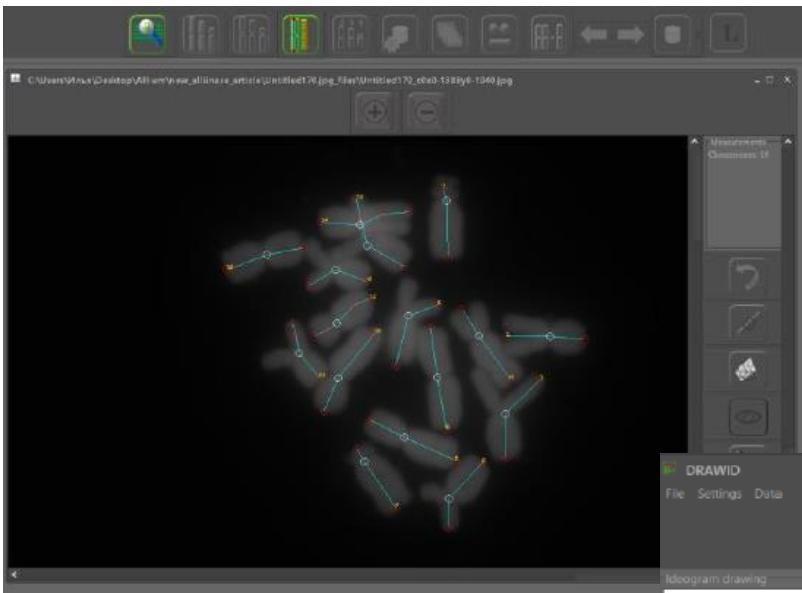
[www.lucia.cz](http://www.lucia.cz)



<http://imagej.nih.gov/ij/>

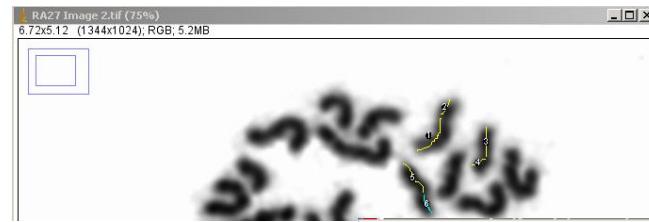
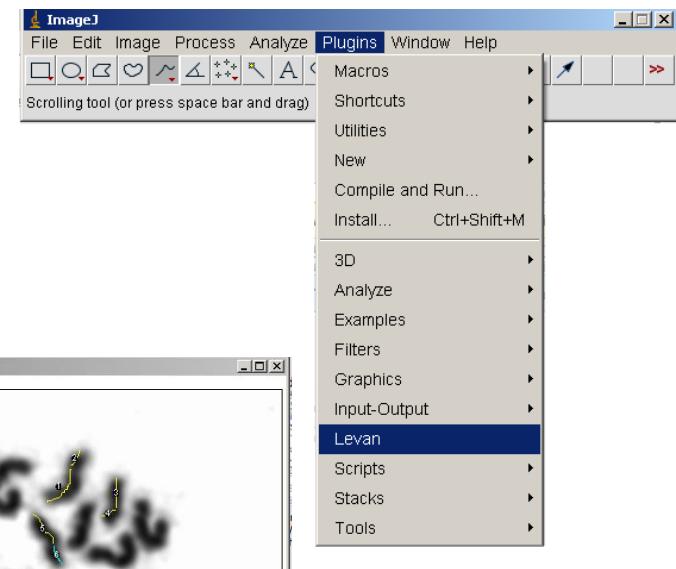
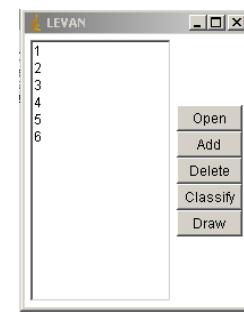
<http://rsb.info.nih.gov/ij/plugins/levan/levan.html>

<http://www.drawid.xyz>

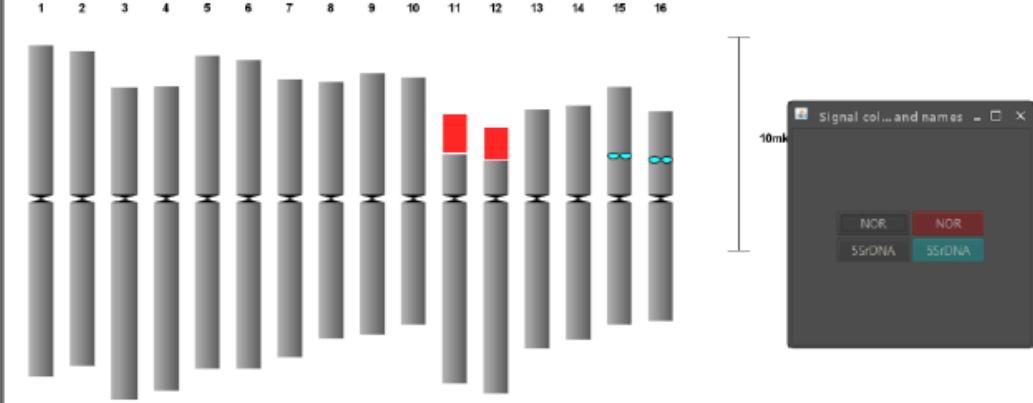
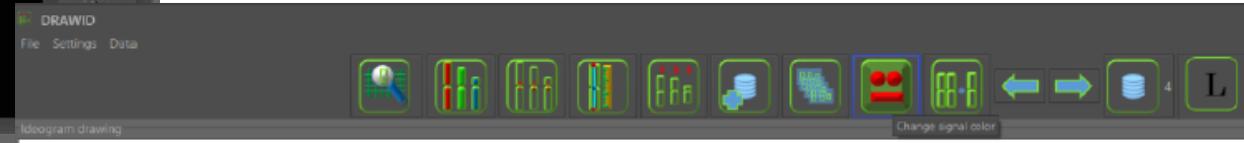


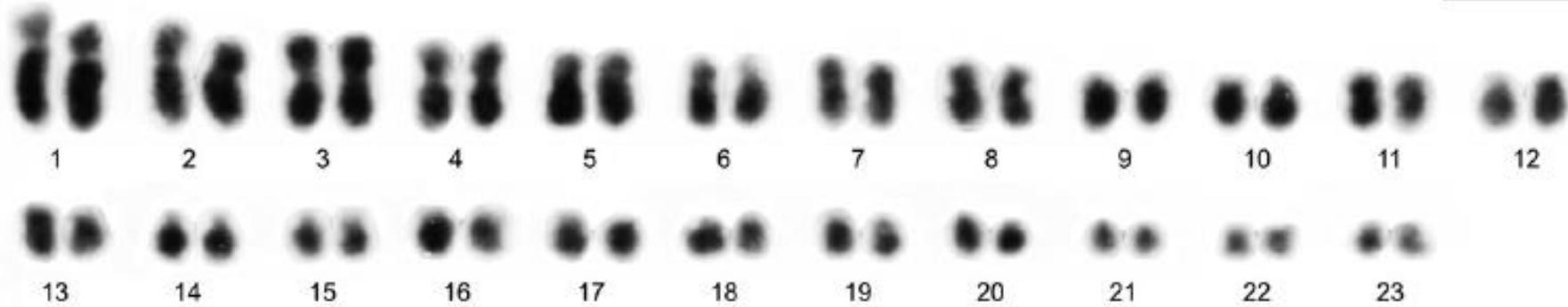
DRAWID V0.26

Make your karyotyping easier!

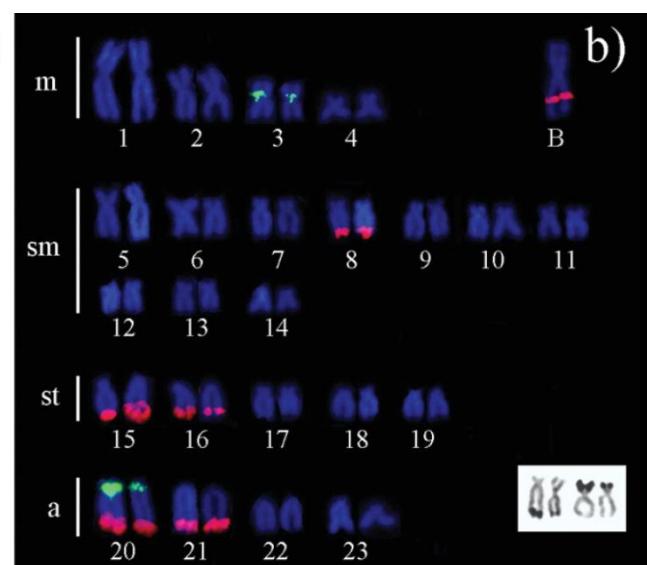
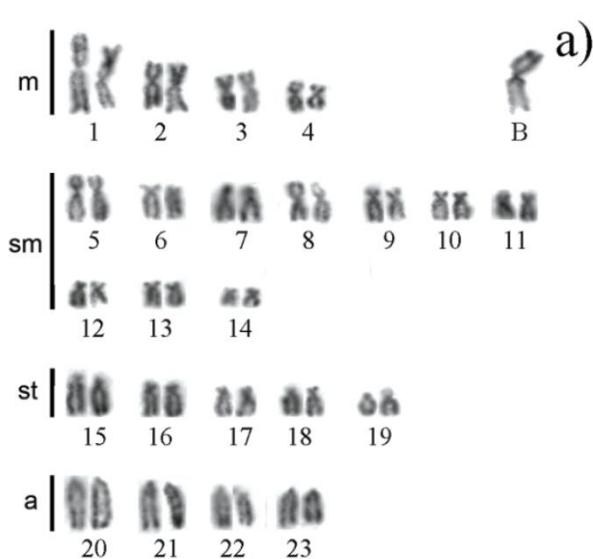


Results						
N	p	q	Total	A.R.	Morphology	
[2,1]	10,54	27,75	38,29	2,63	Submetacentric(sm)	
[6,5]	12,41	22,11	34,52	1,78	Submetacentric(sm)	
[4,3]	8,89	18,30	27,19	2,06	Submetacentric(sm)	

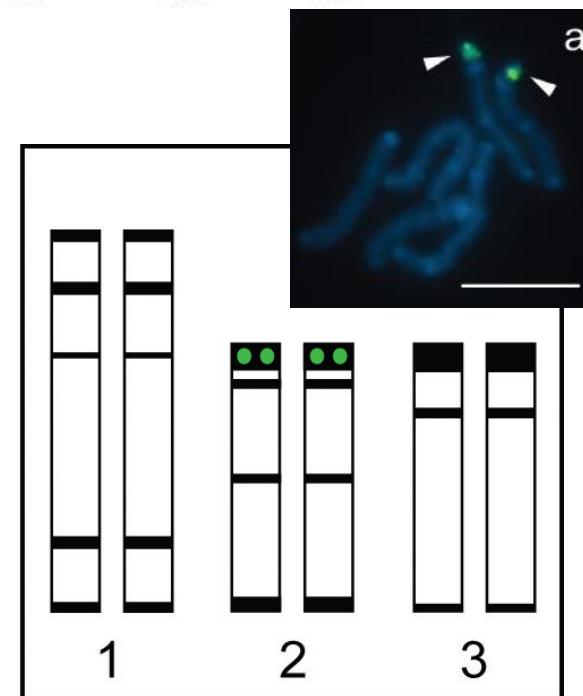




Karyogram of scorpion *Bothriurus rochensis*



Karyogram of *Astyanax fasciatus* deduced after conventional Giemsa staining and double FISH using 5S (green) and 18S rDNA (red) probes.



Idiogram (ideogram) of scorpion *Tityus trivittatus*

# number of chromosomes

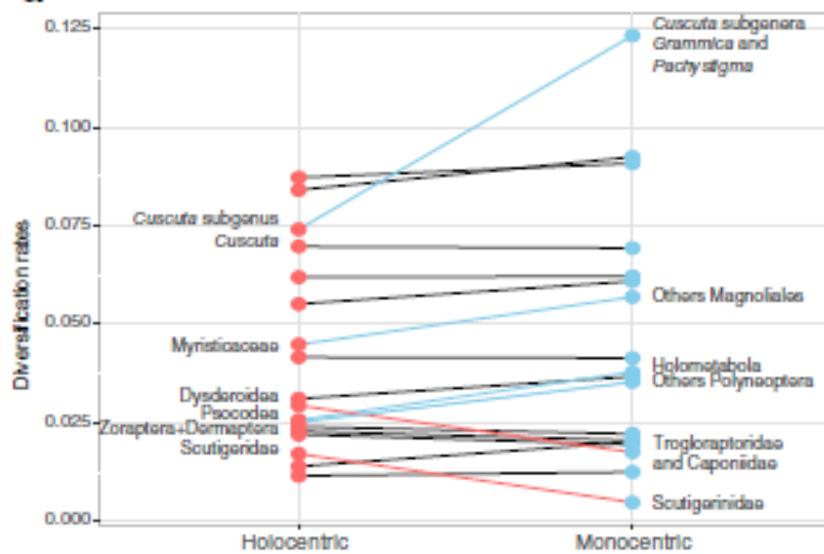
from  $2n=2$

*Parascaris univalens*,

ants *Myrmecia pilosula*, *M. croslandi*,  
(males  $n=1$ )

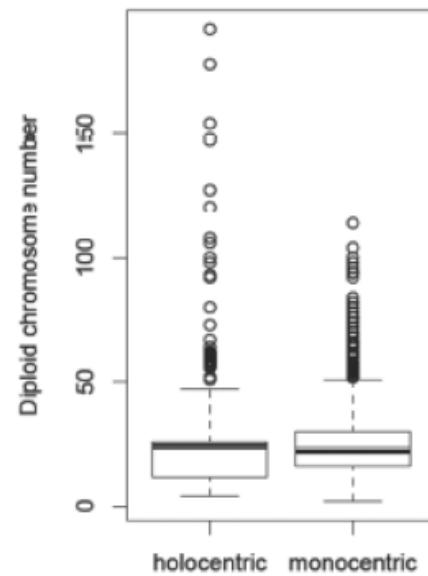
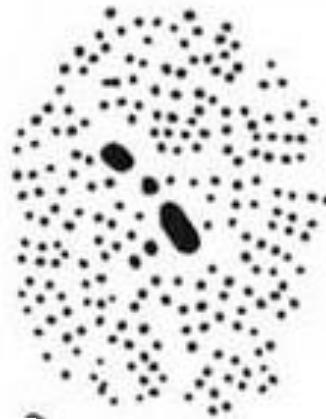


a



Márquez-Corro et al. 2018

to  $2n = 446$  *Plebicula atlantica*



# number of chromosomes

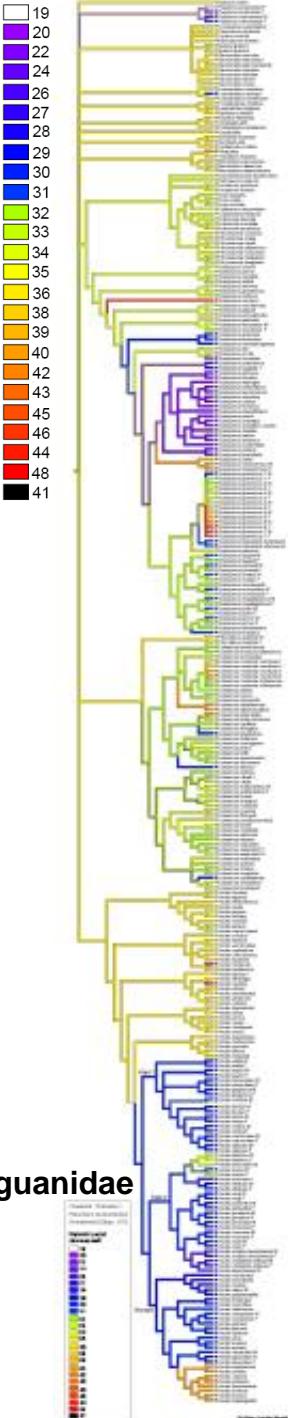
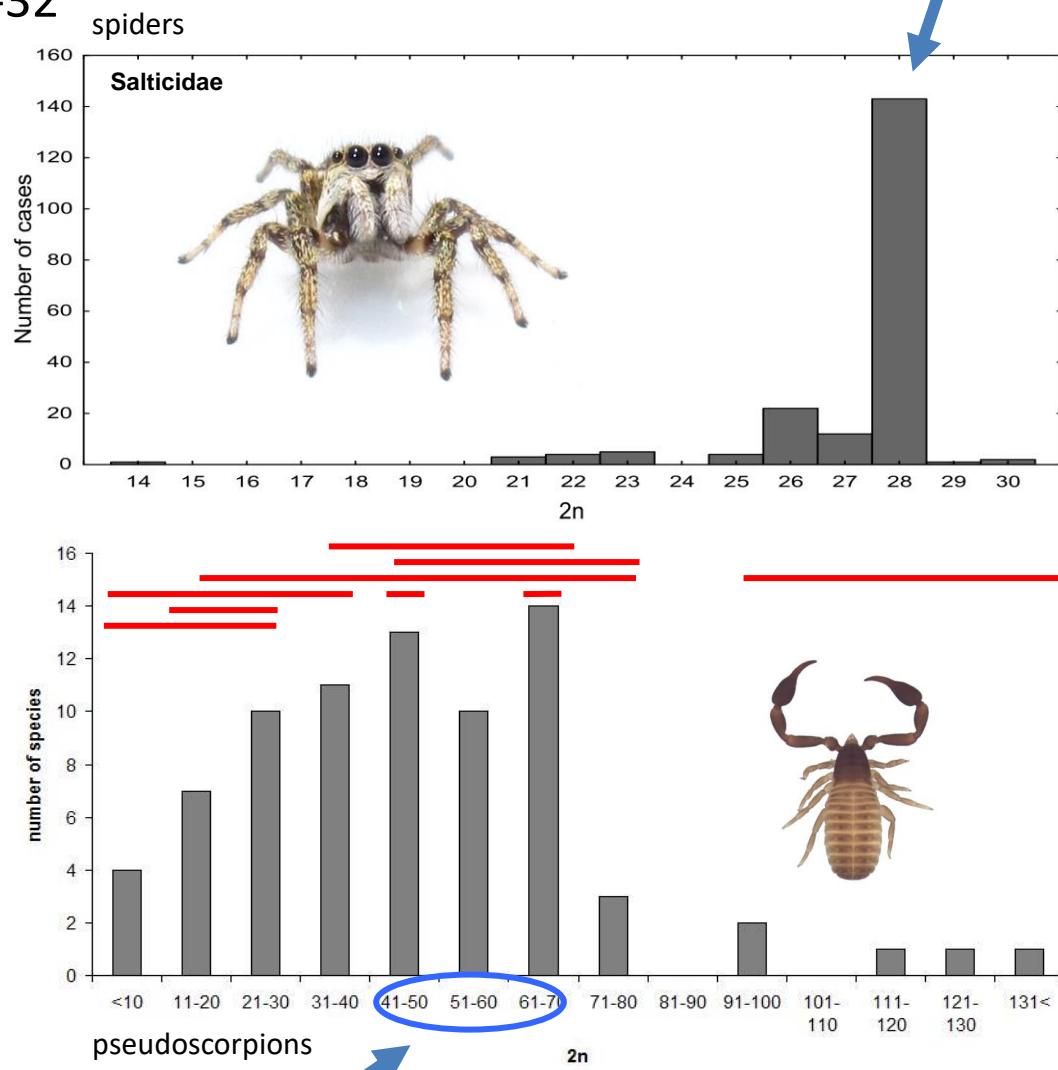
## Modal number of chromosomes

Odonata n=13

Lepidoptera n=28-32

birds n=39-42

Diptera n=2-10



Zima 2000	Palaearctic region		Europe	
	total species	studied species	total species	studied species
Insectivora	81	72 (88.9%)	39	38 (97.4%)
Chiroptera	73	57 (78.1%)	37	36 (97.3%)
Rodentia	299	240 (80.3%)	106	105 (99.1%)

Fish app. 30000 species  
- 1700 karyotyped

<http://coleoguy.github.io/karyotypes/>

Karyotype Data

Cytogenetic data is perhaps the most basic information about a genome (i.e., how many discrete chromosomes is the genome divided among, what type of sex chromosomes are present). Despite the fundamental nature of this data, many questions surrounding the evolution of genomes at this level remain unanswered. Furthermore, as we move into an era of ever more affordable sequencing, this is critical preliminary information that should be evaluated before sequencing and may even suggest particularly attractive targets for future sequencing efforts. Unfortunately, cytogenetic data is often scattered among many journals and often behind paywalls. For these reasons, we have built databases that make this data publicly available.

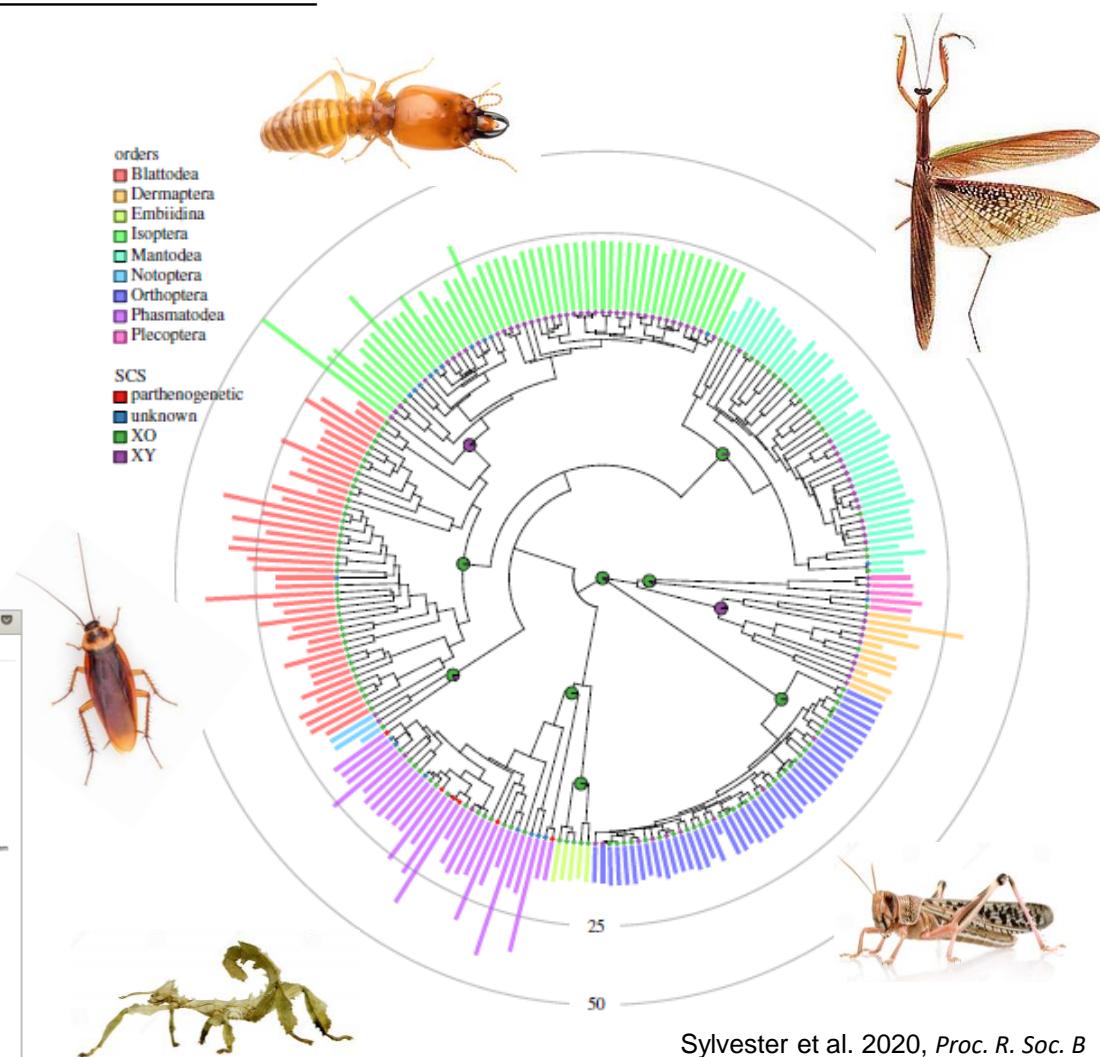
Amphibian Karyotype Database<sup>1</sup>  
2124 records

Coleoptera Karyotype Database<sup>2</sup>  
4960 records

Polyneoptera Database<sup>3</sup>  
823 records

Diptera Karyotype Database<sup>4</sup>  
3443 records

Drosophila Karyotype Database<sup>4</sup>  
1247 records



Zima 2000	Palaearctic region		Europe	
	total species	studied species	total species	studied species
Insectivora	81	72 (88.9%)	39	38 (97.4%)
Chiroptera	73	57 (78.1%)	37	36 (97.3%)
Rodentia	299	240 (80.3%)	106	105 (99.1%)

Fish app. 30000 species  
- 1700 karyotyped

## Arachnids Karyotypes

<https://arthropodacytogenetics.bio.br/>

← → ⌂ Nezabezpečeno | arthropodacytogenetics.bio.br/scorpionsdatabase/families.html ☆ \* ⏪ ⏩ :

### The scorpion cytogenetic database

Current version: 10.0 (Aug 09, 2021)

Marielle Cristina Schneider, Viviane Fagundes Mattos and Doralice Maria Cella

[Introduction](#) [Families](#) [Bibliography](#)  
[Arthropoda Cytogenetics Group](#) [Spider Database](#) [Scorpion Database](#) [Pseudoscorpion Database](#) [Harvestmen Database](#) [Blattodea Database](#) [Chromosomal Analyses](#)

#### Families

Family	Genera	Species
1. <a href="#">Bothriuridae</a>	3	10
2. <a href="#">Buthidae</a>	38	159
3. <a href="#">Chactidae</a>	1	1
4. <a href="#">Chaerilidae</a>	1	10
5. <a href="#">Euscorpiidae</a>	2	16
6. <a href="#">Iuridae</a>	1	1
7. <a href="#">Liocheilidae</a>	3	17
8. <a href="#">Scorpionidae</a>	5	15
9. <a href="#">Scorpiopidae</a>	4	32
10. <a href="#">Urodacidae</a>	1	6
11. <a href="#">Vaejovidae</a>	1	1
<b>Total</b>	<b>60</b>	<b>258</b>

[Introduction](#) [Families](#) [Bibliography](#)  
[Arthropoda Cytogenetics Group](#) [Spider Database](#) [Scorpion Database](#) [Pseudoscorpion Database](#) [Harvestmen Database](#) [Blattodea Database](#) [Chromosomal Analyses](#)

← → ⌂ Nezabezpečeno | arthropodacytogenetics.bio.br/scorpionsdatabase/Bothriuridae.php ☆ \* ⏪ ⏩ :

### The scorpion cytogenetic database

Current version: 10.0 (Aug 09, 2021)

Marielle Cristina Schneider, Viviane Fagundes Mattos and Doralice Maria Cella

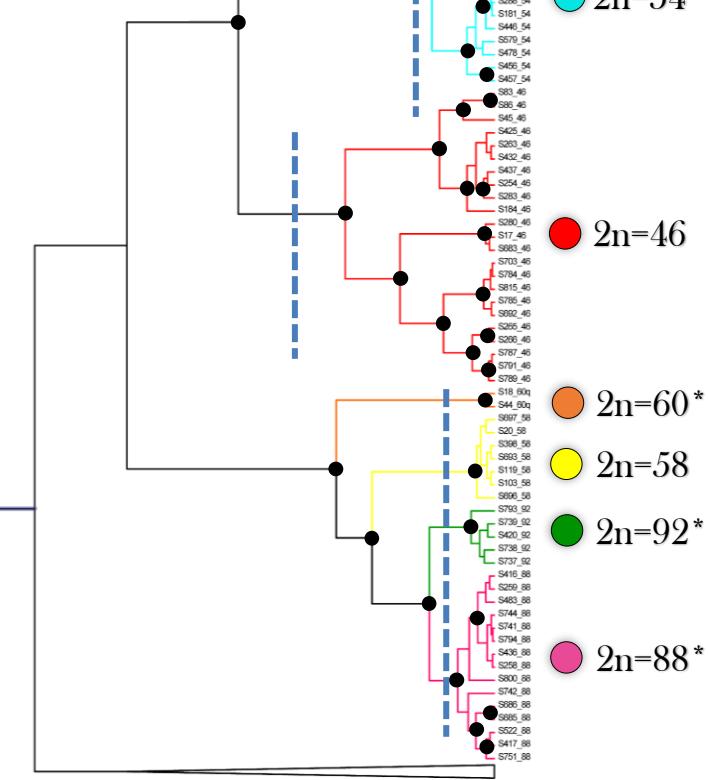
[Introduction](#) [Families](#) [Bibliography](#)  
[Arthropoda Cytogenetics Group](#) [Spider Database](#) [Scorpion Database](#) [Pseudoscorpion Database](#) [Harvestmen Database](#) [Blattodea Database](#) [Chromosomal Analyses](#)

Bothriuridae Simon, 1880

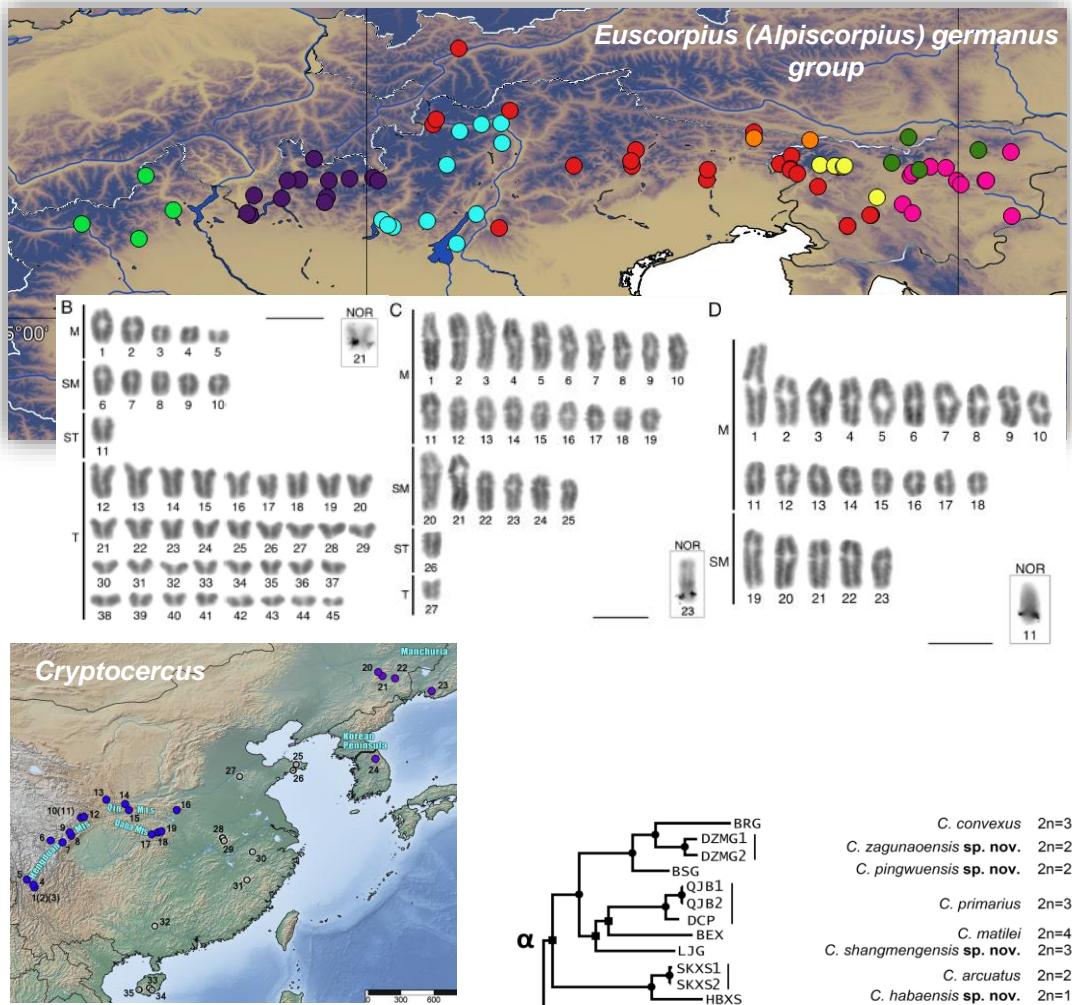
Cited as = species name adopted by the researcher that performed the cytogenetic analysis; 2n = diploid number of males and in parenthesis, diploid number of females; M = metacentric; SM = submetacentric; ST = subtelocentric; A = acrocentric; T = telocentric; ? = dubious description.

Valid name	Cited as	2n	Chromosomal morphology	Collection site	Bibliography
<i>Bothriurus araguaya</i> (Vellard, 1934)	<i>Bothriurus asper araguaiiae</i>	44	---	Brazil	<a href="#">Ferreira_1958</a>
<i>B. araguaya</i> (Vellard, 1934)		42	32ST+8SM+2MT	Brazil	<a href="#">Schneider et al., 2009a</a>
<i>Bothriurus flavidus</i> (Kraepelin 1911)		48	---	Argentina	<a href="#">Giacomozzi, 1977 apud Rodriguez-Gil et al., 2009</a>
<i>Bothriurus prospicus</i> (Mello-Leitão 1934)		50	---	Argentina	<a href="#">Giacomozzi, 1977 apud Rodriguez-Gil et al., 2009</a>
<i>Bothriurus rochensis</i> (San Martín, 1965)		46	16ST+16SM+14MT	Brazil	<a href="#">Schneider et al., 2009a</a>
<i>Bothriurus sp.</i>		36	M?	Brazil	<a href="#">Piza_1947a</a>
<i>Brachistosternus alienus</i> (Lönnberg, 1898)		28	---	Argentina	<a href="#">Giacomozzi, 1977 apud Rodriguez-Gil et al., 2009</a>
<i>B. alienus</i> (Lönnberg, 1898)		46	---	Argentina	<a href="#">Adílardi et al., 2013</a>
<i>Brachistosternus ferrugineus</i> (Thorell, 1876)		46	MT+SM+A	Argentina	<a href="#">Rodriguez-Gil et al., 2009</a>
<i>Brachistosternus montanus</i> (Roig Alcina, 1977)		46	MT+SM+A	Argentina	<a href="#">Rodriguez-Gil et al., 2009</a>
<i>Brachistosternus pentheri</i> (Mello-Leitão, 1931)		46, 42	---	Argentina	<a href="#">Rodriguez-Gil et al., 2009</a>

# Scorpiones



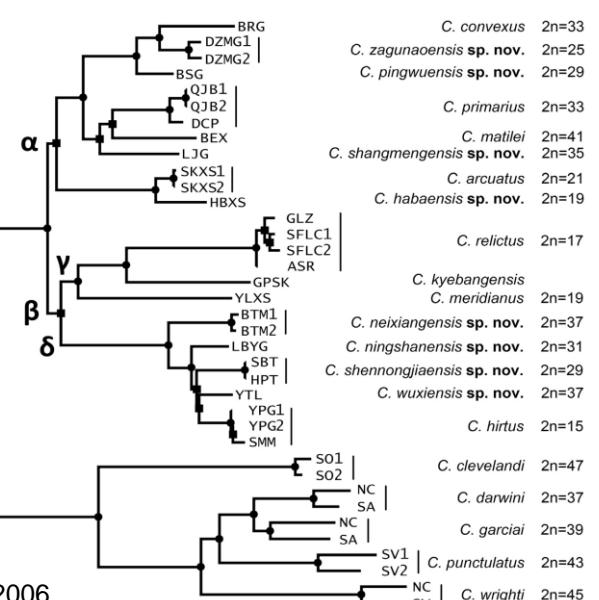
Štundlová et al. 2019



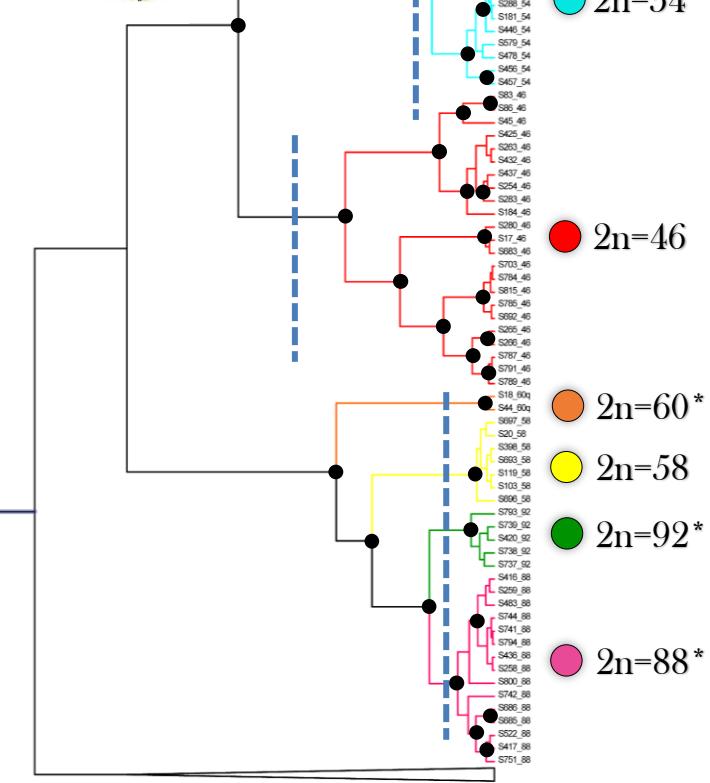
## Cryptocercus



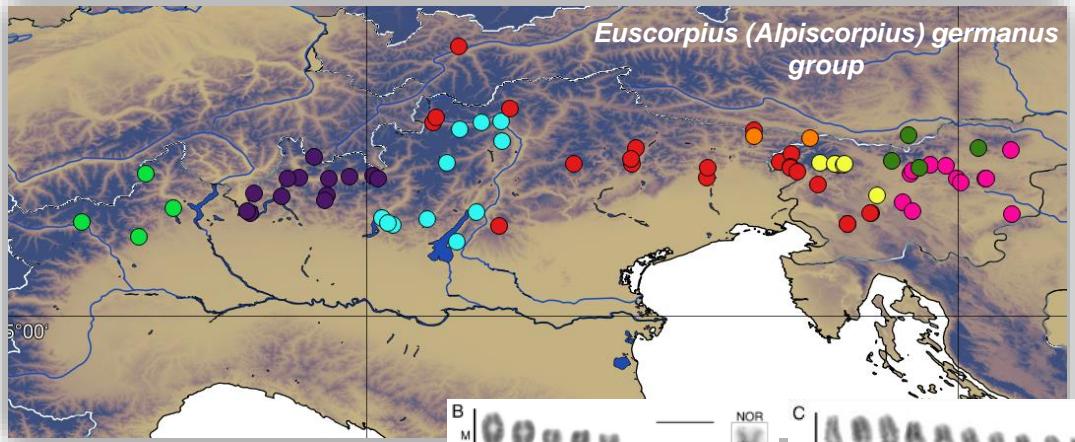
Che et al. 2006



# Scorpiones

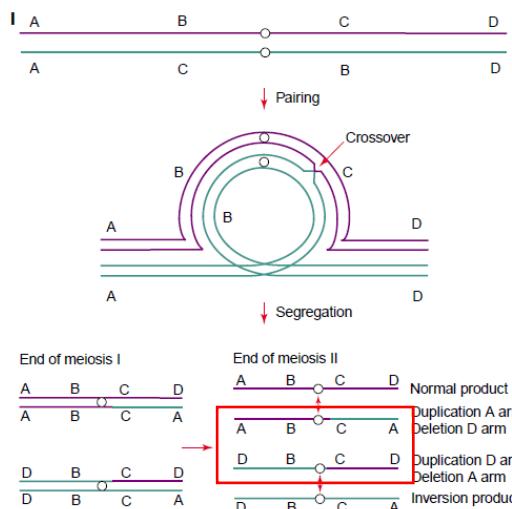
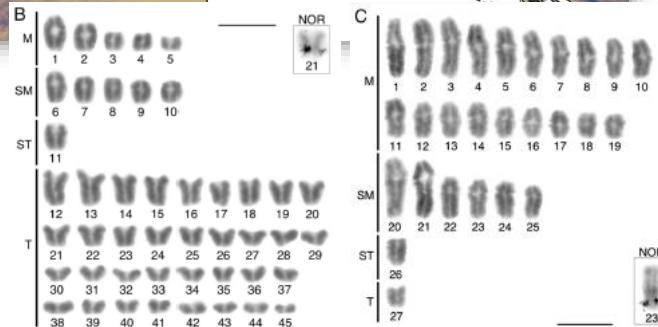


Štundlová et al. 2019

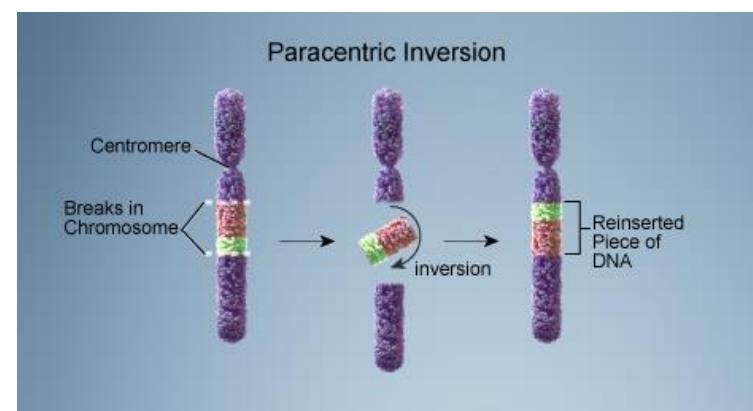
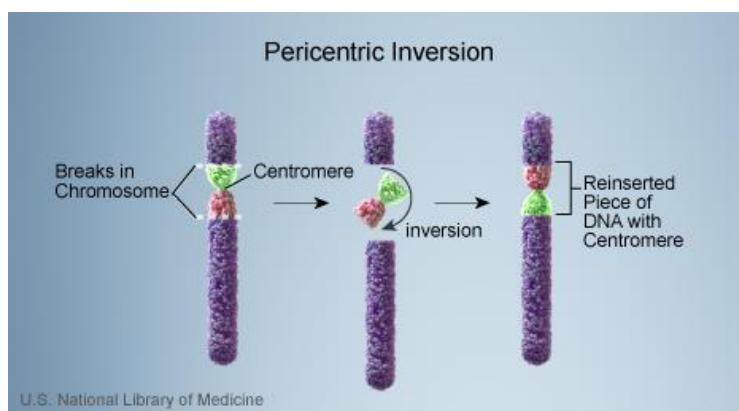
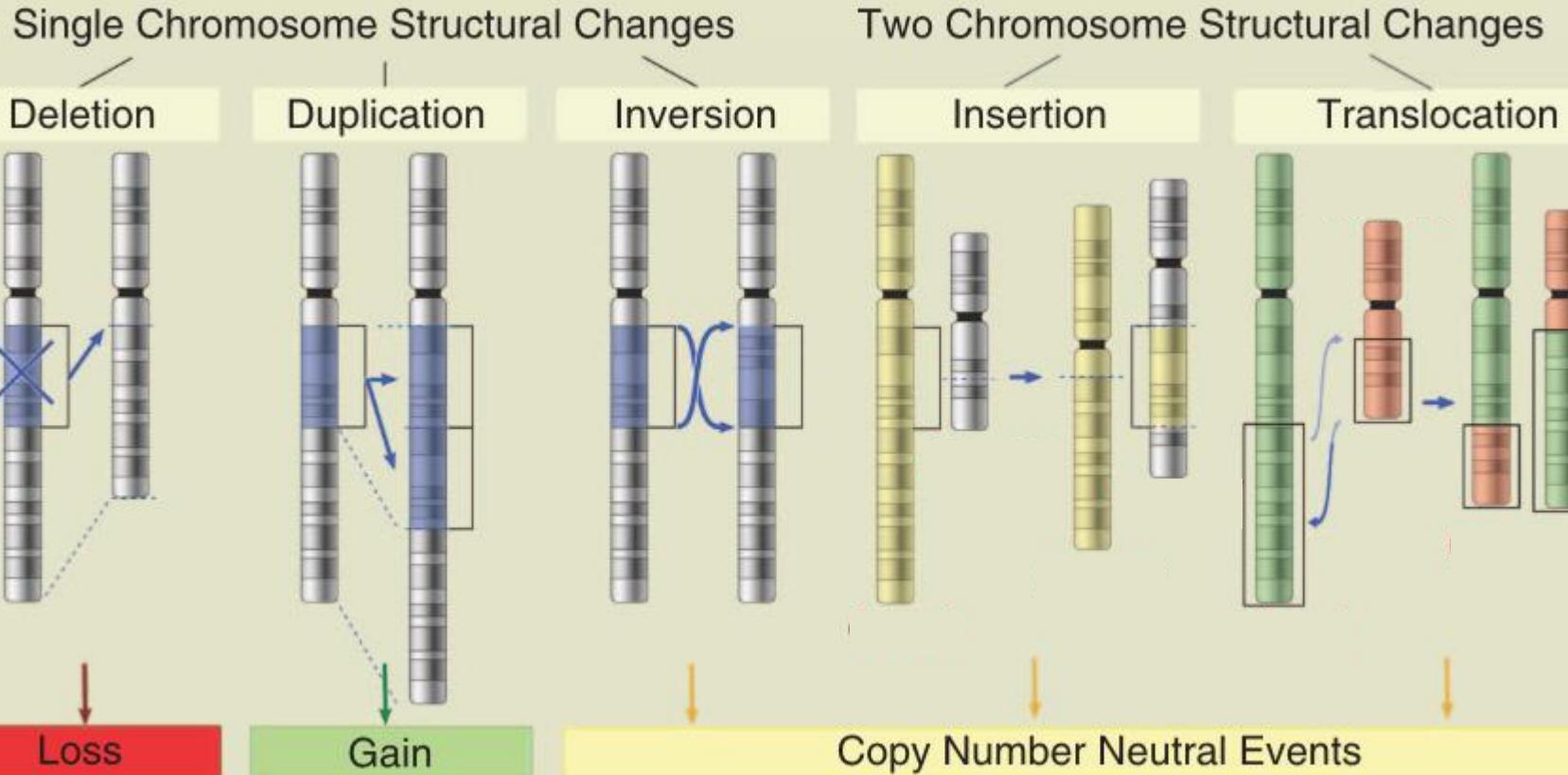


## chromosome speciation ?

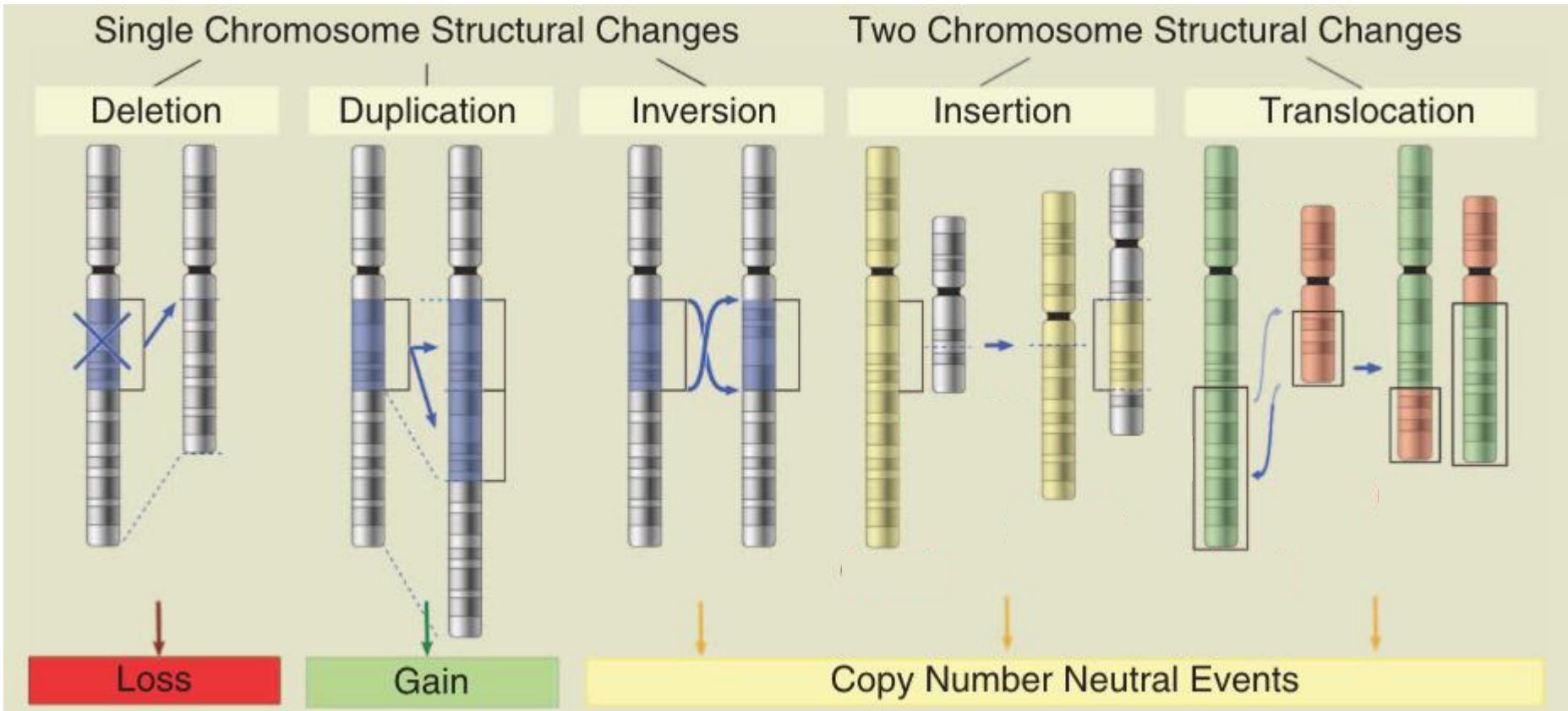
*"hybrid-sterility model"*  
predicted that the karyotypic  
hybrids generate unbalanced  
gametes and thus reduce fertility.



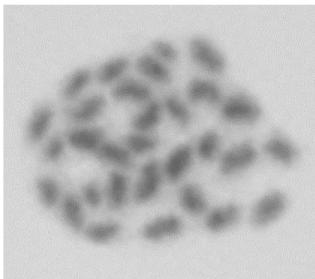
# types of chromosomal rearrangements



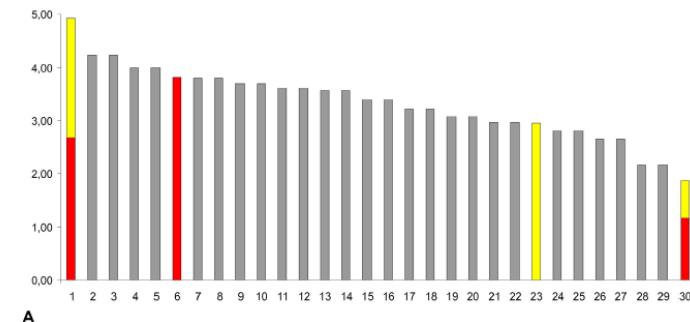
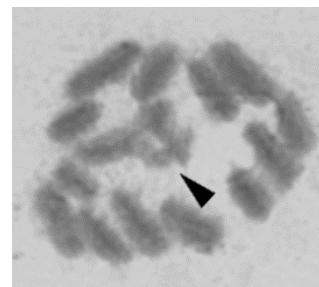
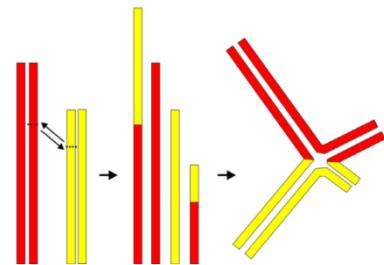
# types of chromosomal rearrangements



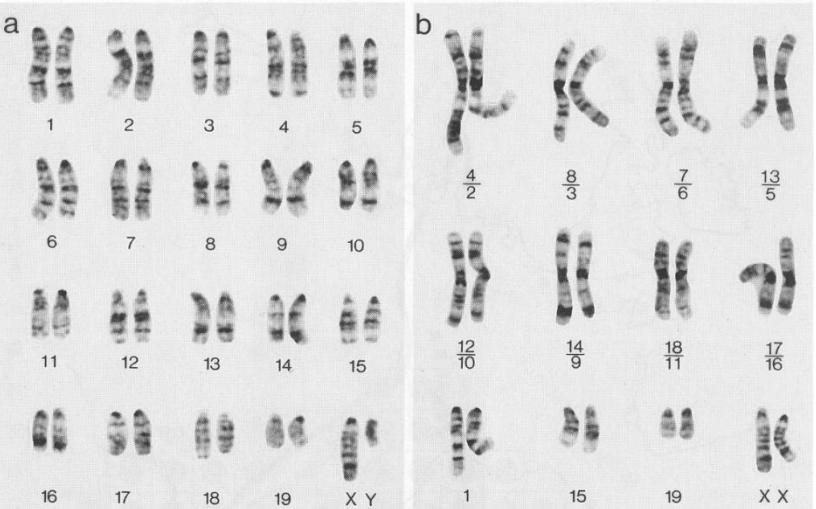
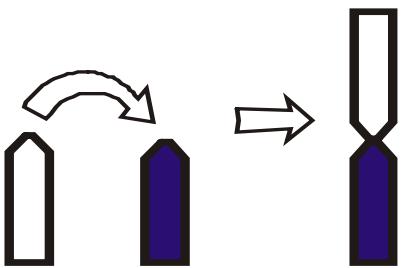
Mitotic metaphase



Meiotic pachytene

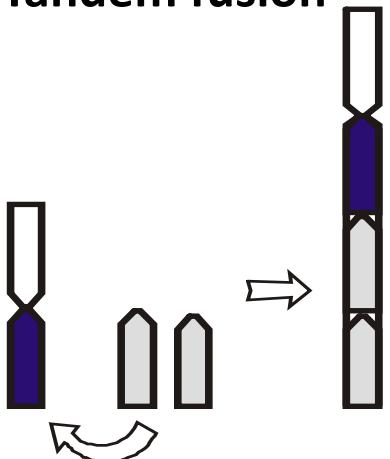


# Centric fusions - Robertsonian translocations or fissions

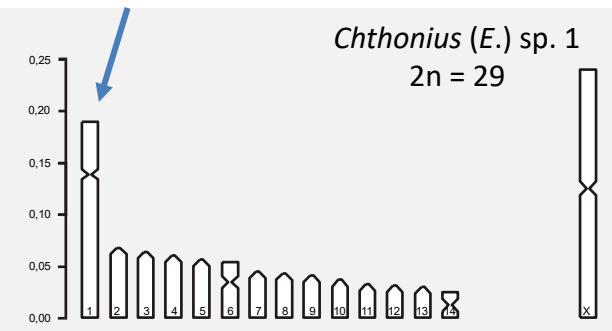
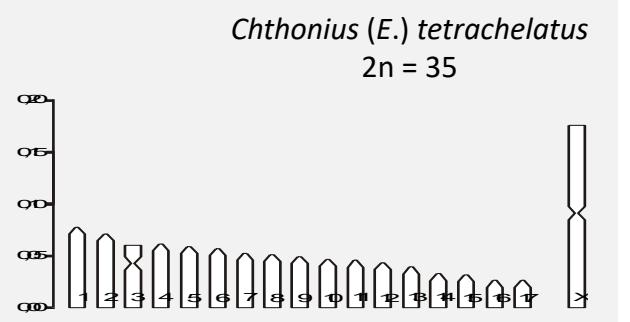


Species	Common name	2n	NF
<i>Salmoninae (cont.)</i>			
<i>Salvelinus confluentus</i>	Bull trout	78	100
<i>fontinalis</i>	Brook trout	84	100
<i>namaycush</i>	Lake trout	84	100
<i>leucomelas</i>	Potted char	84	100
<i>pluvius</i>	Japanese char	84–86	100
<i>alpinus/malma</i> complex	Dolly Varden char	82	98
<i>albus</i>	White char	78–80	98
<i>alpinus</i>	Arctic char	78	98
<i>elgysticus</i>	Small mouthed char	76–78	98
<i>boganiidae</i>	Boganiid char	76–78	98
<i>kronicus</i>	Stone char	78–82	100
<i>taranietsi</i>	Eastern Arctic char	76–78	98–100
<i>levanidovi</i>	Levanidovi char	78–80	98
<i>malma</i>			
<i>lordi</i>	Dolly Varden char	78	98
<i>m. malma</i>	Dolly Varden char	82	98
<i>m. kraschennkovi</i>	Dolly Varden char	82	98
<i>Salvethymus svetovidovi</i>	Longfinned char	56	98

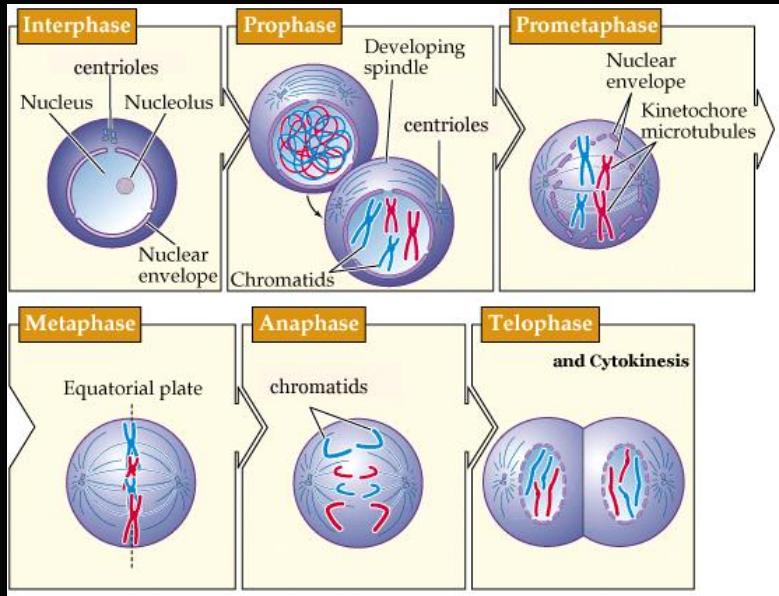
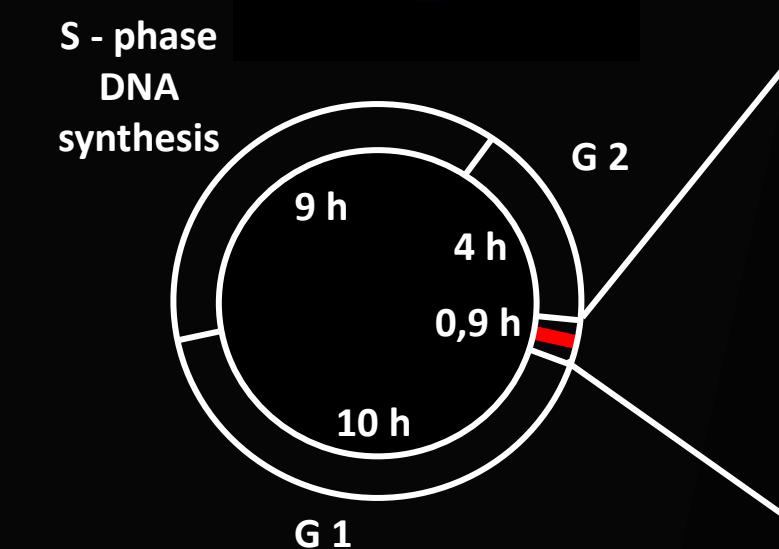
## Tandem fusion



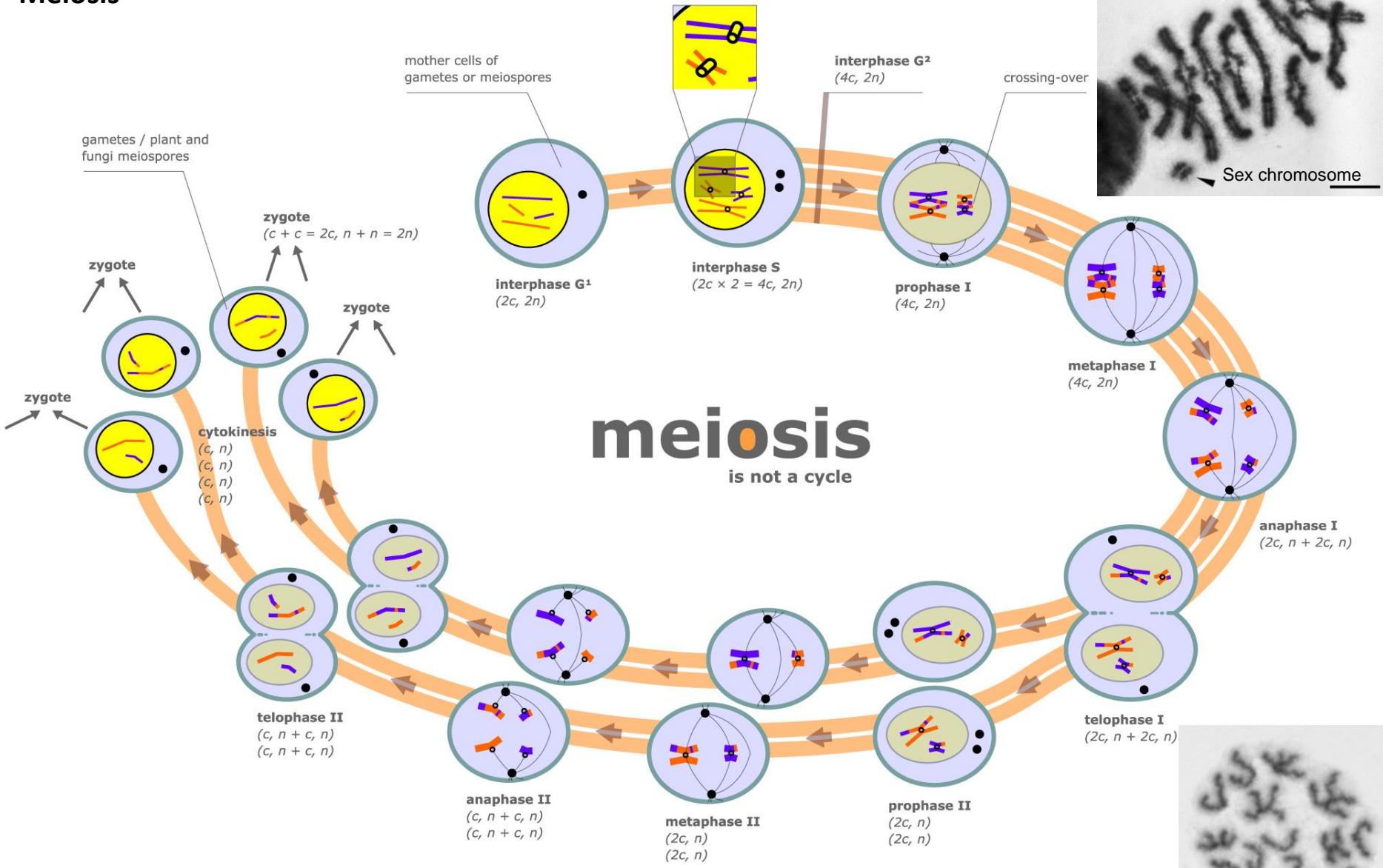
pseudoscorpions



# Mitosis



# Meiosis



# Cytogenetic techniques

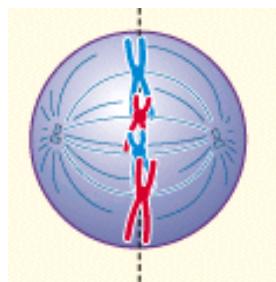
## The most important – good quality of chromosome preparation

### - Dividing cells

bone marrow, blood, amniotic fluid, cord blood, tumor, and tissues (including skin, umbilical cord, chorionic villi, liver, and many other organs)

In invertebrates very often salivary gland, embryo, testis

A mitotic inhibitor (**colchicine**, colcemid) is added to the culture. This stops cell division at mitosis which allows an increased yield of mitotic cells for analysis.



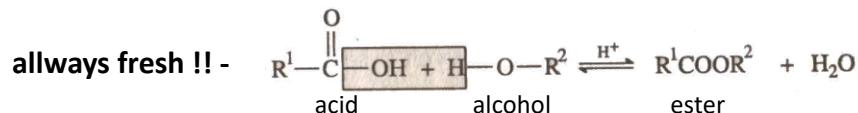
### - Hypotonic solution

Potassium chloride (KCl), Citric acid ( $\text{Na}_3\text{C}_6\text{H}_5\text{O}_7$ )

### - Fixation

methanol (or ethanol) : glacial acetic acid (3:1)

Carnoy's fixative - ethanol : chloroform : glacial acetic acid (6:3:1)



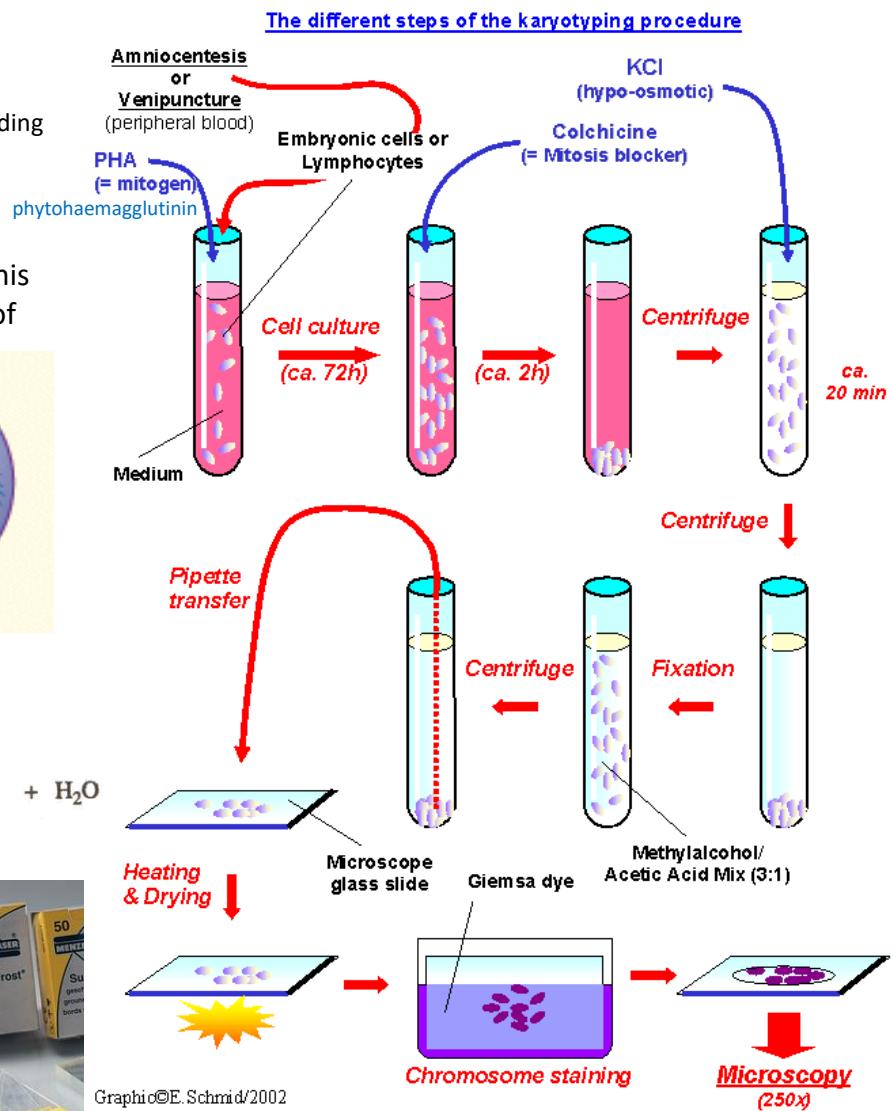
### - Spreading

(good quality of microscope slides !!)

- „dropping“
- „squashing“
- „plate spreading“



Graphic © E. Schmid/2002



# Conventional staining – homogeneous staining

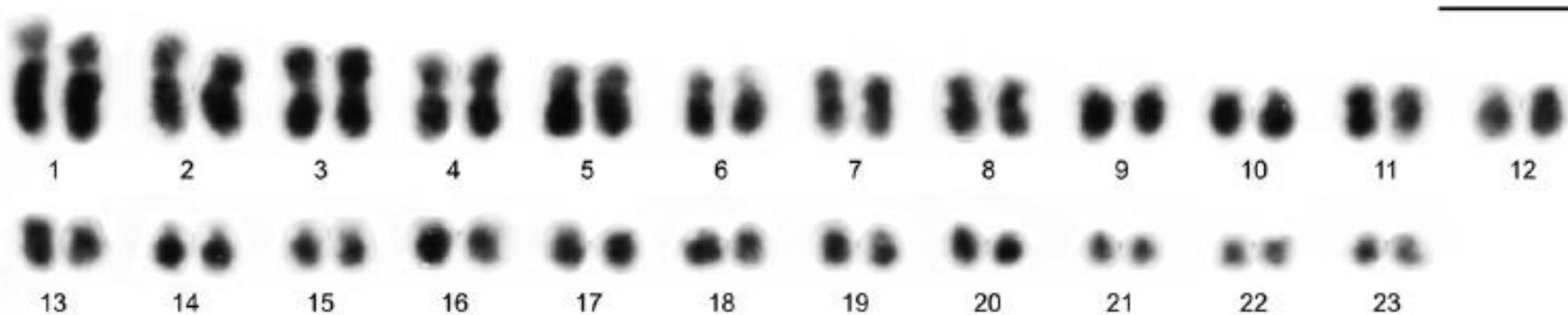
Giemsa

Haematoxylin

Acid-Schiff staining

Carbol fuchsin

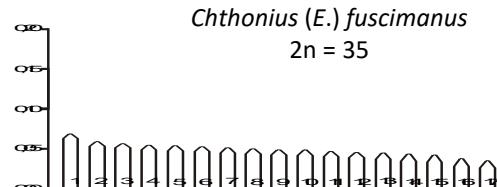
Number, morphology and size of chromosomes



Scorpion: *Bothriurus rochensis*



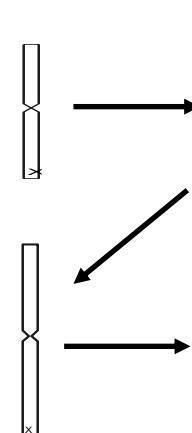
pseudoscorpions:



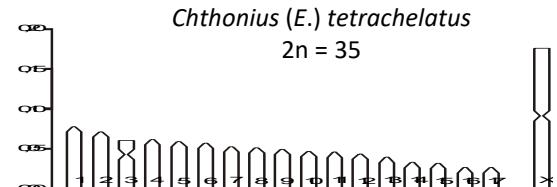
*Chthonius (E.) fuscimanus*  
 $2n = 35$



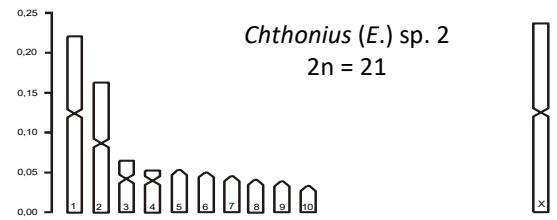
*Chthonius (E.) sp. 1*  
 $2n = 29$



*Chthonius (E.) tetrachelatus*  
 $2n = 35$



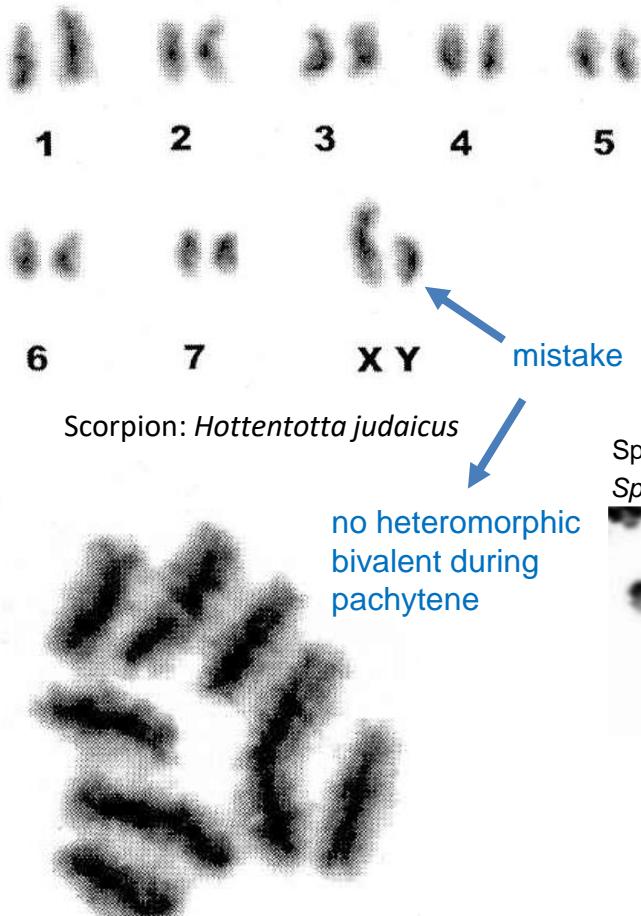
*Chthonius (E.) sp. 2*  
 $2n = 21$



# Conventional staining – homogeneous staining

Giemsa

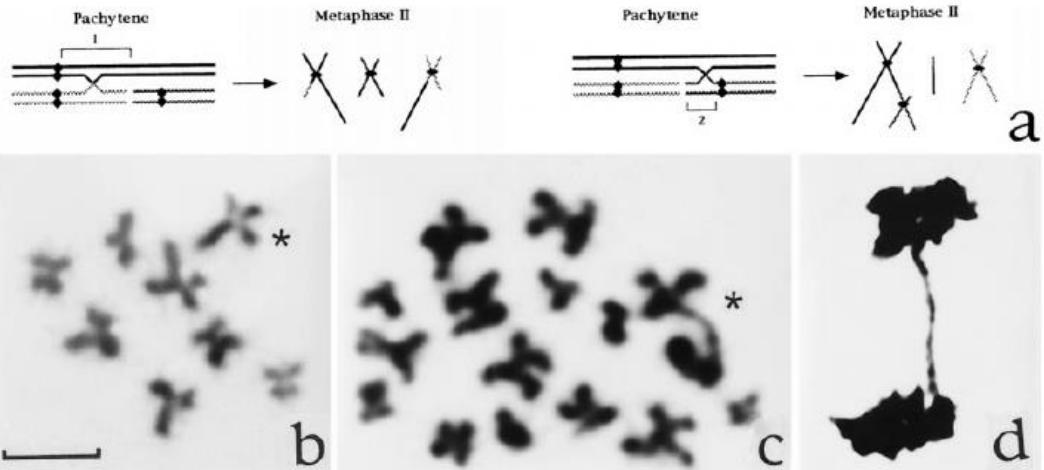
sex chromosomes, rearrangements



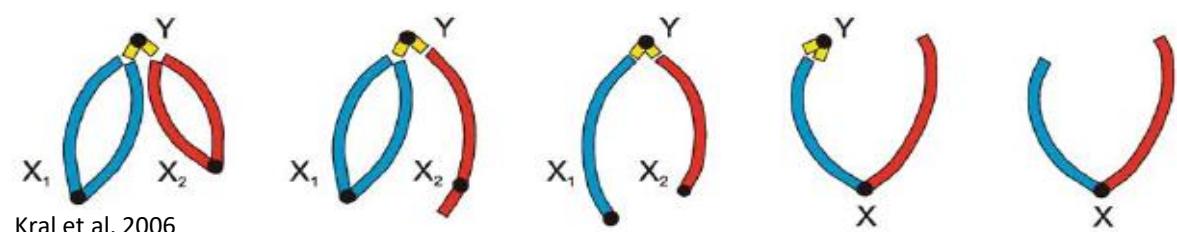
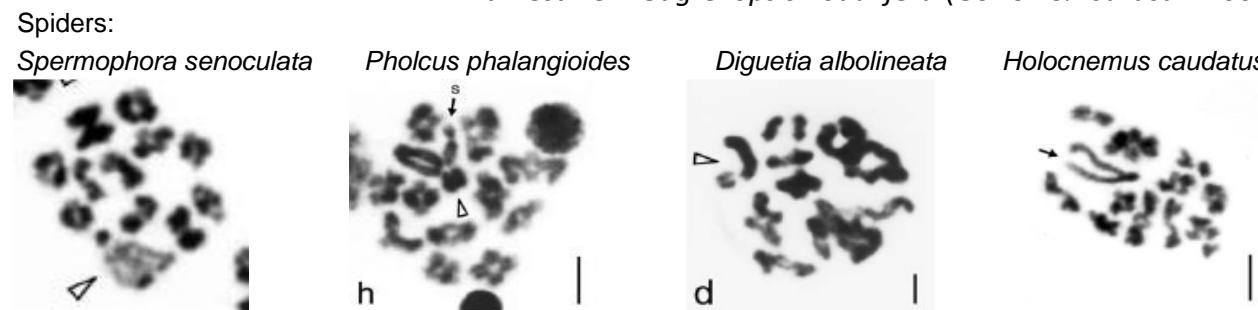
Scorpion: *Hottentotta judeaicus*

no heteromorphic bivalent during pachytene

Qumsiyeh et al. 2013



Harvestmen: *Gagrellopsis nodulifera* (Gorlov & Tsurusaki 2000)

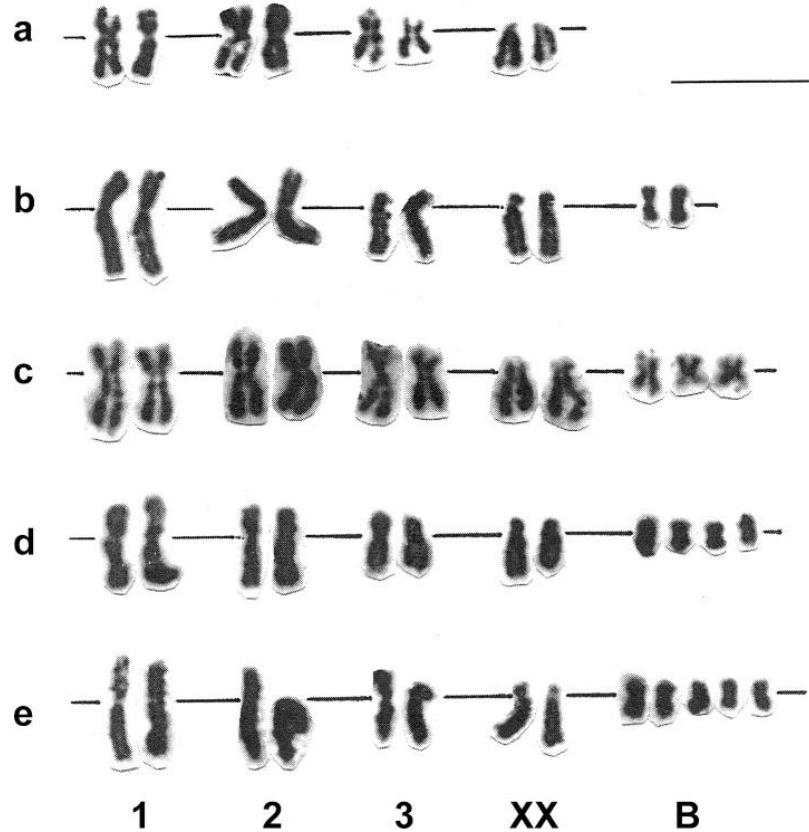


Kral et al. 2006

# Conventional staining – homogeneous staining

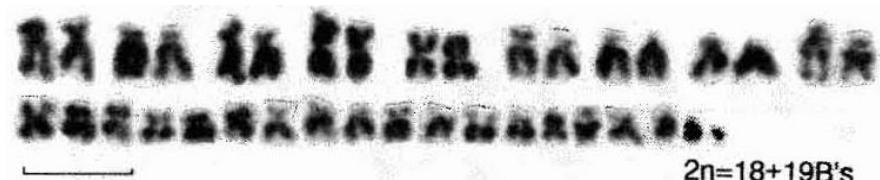
Giemsa

B chromosomes



*Acanthocephalus lucii*. Chromosome sets of 5 female individuals.

(a)  $2n = 6 + XX$ ; (b–e)  $2n = 6 + XX + 2-5B$  (Špakulová et al. 2002)



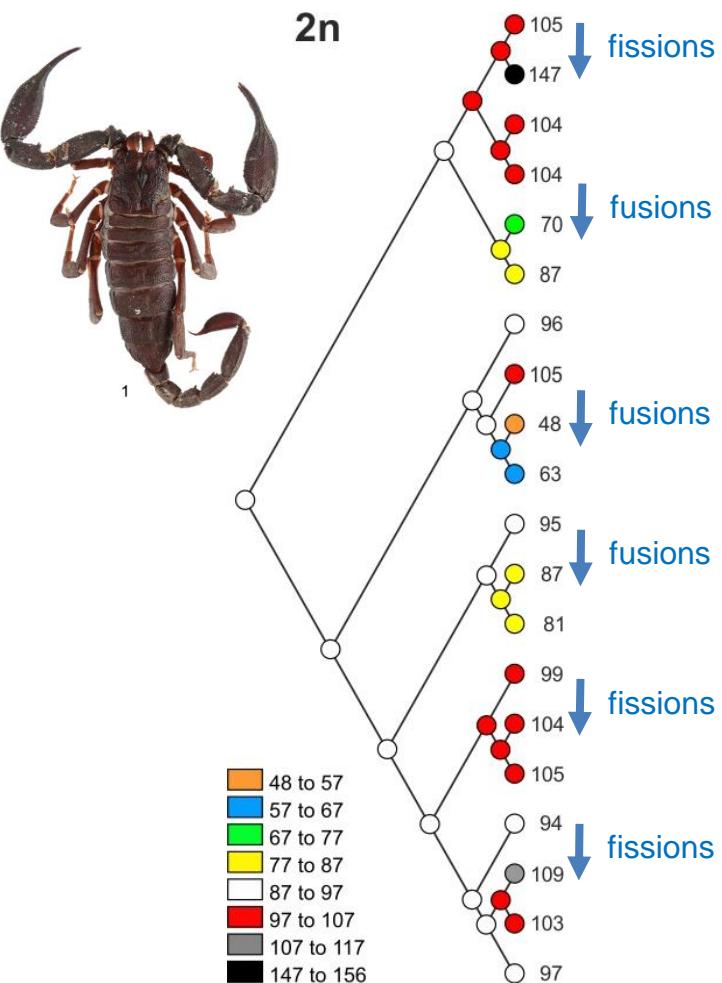
Hervestmen *Metagagrella tenuipes*  
Tsurusaki 1993

# Conventional staining – homogeneous staining

## Ancestral state

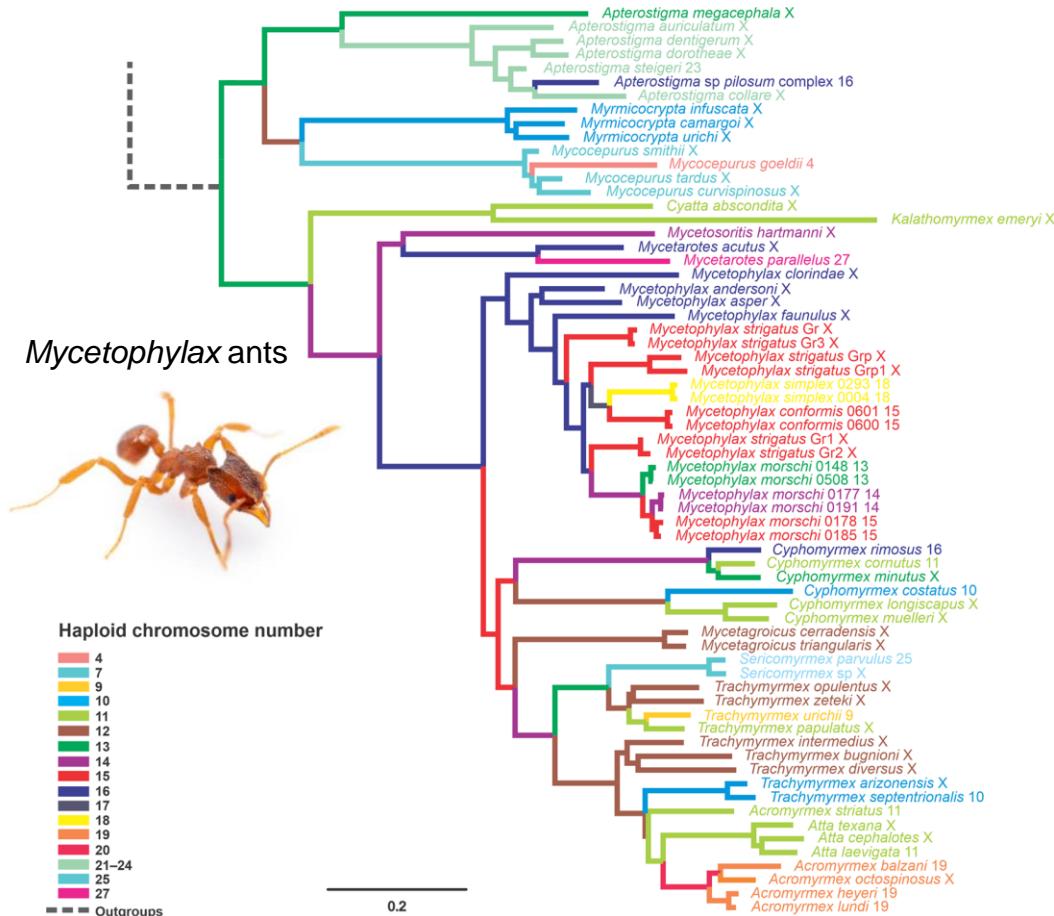
Mesquite

<http://www.mesquiteproject.org/>



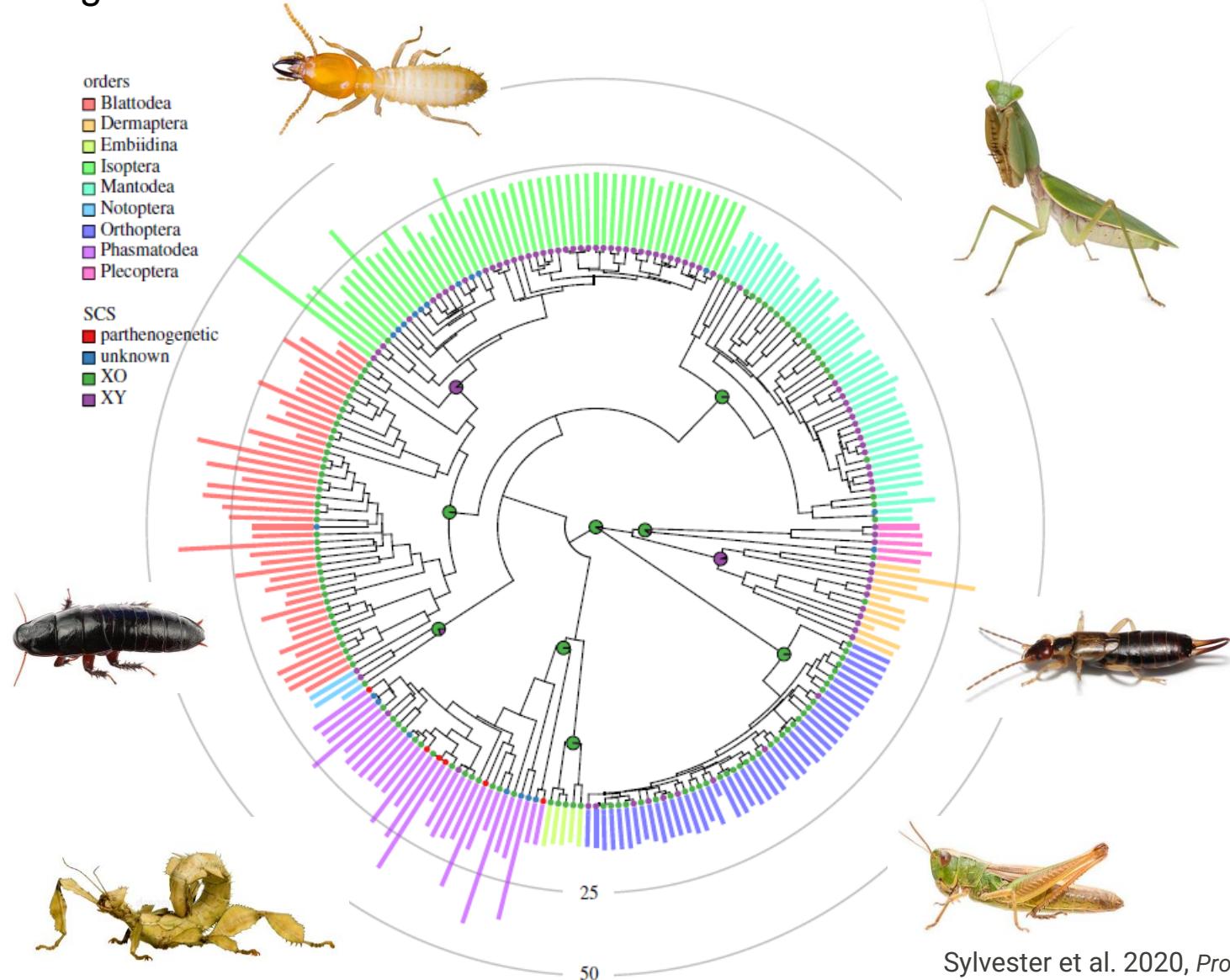
ChromEvol v. 2.0

[http://www.tau.ac.il/~itaym/ay/cp/chrom\\_Evol/](http://www.tau.ac.il/~itaym/ay/cp/chrom_Evol/)



# Conventional staining – homogeneous staining

R package chromePlus to estimate rates of chromosome number evolution



## Selective staining – for specific regions, large blocks

### C-banding - constitutive heterochromatin

0.2 M HCl for 20-45 min (depurination)

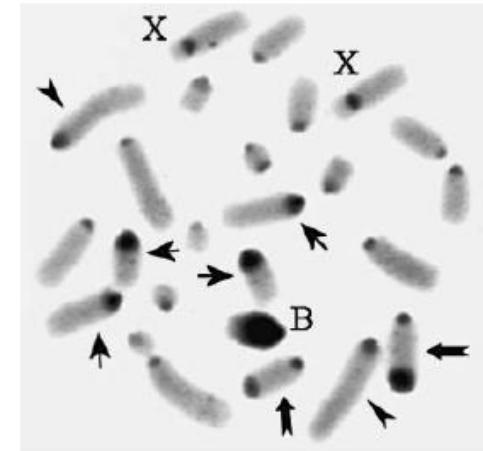
Rinse with DI water

4% Ba(OH)<sub>2</sub> (barium hydroxid) at 60 °C (denaturation)

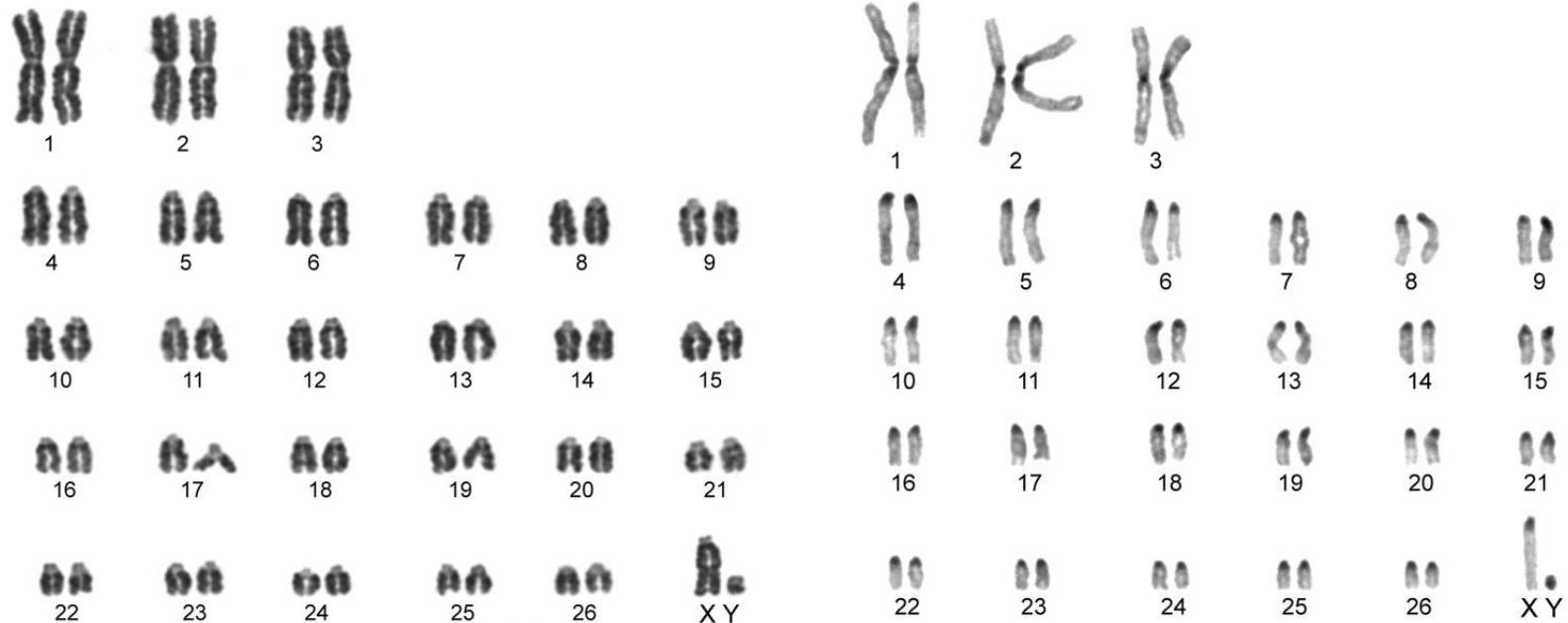
Rinse with DI water

2x SSC at 60 °C for 20-75min (renaturation)

Rinse with DI water



*Podysma krylonensis*  
Bugrov et al. 2004



## Selective staining – for specific regions, large blocks

### C-banding - constitutive heterochromatin

0.2 M HCl for 20-45 min (depurination)

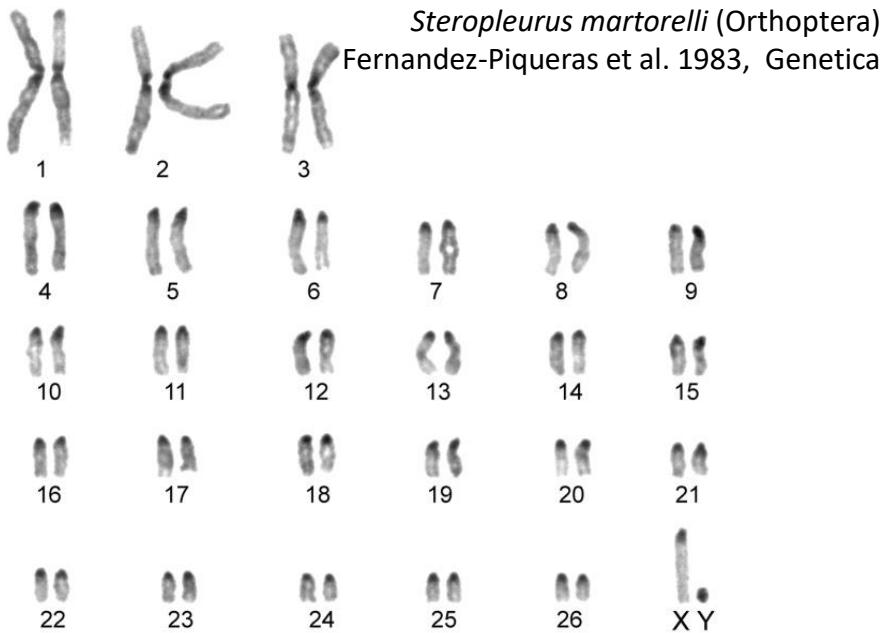
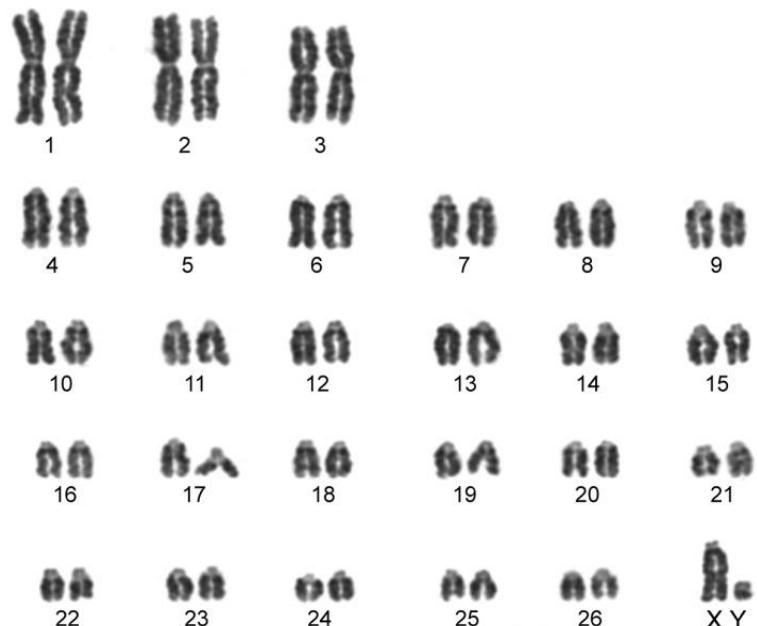
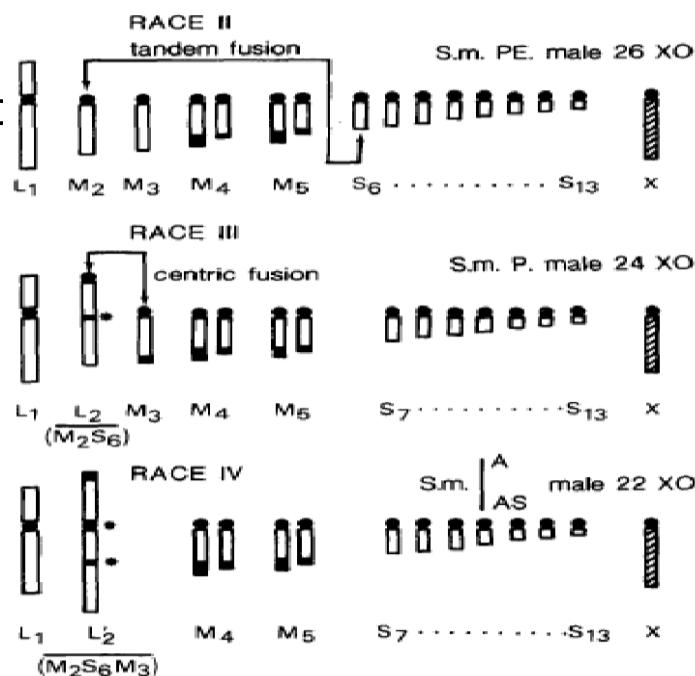
Rinse with DI water

4% Ba(OH)<sub>2</sub> (barium hydroxid) at 60 °C (denaturation)

Rinse with DI water

2x SSC at 60 °C for 20-75min (renaturation)

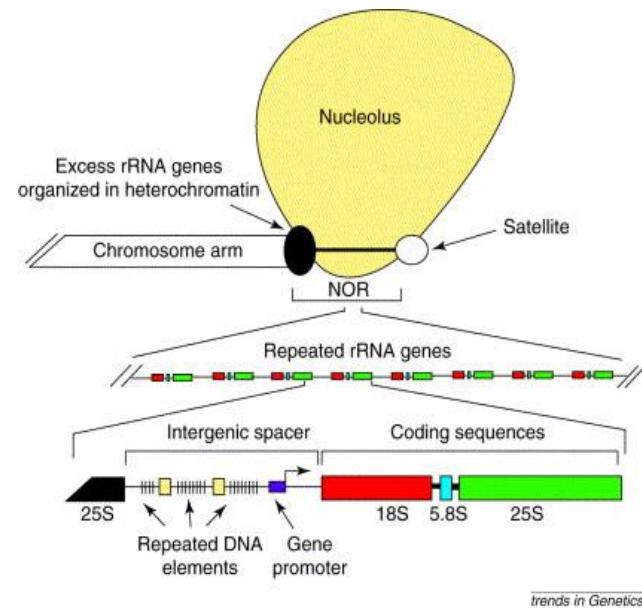
Rinse with DI water



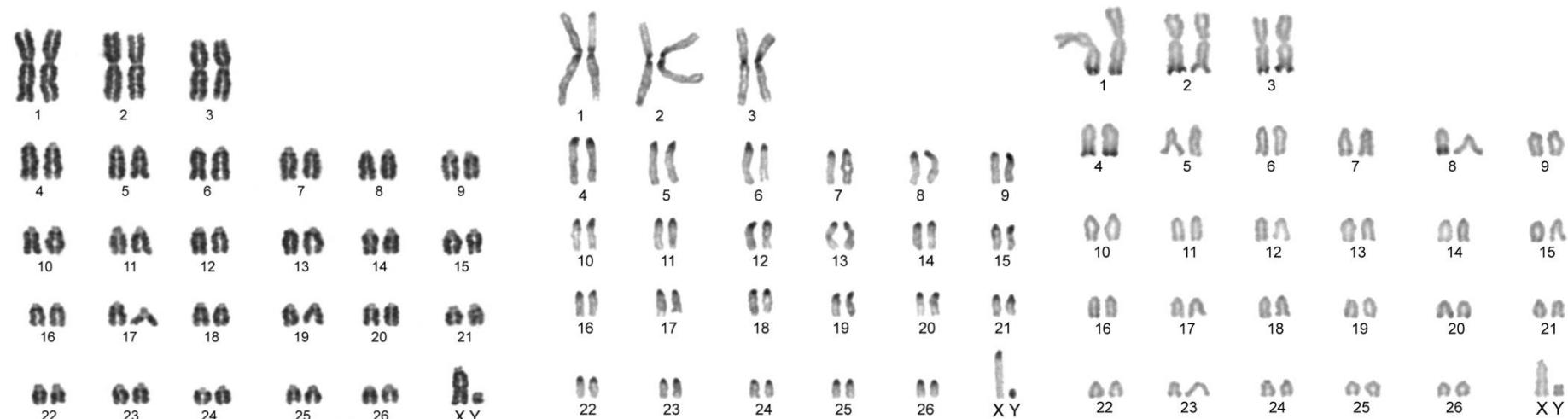
## Selective staining – for specific regions, large blocks

### Ag-NOR staining - NOR = Nucleolar Organizing Region

The region contains several tandem copies of ribosomal DNA genes.



- 1 g of AgNO<sub>3</sub> in 1 mL of 0.02 g sodium citrate (C<sub>6</sub>H<sub>5</sub>Na<sub>3</sub>O<sub>7</sub>·2 H<sub>2</sub>O) per 500 mL distilled water, adjusted to pH 3.0 with formic acid.
- Add 1-2 drops of the above solution onto the slides and place a cover slip over the preparation.
- Incubate slides in a moist chamber at 55–60°C for app. 30 min.



## Selective staining – for specific regions, large blocks

### G- banding

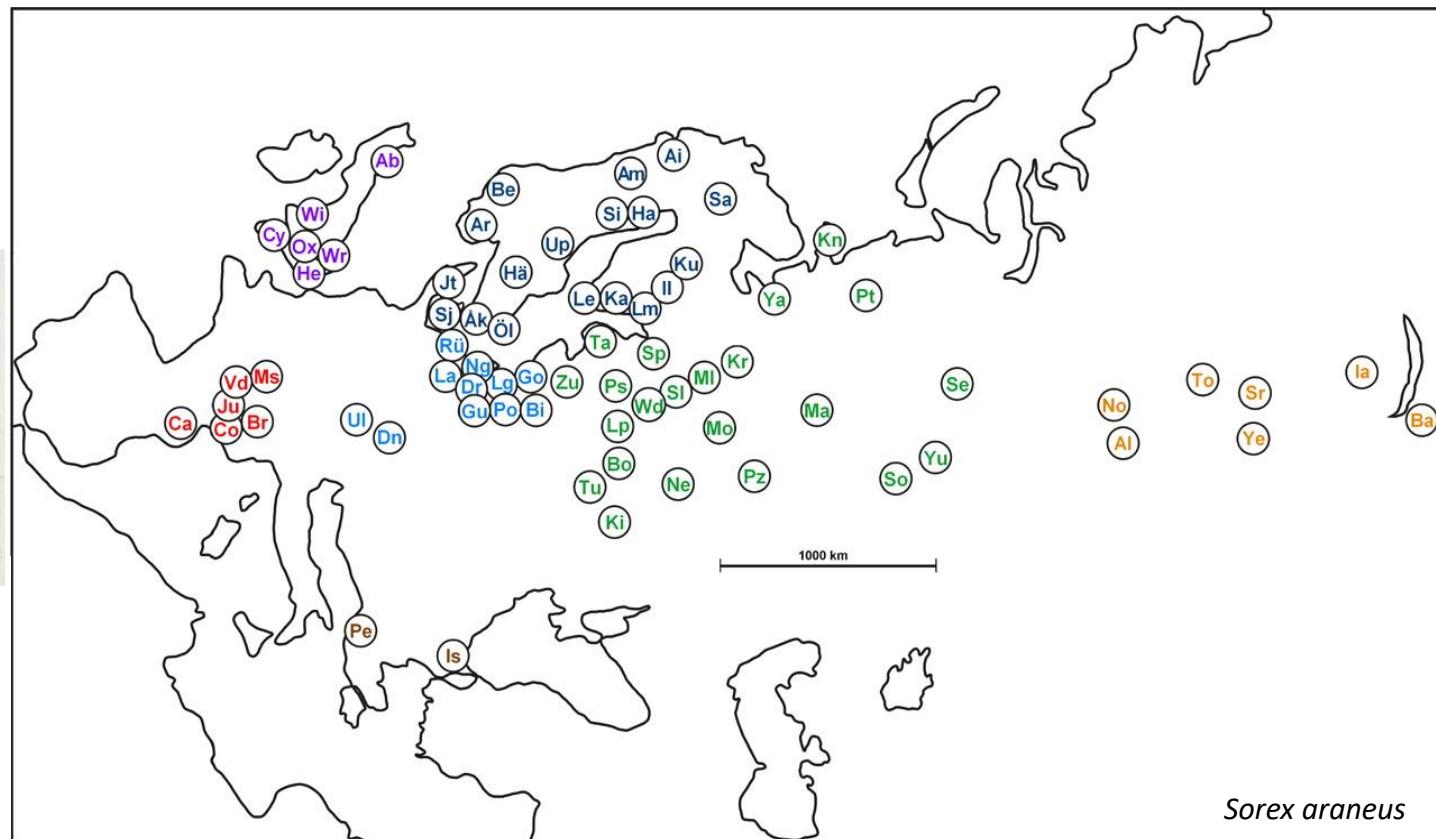
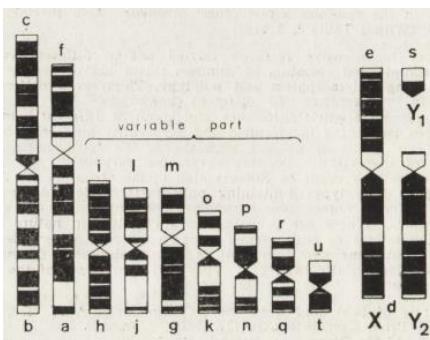
- obtained by the action of **trypsin** (10-20s at room temperature in a fresh 0.25% trypsin and then washed in PBS to block the action of trypsin)  
similar pattern also in **Q-banding** (stained by **quinacrin**)

#### *Sorex araneus*

2n=20-33

FN=40

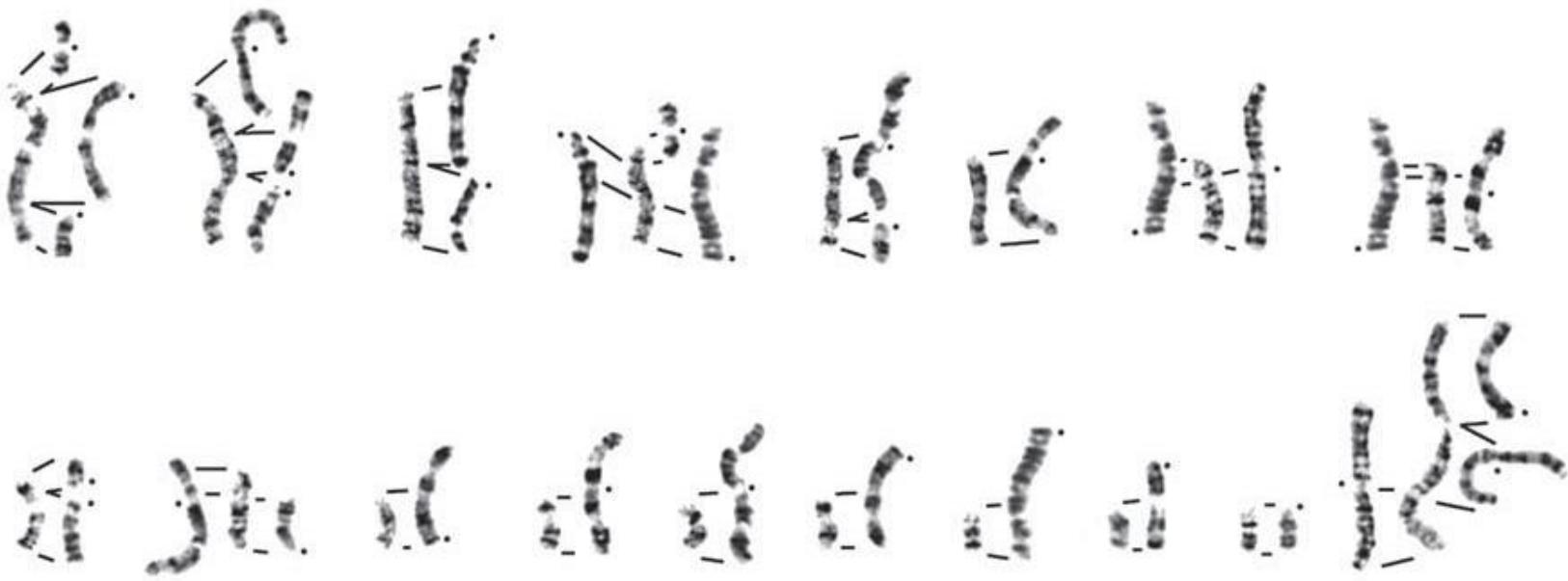
Chrom. races=72



## Selective staining – for specific regions, large blocks

### G- banding

- obtained by the action of **trypsin** (10-20s at room temperature in a fresh 0.25% trypsin and then washed in PBS to block the action of trypsin)  
similar pattern also in **Q-banding** (stained by **quinacrin**)

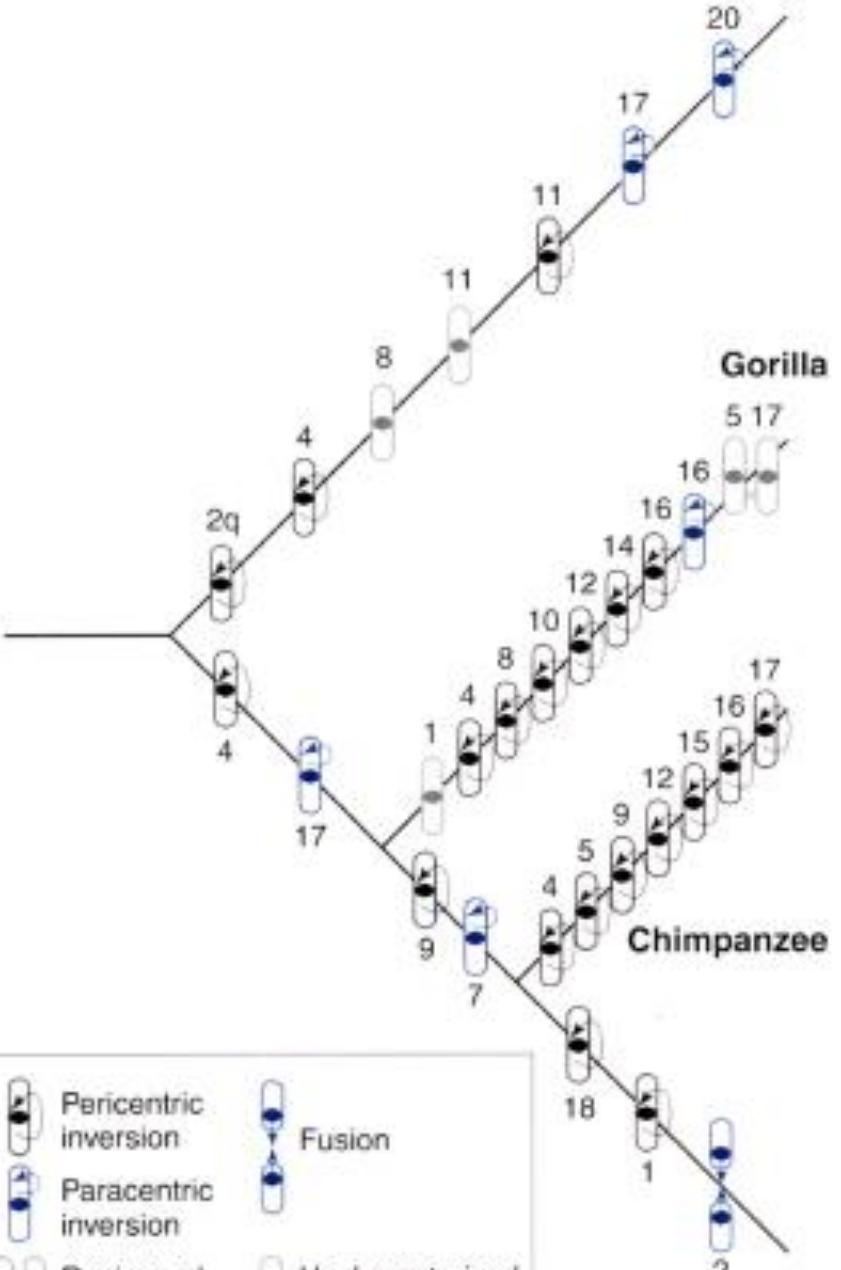


Comparison of G-banded chromosomes of *Sorex minutus* and *S. granarius*

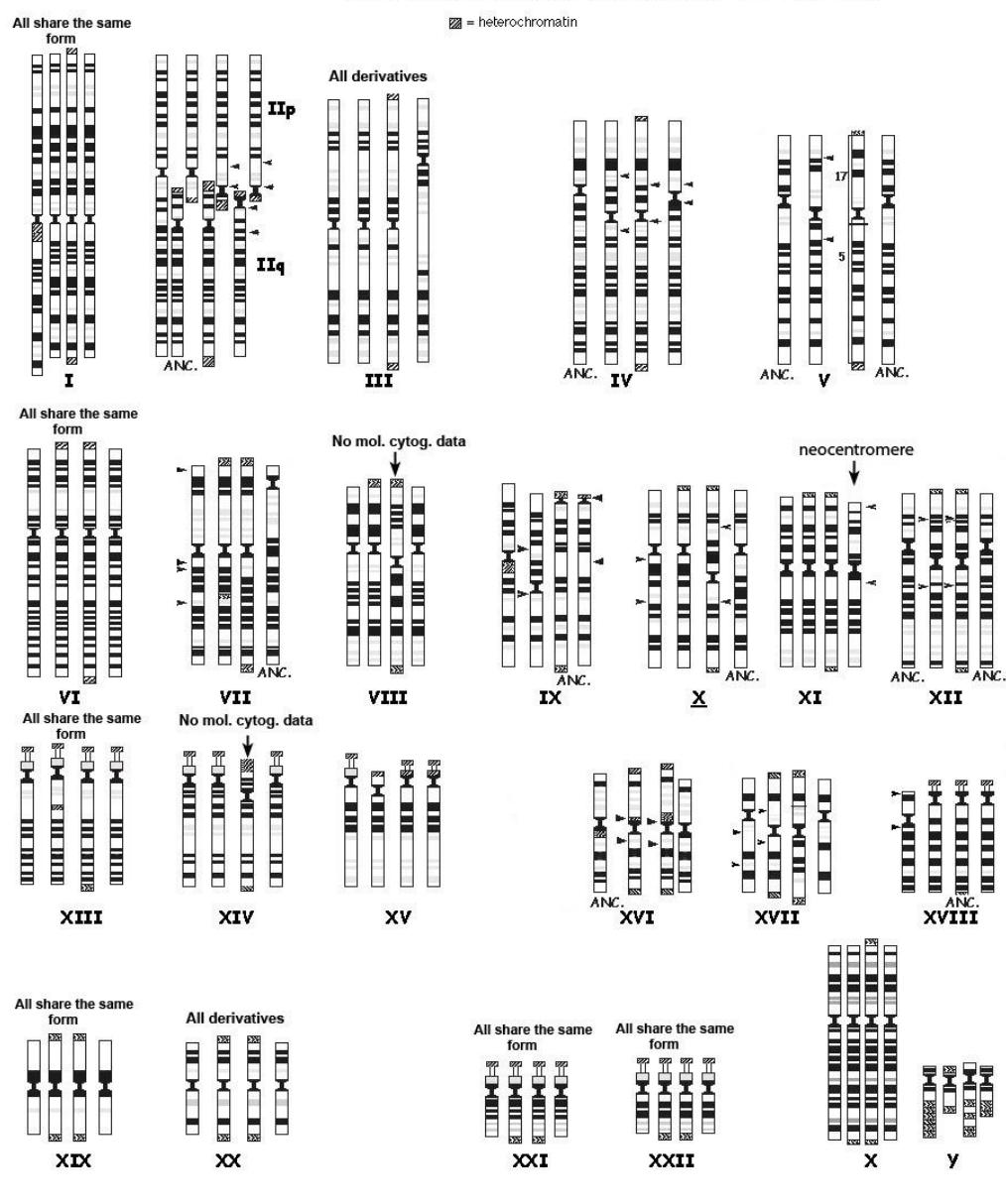


Biltueva et al. 2011

# Orangutan 2n=48



## GREAT APES COMPARATIVE KARYOTYPE (HSA - PTR - GGO - PPY)

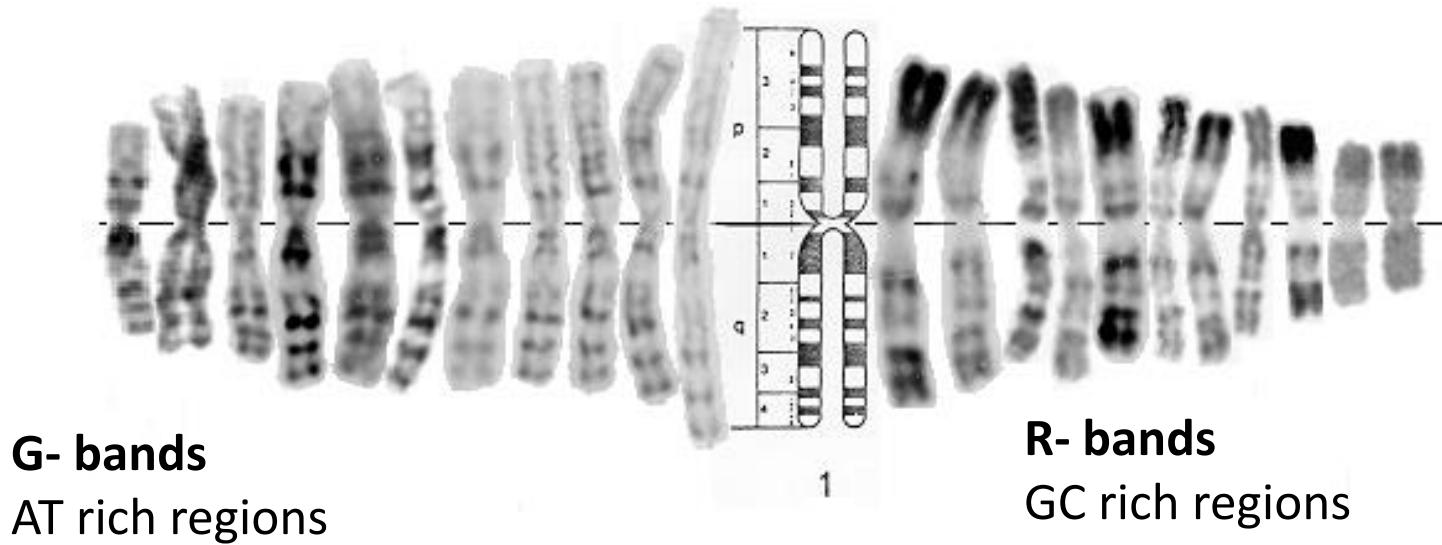


**Human 2n=46**

## Selective staining – for specific regions, large blocks

**R- banding** – bands reverse to G-banding

- the thermal denaturation of chromosomes (30-90 minutes at 87°C)

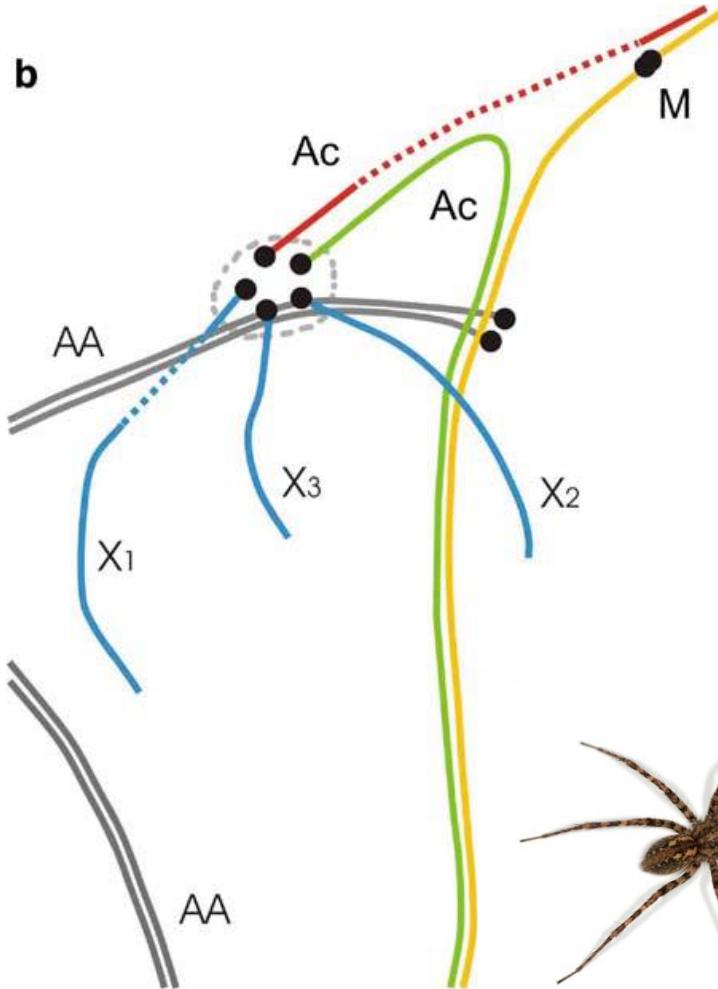
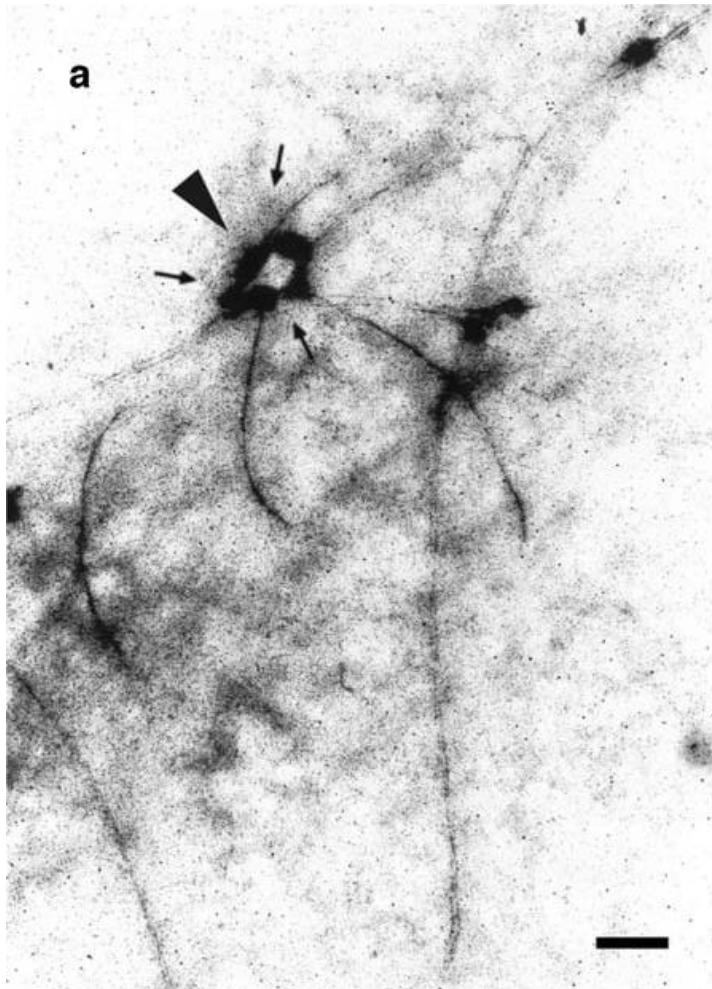


## Fluorochrome staining

AT rich regions: DAPI ( $4',6\text{-diamidin-2-fenylindol}$ ), chinakrin, Hoechst 33258

GC rich regions: chromomycin A<sub>3</sub>, mithramycin, olivomycin

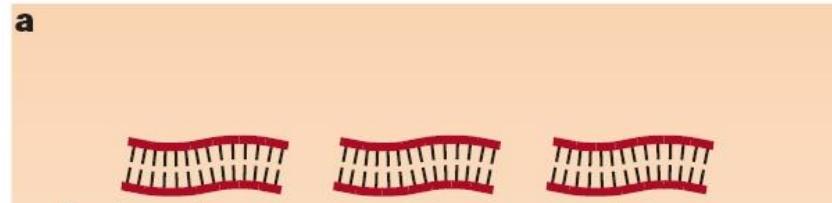
# Transmission electron microscopy (TEM)



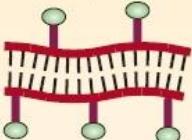
Ultrastructure of pairing of the X univalents with acrocentric chromosomes of the trivalent, *Malthonica ferruginea* male.  
(Král 2007)

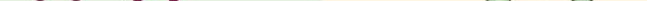
# FISH - Fluorescence *In Situ* Hybridization

a



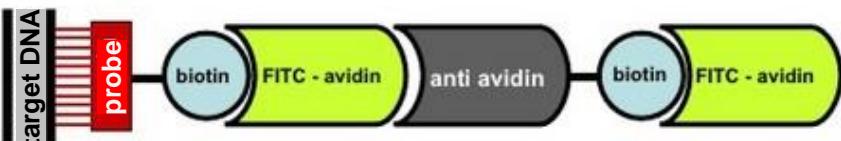
**b** indirect labeling direct labeling



**C** 



**d** ↓ ↓



A small icon of a lightbulb with rays emanating from it, labeled "U.V. lamp".

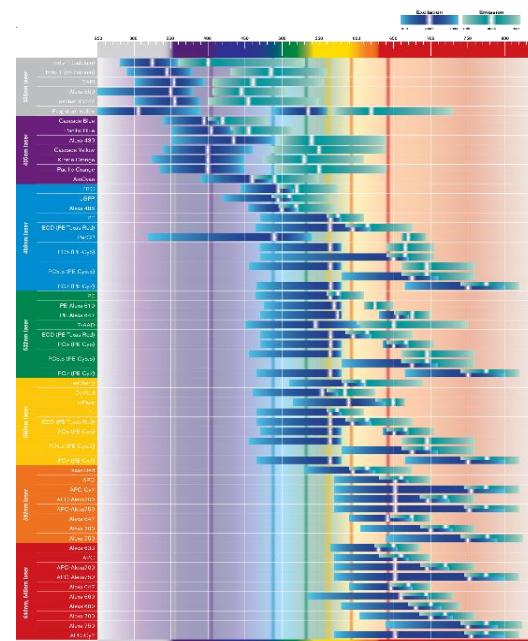
## Excitation filter

Dichroic  
mirror

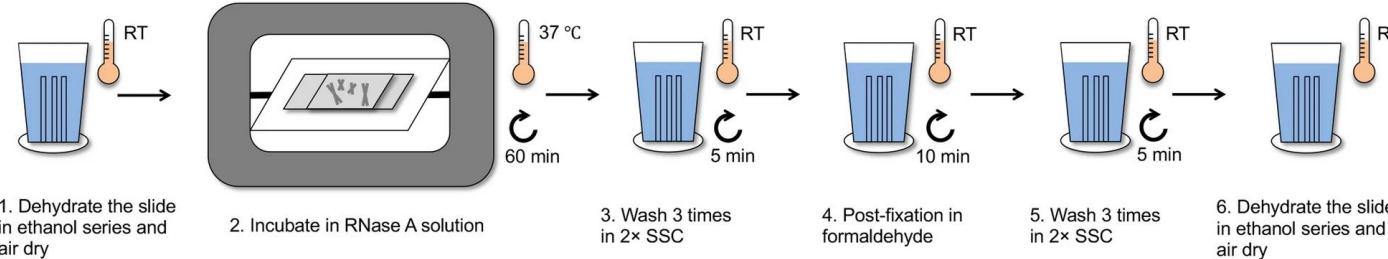
Target

The diagram illustrates the energy levels of a molecule. It features a central vertical axis representing energy. At the bottom is a thick black horizontal bar labeled "ground state". Above it is a thin black horizontal bar labeled "excited states". A red arrow points downwards from the excited states level to the ground state, labeled "emission". A green arrow points downwards from the excited states level to another thin black horizontal bar positioned between the ground state and the excited states, labeled "non-radiative (quenching)". On the left side, the word "excitation" is written next to a grey curved arrow pointing upwards towards the excited states level. On the right side, the words "excited states" are written above the top horizontal bar, and "non-radiative (quenching)" are written below the middle horizontal bar.

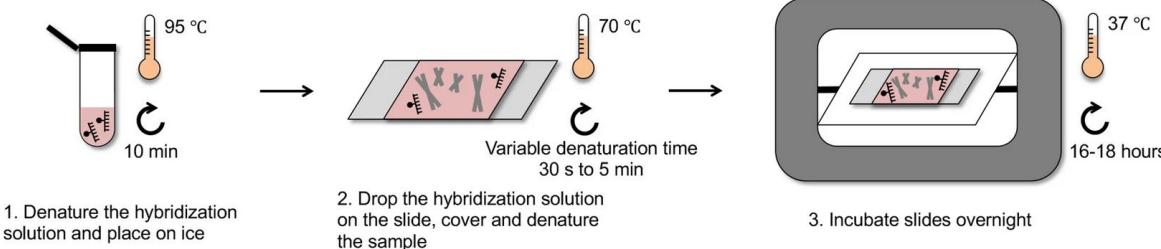
## Sample



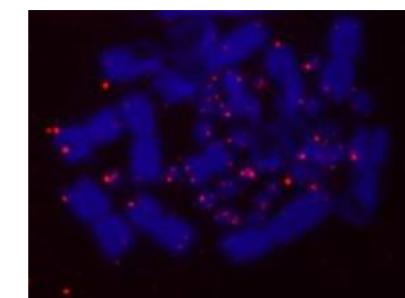
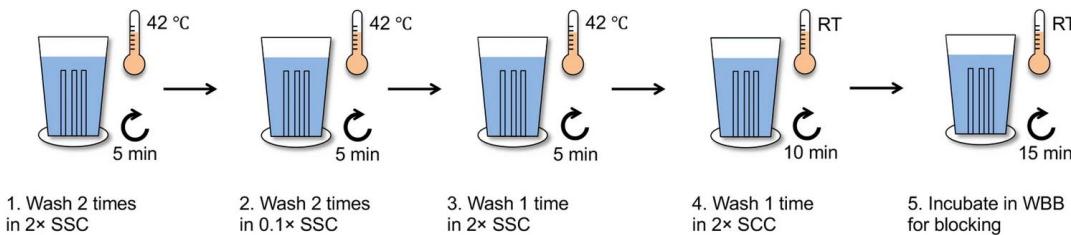
### (a) RNase pre-treatment and formaldehyde post-fixation



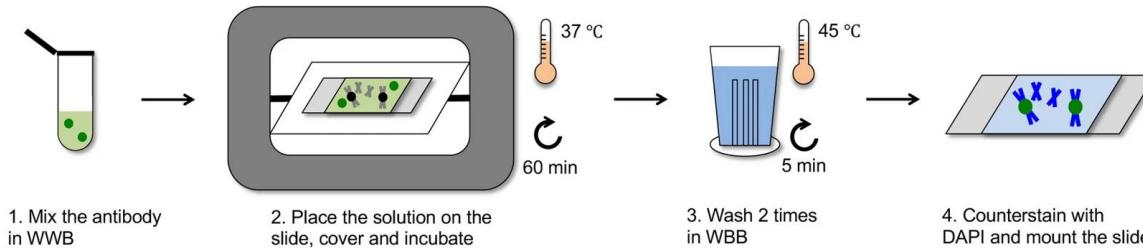
### (b) Denaturation and hybridization



### (c) Post-hybridization washes and blocking

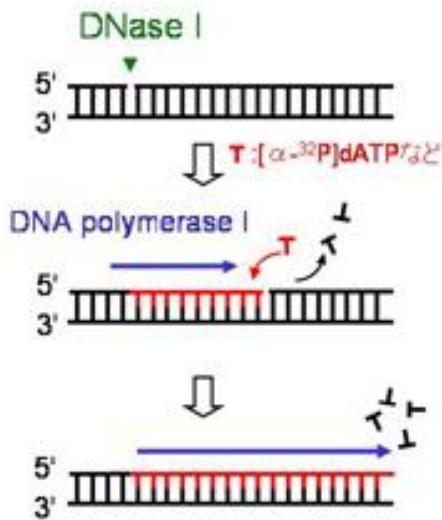


### (d) Immunological probe detection and counterstaining

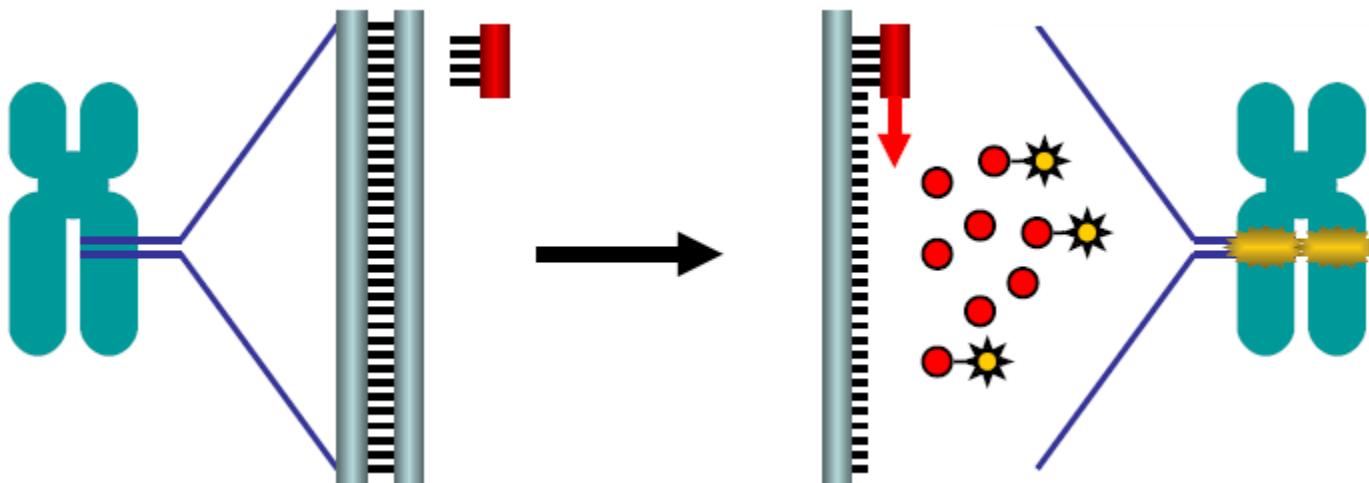


# NICK translation

- DNA Polymerase I is used to replace some of the nucleotides of a DNA sequence with their labeled analogues



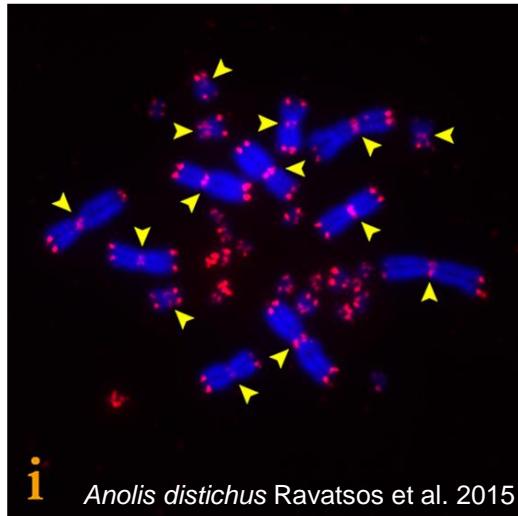
## Primed *in situ* Labelling (PRINS)



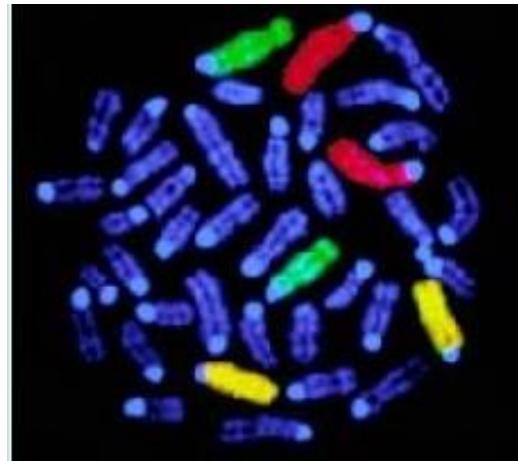
- Centromere-FISH (ACM-FISH)**
- armFISH**
- Catalyzed Reporter Deposition-FISH (CARD-FISH)**
- Cellular Compartment Analysis of Temporal (Cat) Activity by Fish (catFISH)**
- Cytochalasin B (CB-FISH)**
- Chromosome Orientation (CO)-FISH**
- Combined Binary Ratio (COBRA)-FISH**
- Chromosome Orientation and Direction (COD)-FISH**
- Combinatorial Oligonucleotide (COMBO)-FISH**
- Comet-FISH**
- Cryo-FISH**
- Double Fusion FISH (D-FISH)**
- DNA Breakage Detection FISH (DBD-FISH)**
- e-FISH**
- Fiber-FISH**
- Flow-FISH**
- Fusion-Signal FISH**
- Halo-FISH**
- Harlequin-FISH**
- Immuno-FISH**
- Locked Nucleic Acids (LNAs)-FISH**
- Multiplex (M)-FISH**
- Multilocus or ML-FISH**
- Premature Chromosome Condensation (PCC)-FISH**
- Peptide Nucleic Acid (PNA)-FISH**
- Quantitative-FISH (Q-FISH)**
- Quantum Dot (QD)-FISH**
- Rainbow-FISH**
- Raman-FISH**
- Replicative Detargeting FISH (ReD-FISH)**
- Reverse-FISH**
- Recognition of Individual Genes (RING)-FISH**
- RNA-FISH**
- Cross Species Color Banding (Rx)-FISH**
- Split-Signal FISH**
- Stellaris RNA FISH (Single-Molecule RNA FISH)**
- T-FISH**
- 3-D FISH**
- Zoo-FISH**

## Types of probes

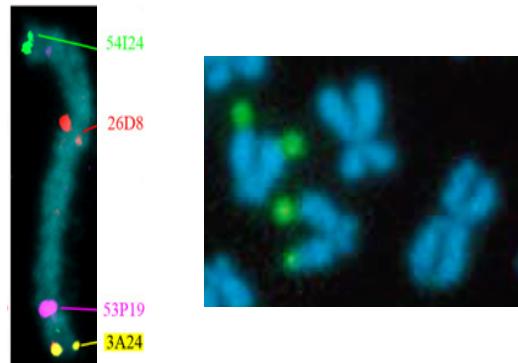
- Satelite DNA
  - centromeric
  - telomeric



- painting probes



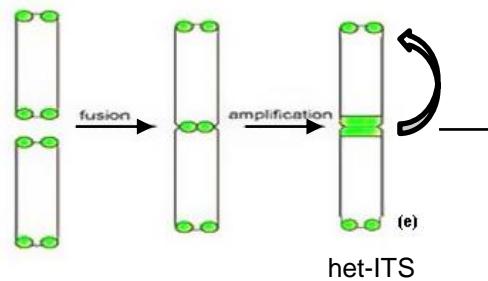
- locus specific



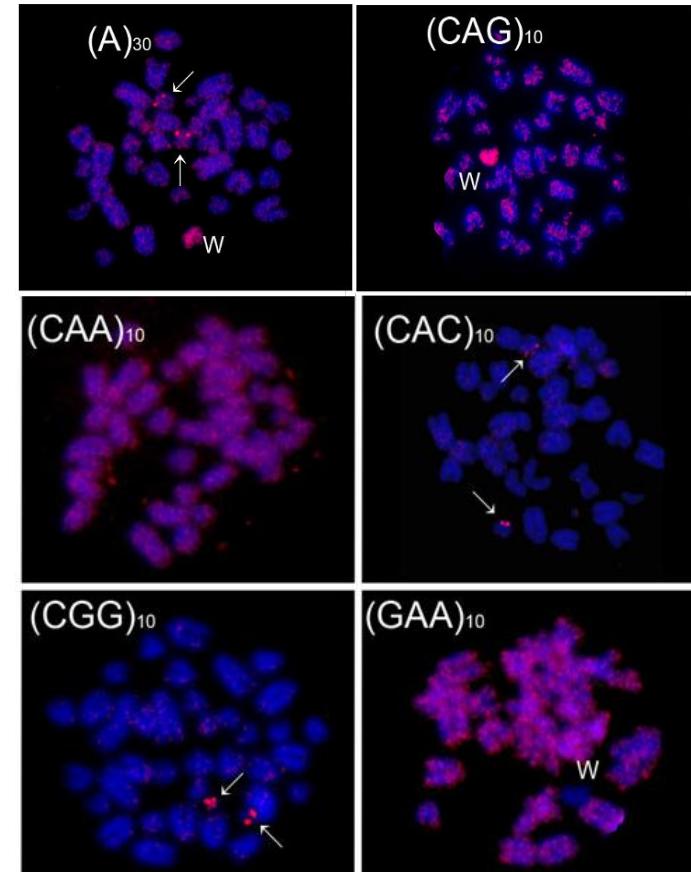
### telomere

Insects  
Vertebrates, Anellida, Mollusca  
Nematoda

(TTAGG) $n$   
(TTAGGG) $n$   
(TTAGGC) $n$



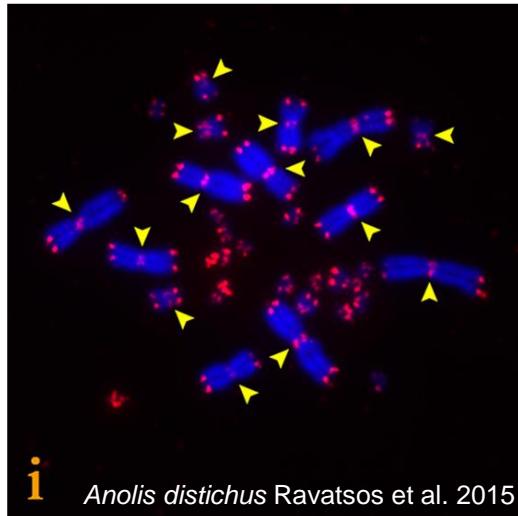
het-ITS      sutelo-ITS



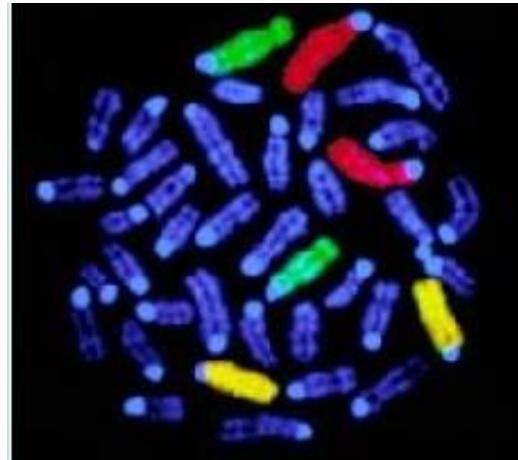
*Eremias velox* Pokorná et al. 2011

## Types of probes

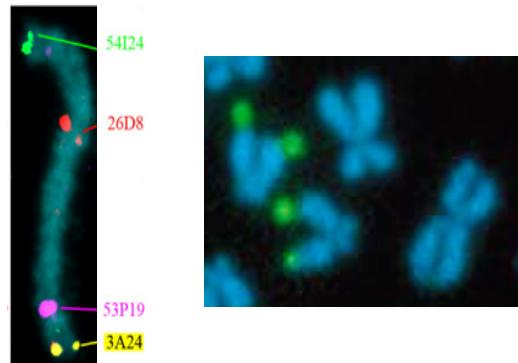
- Satelite DNA
  - centromeric
  - telomeric



- painting probes



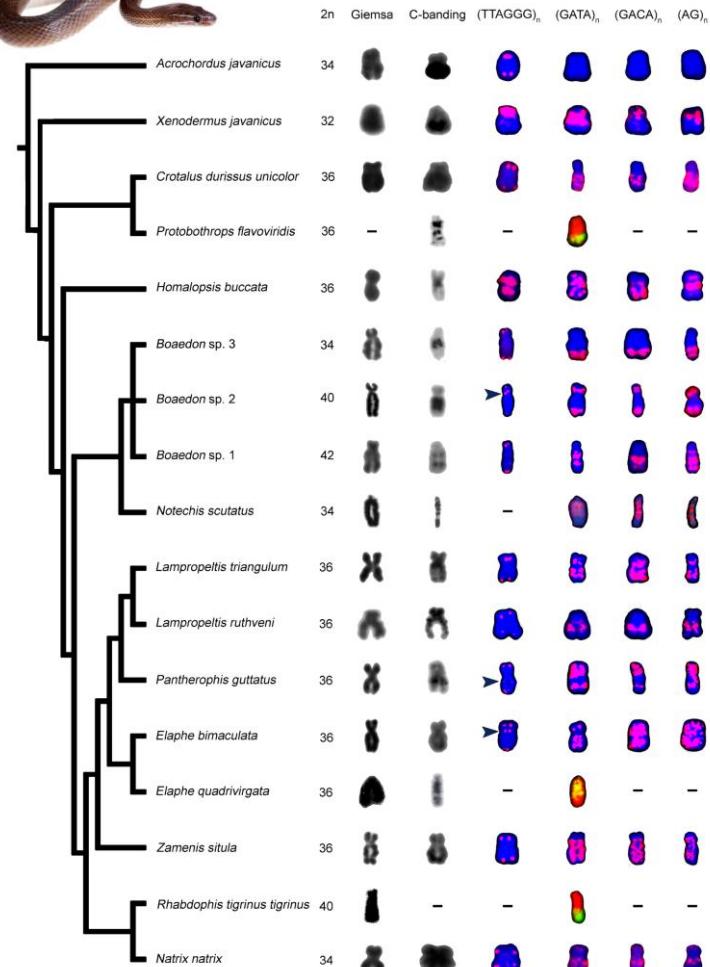
- locus specific



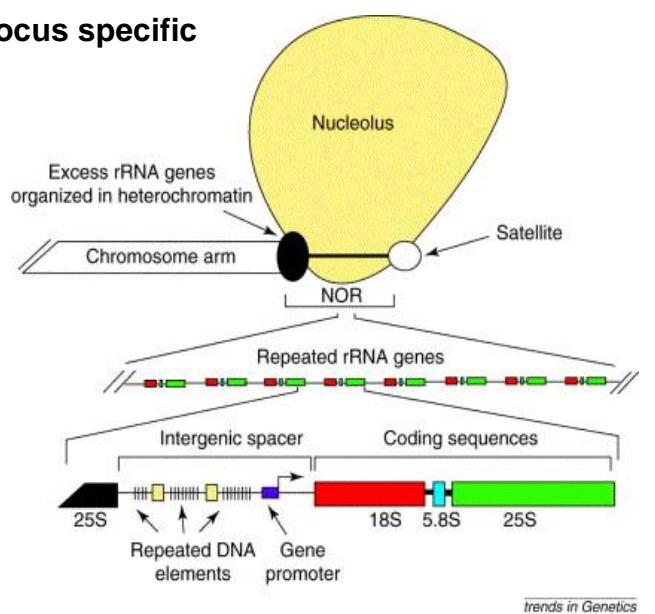
## telomere

Insects  
Vertebrates, Anellida, Mollusca  
Nematoda

(TTAGG) $n$   
(TTAGGG) $n$   
(TTAGGC) $n$



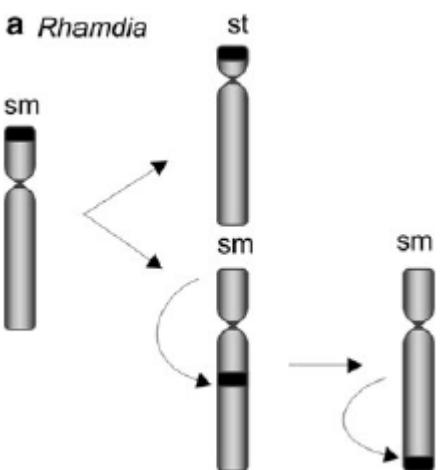
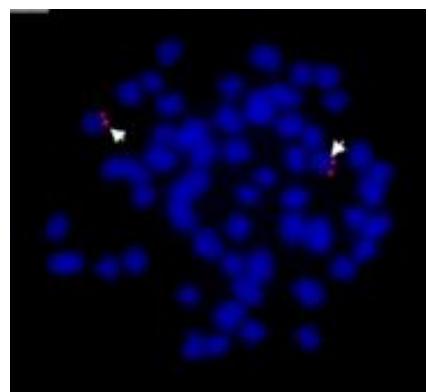
## locus specific



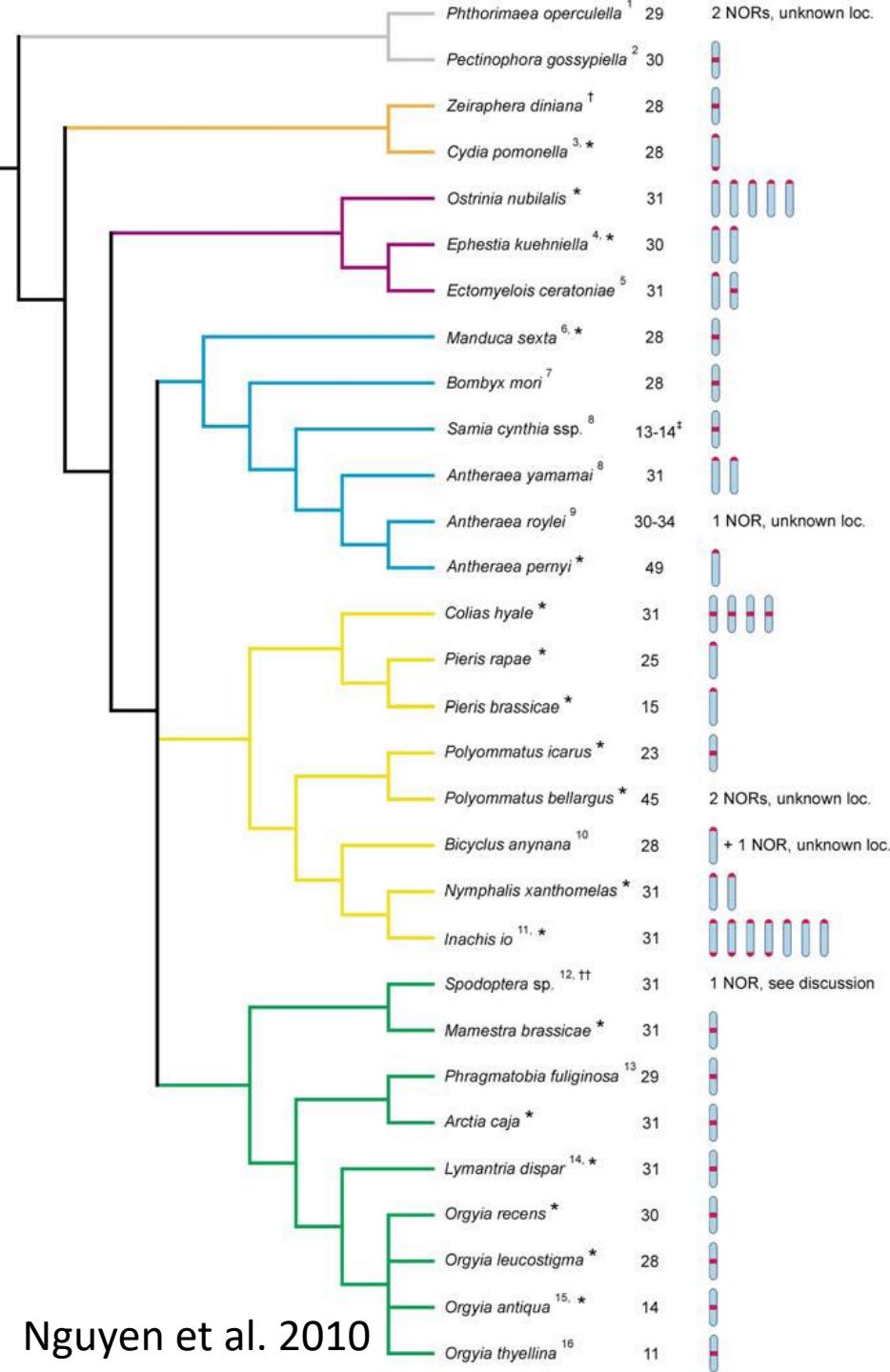
## Ribosomal DNA (rDNA)

- loci encoding 5S and 45S (18S-5.8S-28S) rRNAs

## 18S rDNA probe

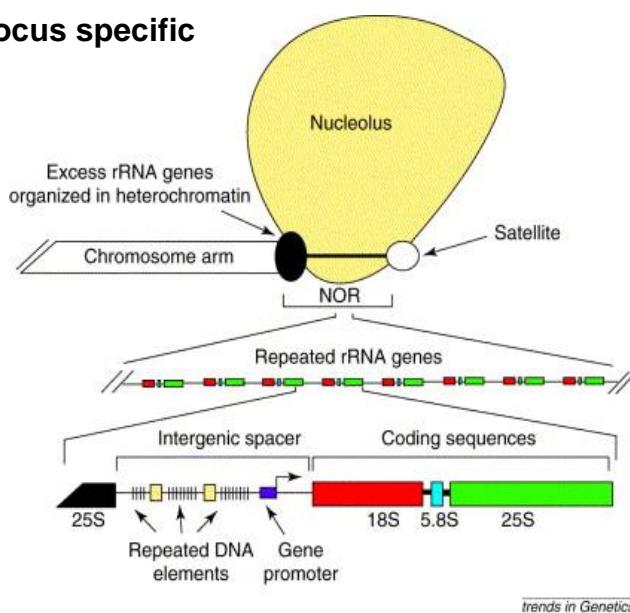


Borba et al. 2014



Nguyen et al. 2010

**locus specific**



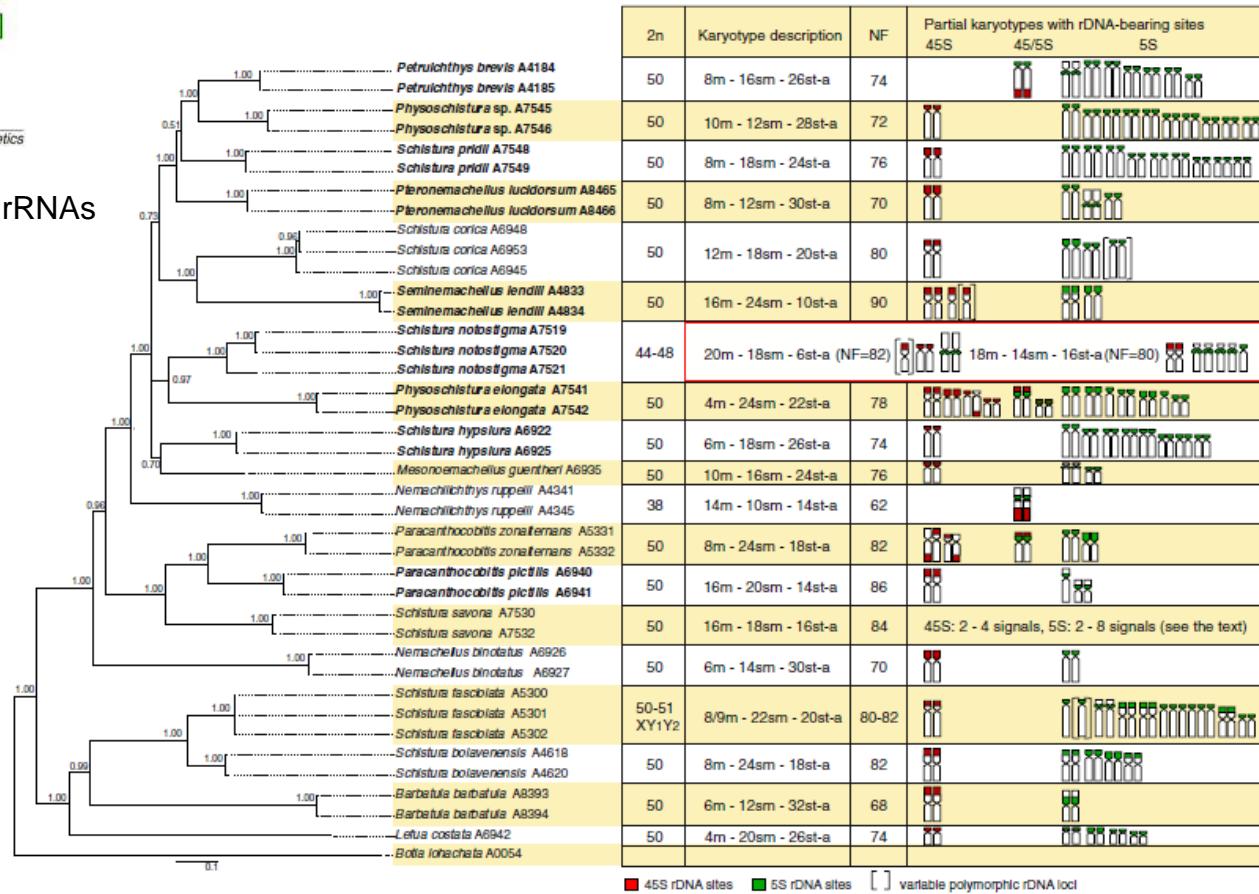
## Ribosomal DNA (rDNA)

- loci encoding 5S and 45S (18S-5.8S-28S) rRNAs

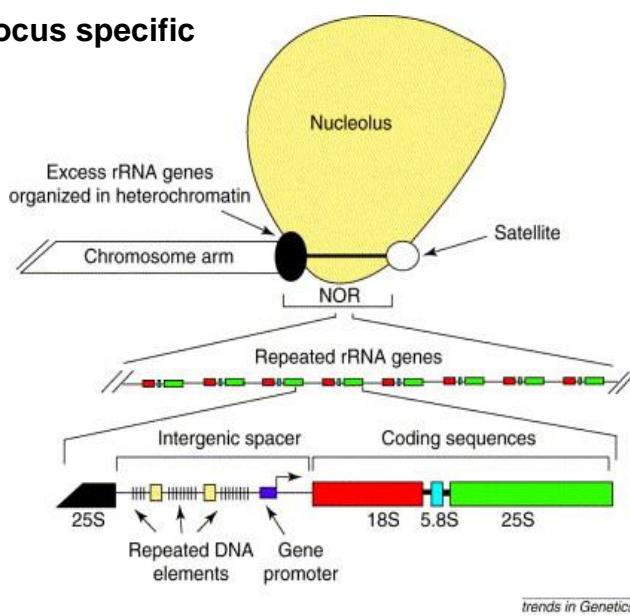


## Nemacheilidae

Sember et al. 2015



# locus specific



## Ribosomal DNA (rDNA)

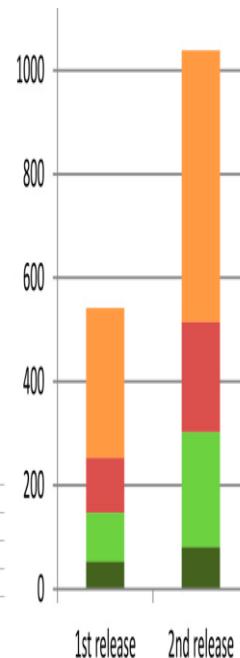
- loci encoding 5S and 45S (18S-5.8S-28S) rRNAs

The screenshot shows the 'animal rRNA database' interface. At the top, there's a search bar with 'Type...' and a magnifying glass icon. Below it, the title 'animal rRNA database' is displayed with a release date of 'release 2.0, October 2017'. There are several checkboxes for 'Select output fields' including 'Family', 'Genus', 'Specific epithet', 'Arrangement', and 'Infraspecific category'. Below this is a section for 'Write conditions' with dropdown menus for 'Family', 'Genus', 'Specific epithet', 'Chromosome number from', and 'Poly level from'. A 'Select filters' section is also present. At the bottom, there's a 'Search' button and some help text.

<http://www.animalrdnadb.com>

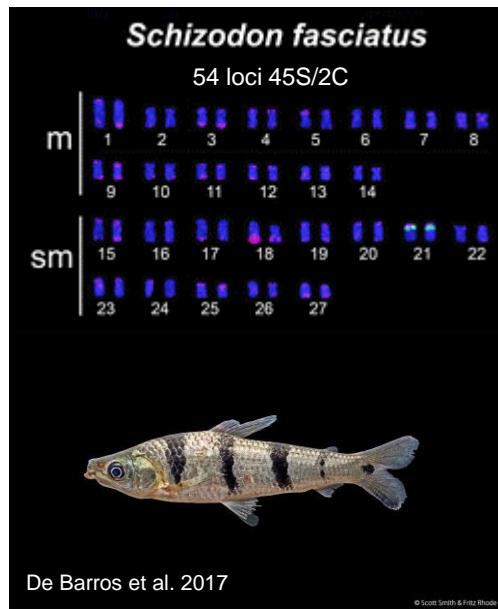
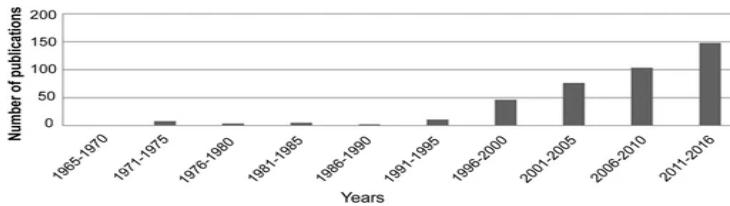
**2500 species**

1068 Arthropods  
653 fish

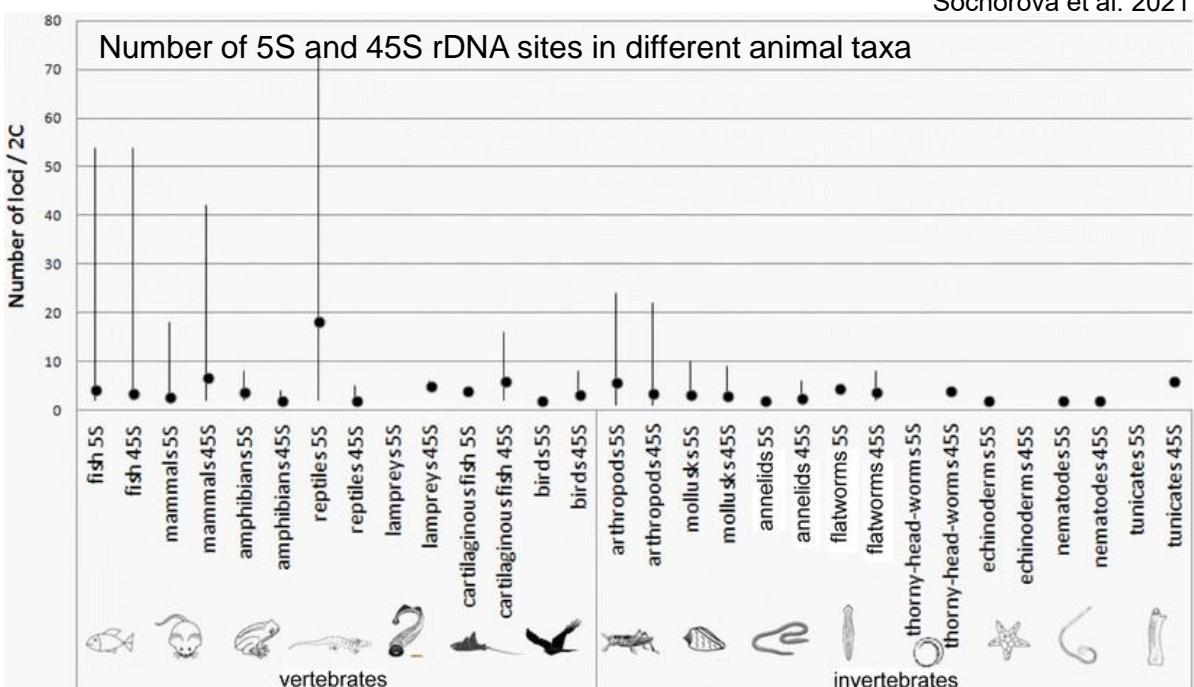


Sochorová et al. 2021

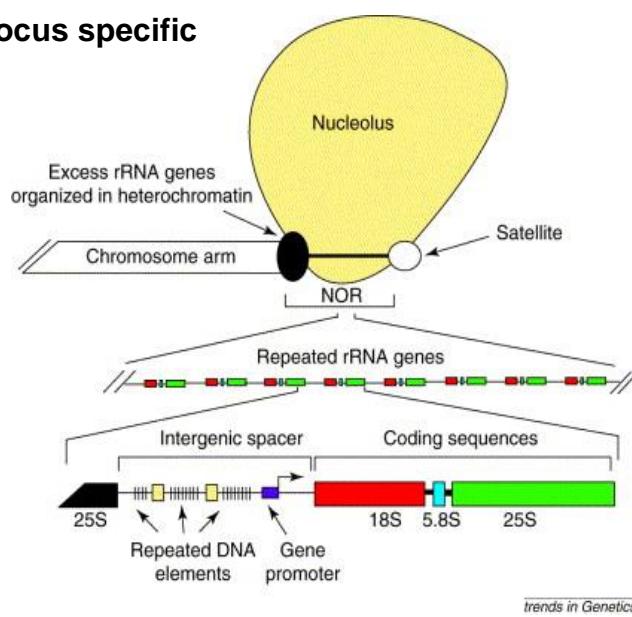
Sochorová et al. 2018



De Barros et al. 2017



# locus specific



## Ribosomal DNA (rDNA)

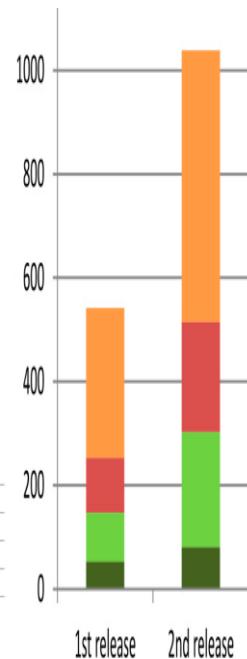
- loci encoding 5S and 45S (18S-5.8S-28S) rRNAs

A screenshot of the 'animal rRNA database' interface. The top navigation bar includes links for Home, Publications, Help, Units, Submit your data, Contact and Comments, How to cite? IUP, IBB CSIC, and Release 1.0, October 2017. The main search bar has a placeholder 'Type...'. Below the search bar are several checkboxes for 'Select output fields': Family, Genus, Specific epithet, Specific authority, Infraspecific category, Chromosome number (n), Polyploid, Number of 5S signals, Range of 5S signals, Position of 5S signals (SSP), Number of 45S signals, Range of 45S signals, Position of 45S signals (SSP), Arrangement, Number of chromosomes with both 5S and 45S signals (S), Number of chromosomes with co-localized 5S and 45S signals (CoL), and Original reference. There are also 'Write conditions' and 'Select filters' sections. At the bottom, there is a 'Search' button and a note: 'For help with searching and querying the database, go to HELP'.

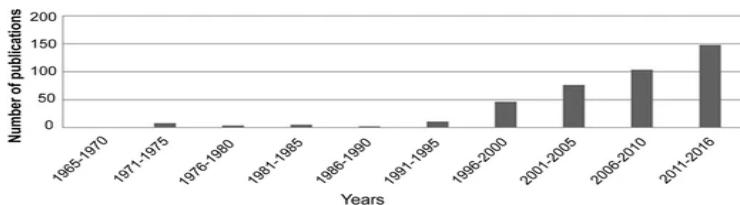
<http://www.animalrdnadatabase.com>

**2500 species**

1068 Arthropods  
653 fish



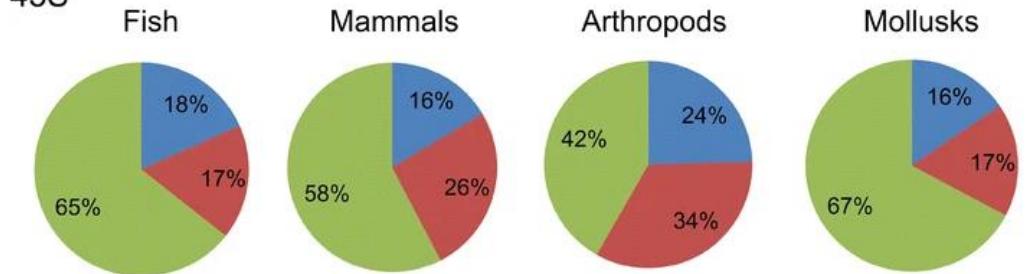
Sochorová et al. 2018



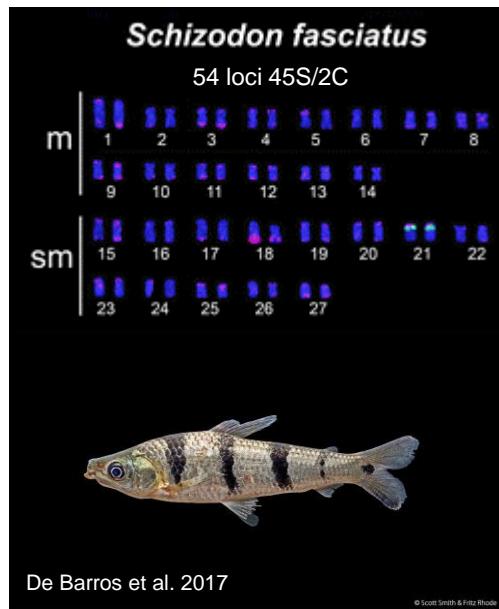
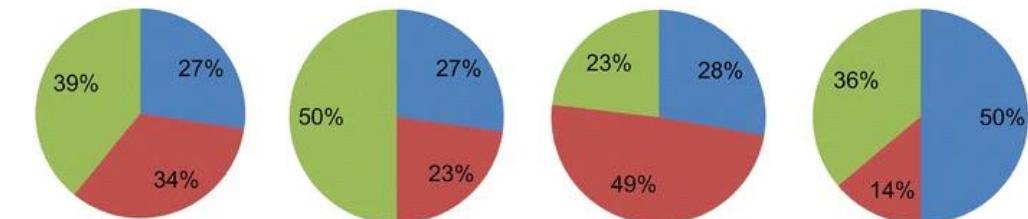
Sochorová et al. 2021

## Position of rDNA sites on chromosomes

45S

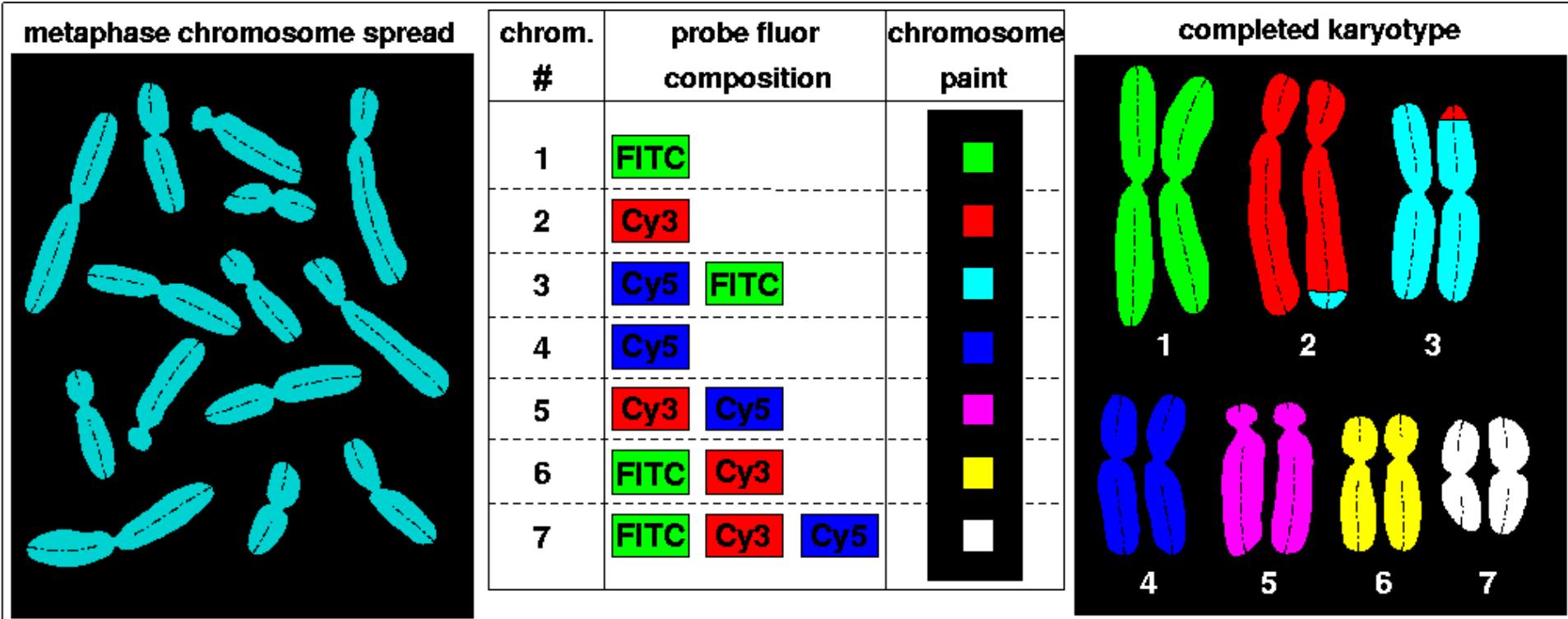


5S

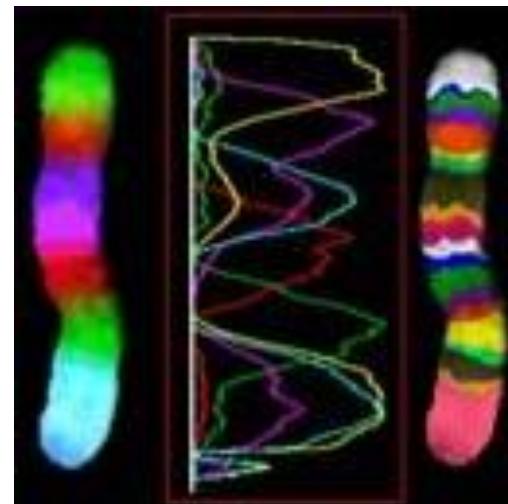
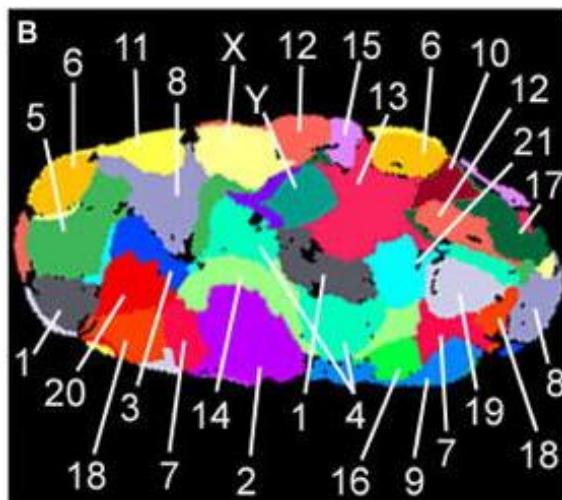
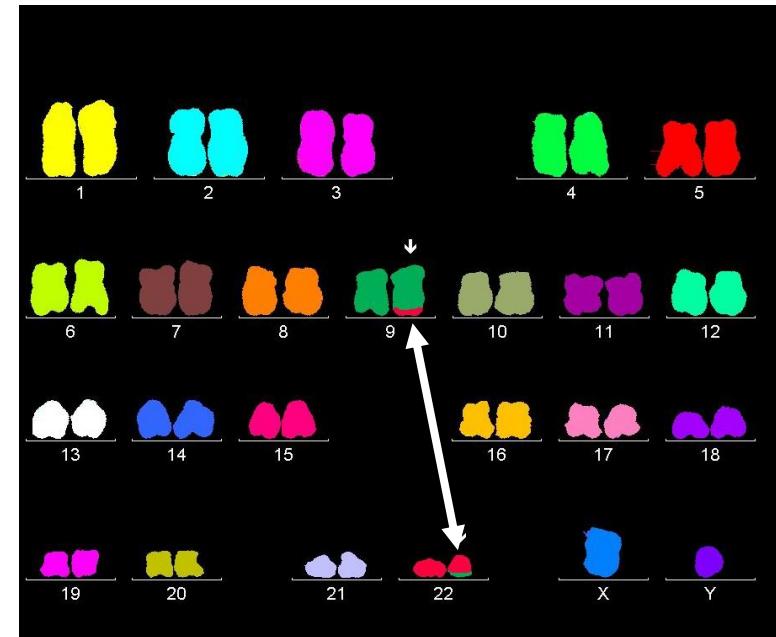
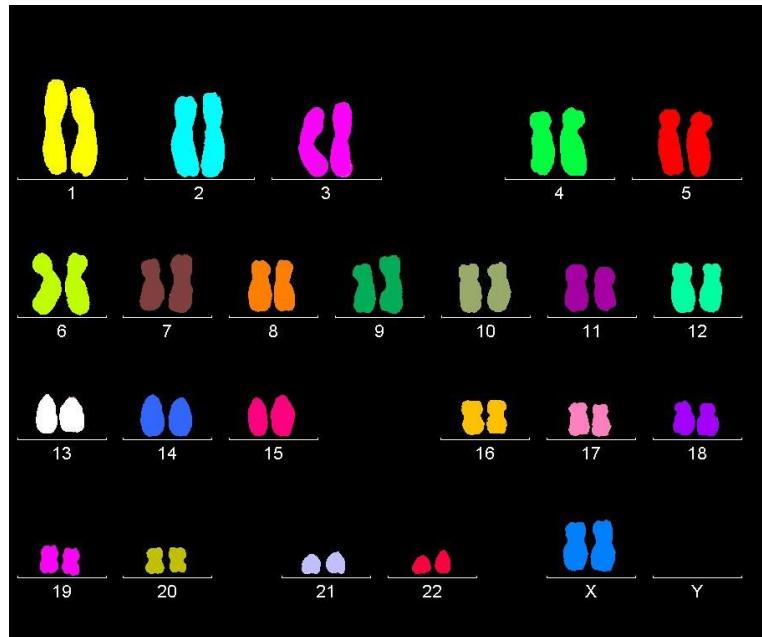


# M-FISH

multiplex FISH or multicolour FISH

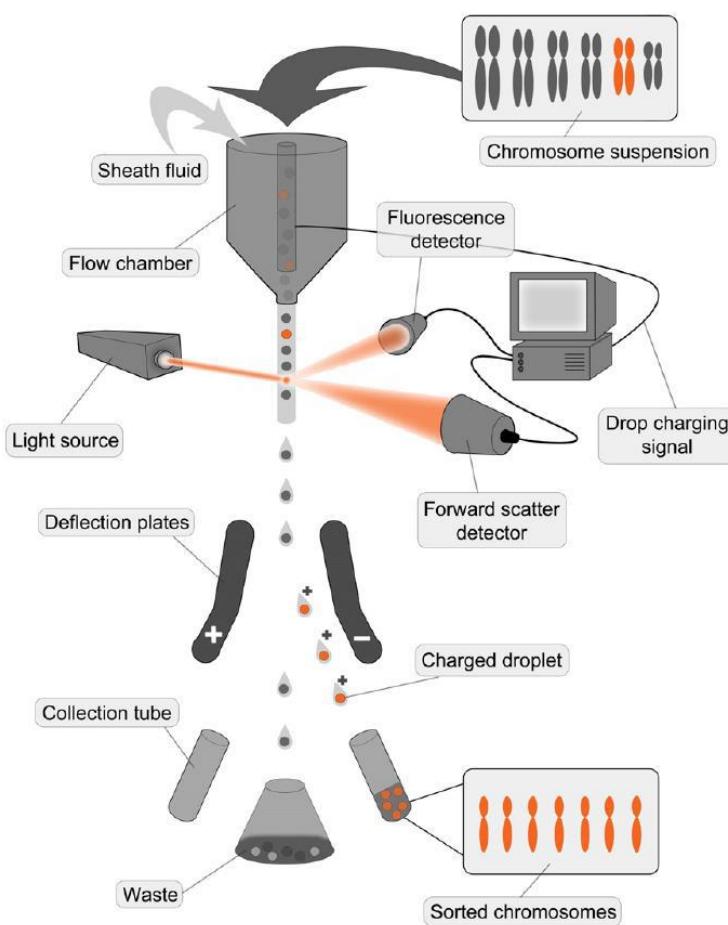


# M-FISH

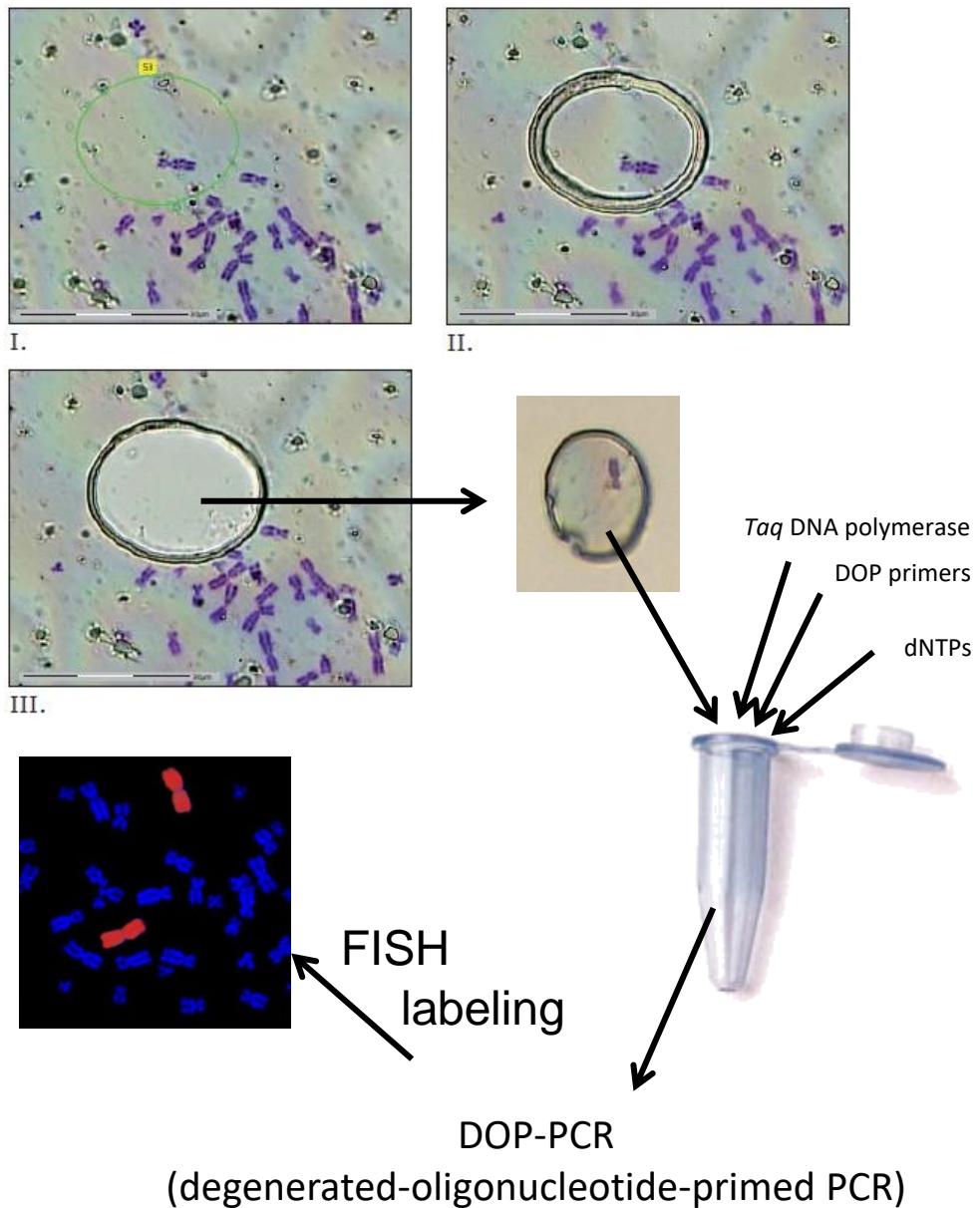


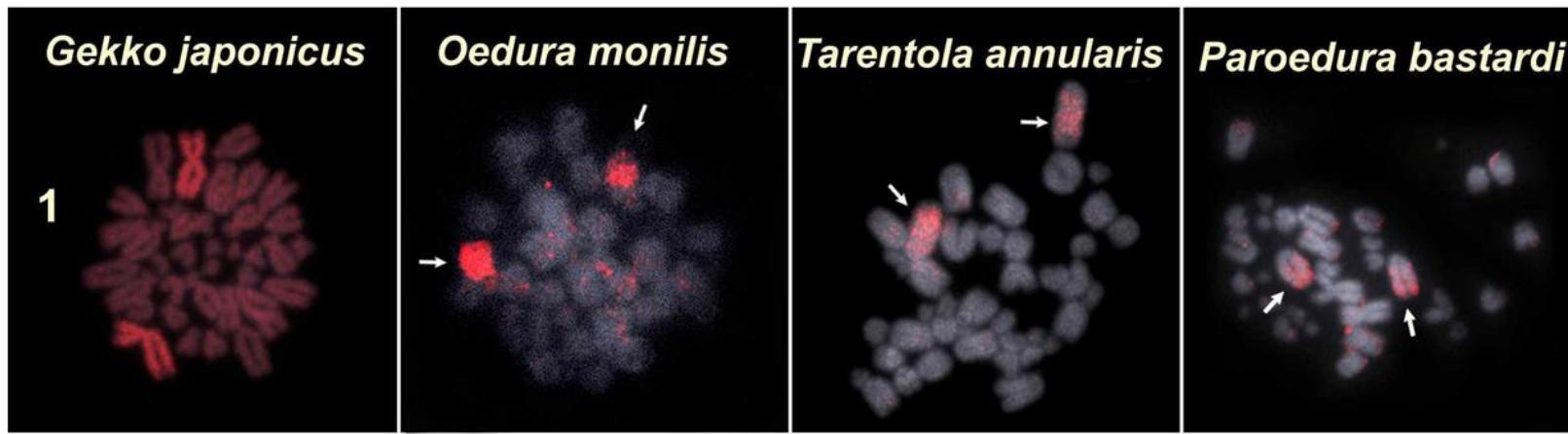
**Multicolour banding  
(mBAND)**

## Chromosome sorting (flow cytometer)

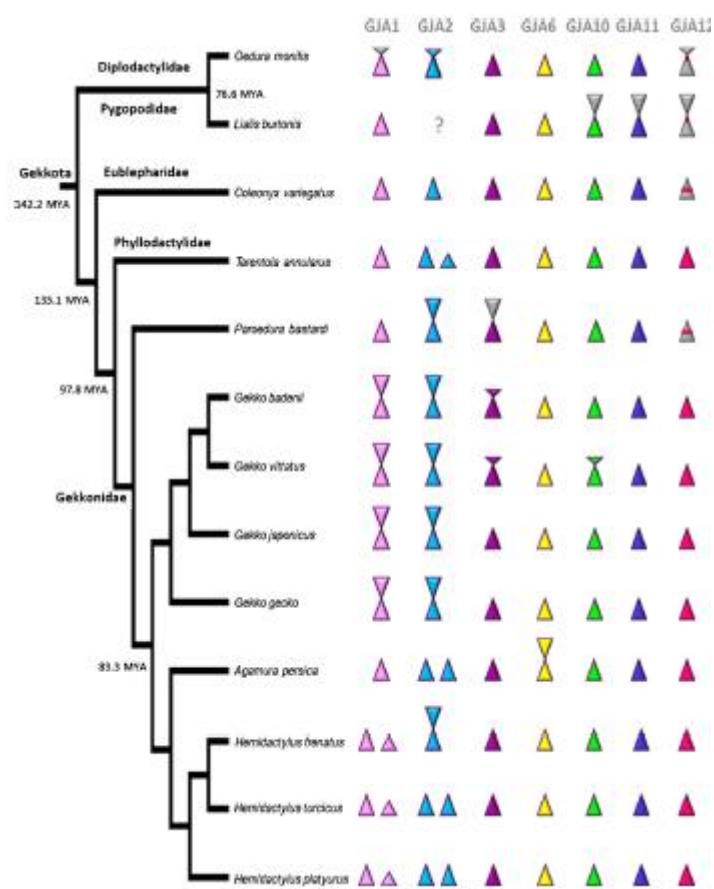


## Microdissection



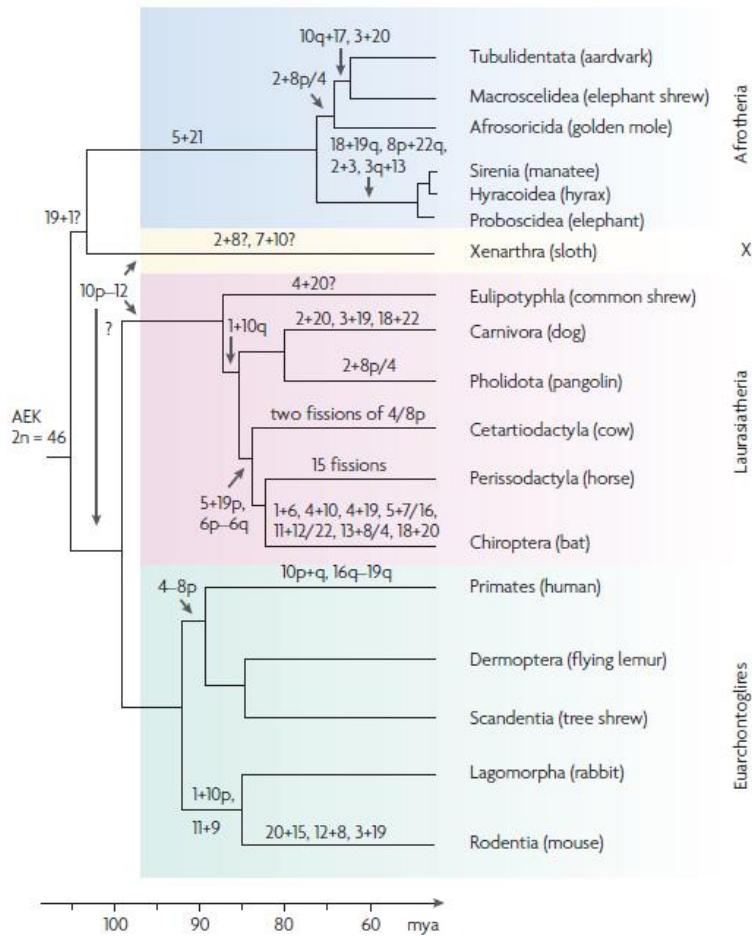


Pokorná et al. 2015, *Chrom. Res.*

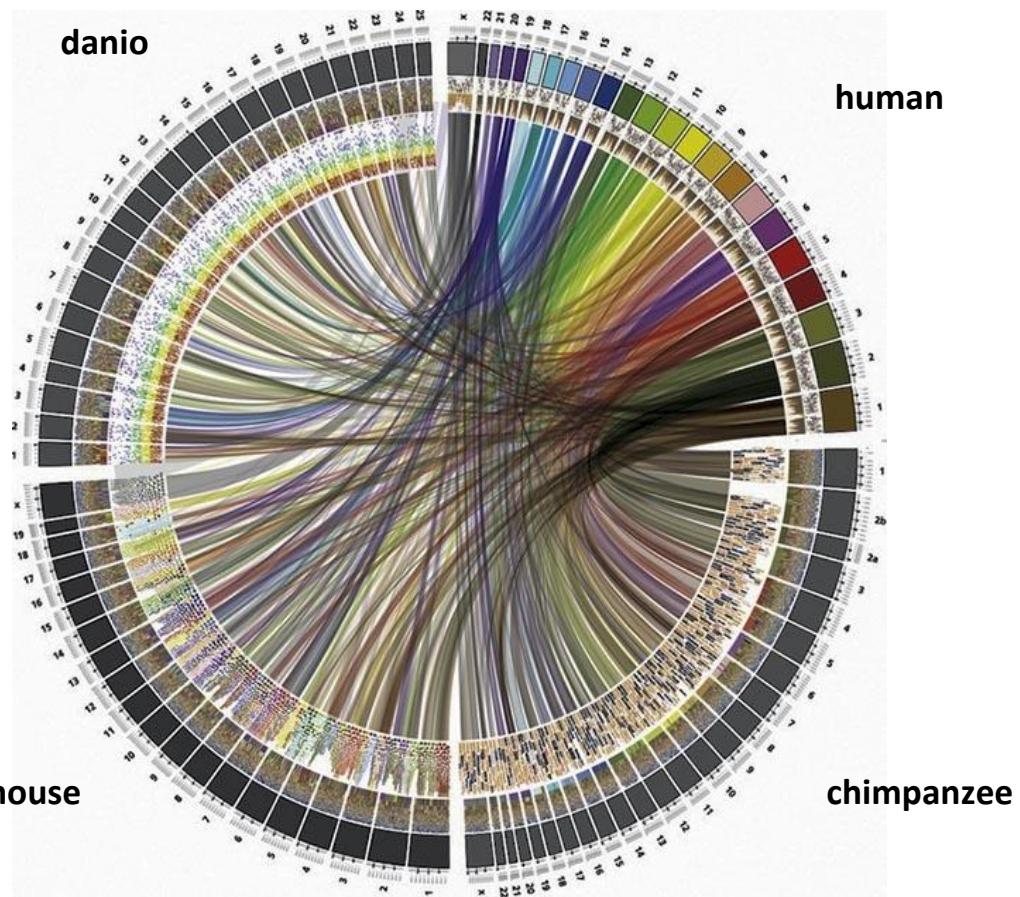


# ZOO-FISH

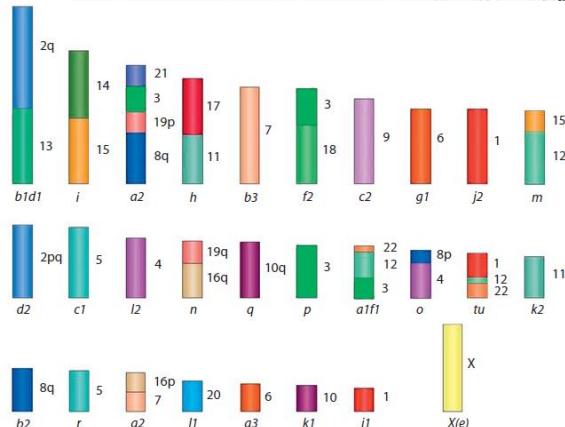
- cross-species chromosome painting, which uses painting probes specific for whole chromosomes, enables detecting homologous synteny blocks, the occurrence of which is evidence that species share a common ancestry and are related.



Ferguson-Smith & Trifonov 2007

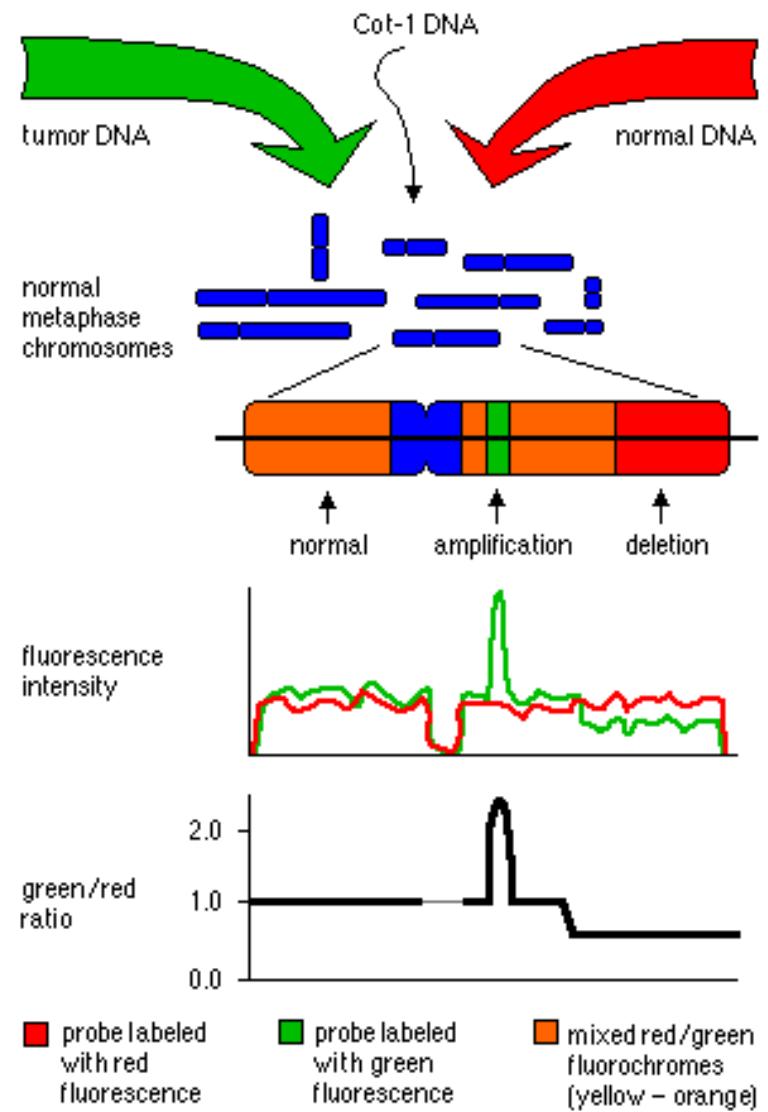
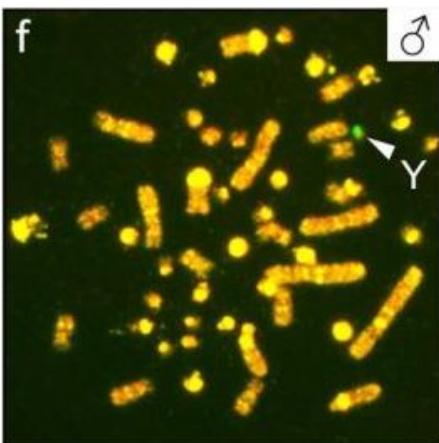
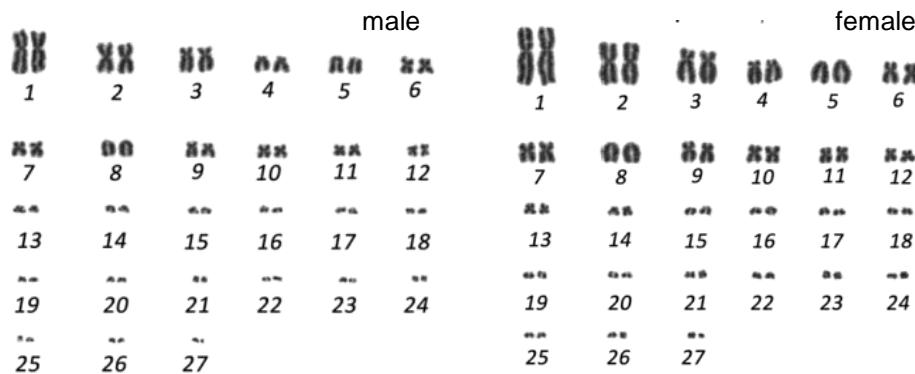


Biltueva et al. 2011

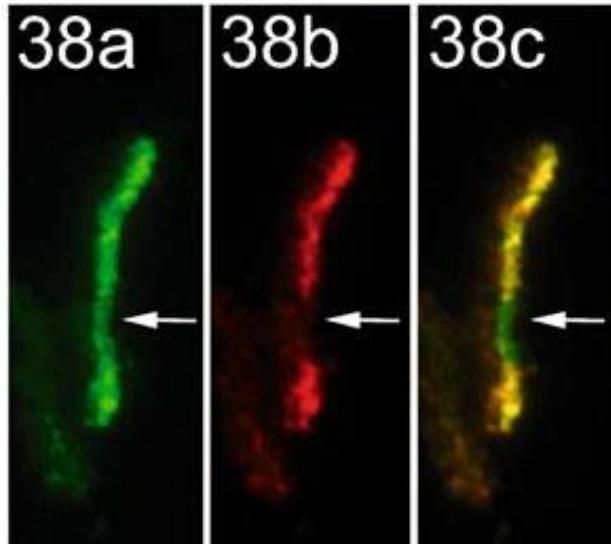


Ancestral karyotype of the genus *Sorex*  
Used painting probes of human

# CGH – comparative genomic hybridization



# CGH – comparative genomic hybridization



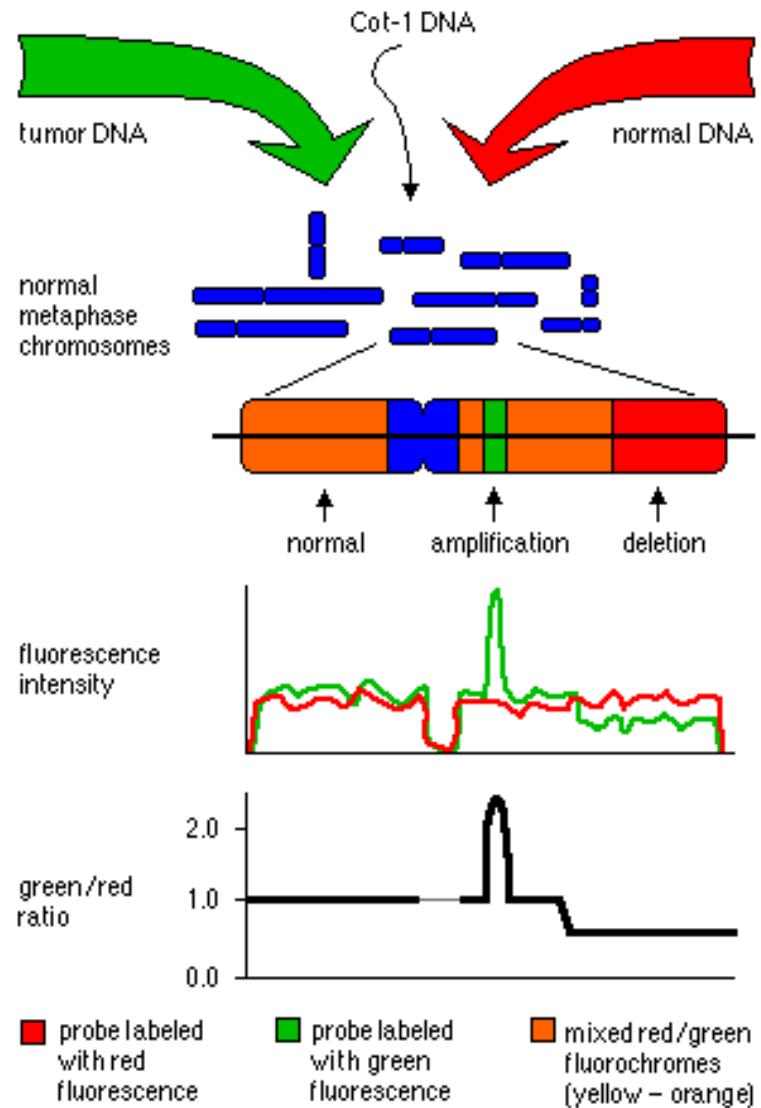
## Sex chromosomes

CGH in pachytene of *Galleria mellonella*

female genomic probes were labelled with Alexa Fluor 488 (green)  
male-derived genomic probes with Cy3 (red)

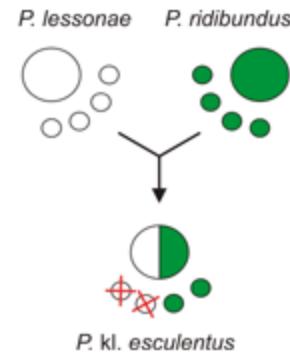
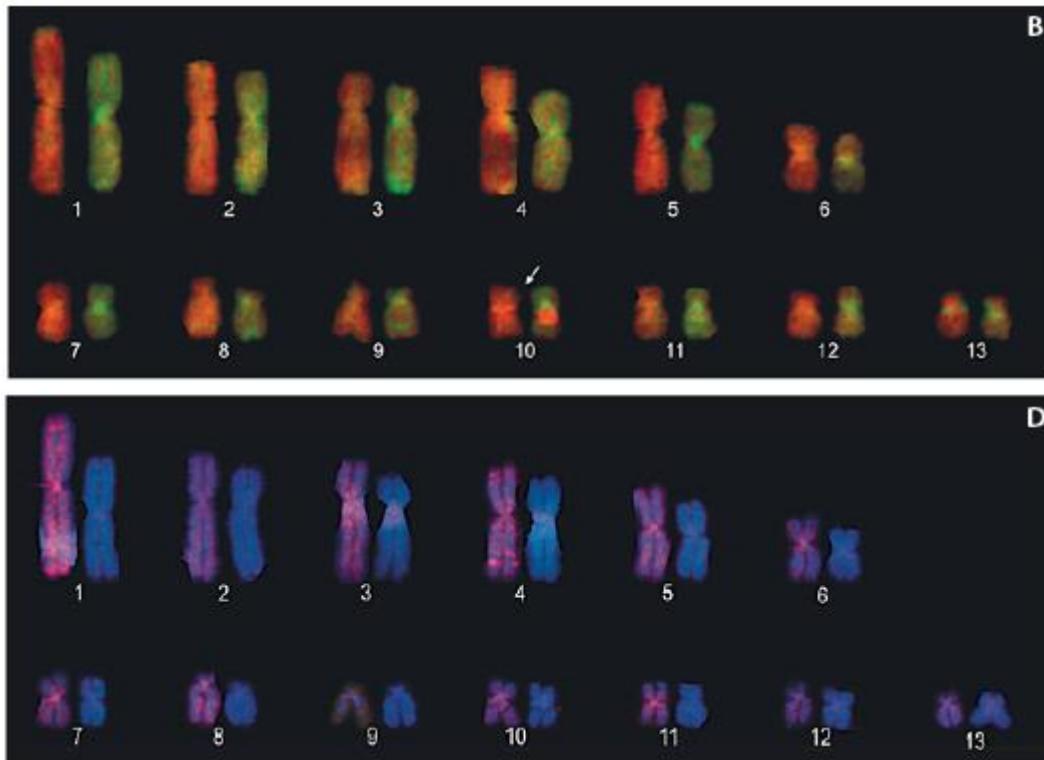
Arrow indicates a region of the W chromosome exclusively  
stained by female genomic probe.

Vítková et al. 2007



## GISH – genomic *in situ* hybridization

- a type of FISH, uses total genomic DNA from one species as the labeled probe and unlabeled genomic DNA from another species at a much higher concentration as blocking DNA, substantially increasing the hybridization specificity



GISH on chromosomes of the water frog *Pelophylax esculentus* obtained from bone marrow of a single female.

**B.** Metaphase chromosomes hybridized with the Alexa Fluor 488-labeled genomic probe from *P. lessonae* (green signals); chromosomes were counterstained with PI (red)

**D.** Metaphase chromosomes hybridized with the Cy3-labeled genomic probe from *P. ridibundus* (red signals); chromosomes were counterstained with DAPI (blue). (Zalesna et al. 2011)

Thank you for your attention

