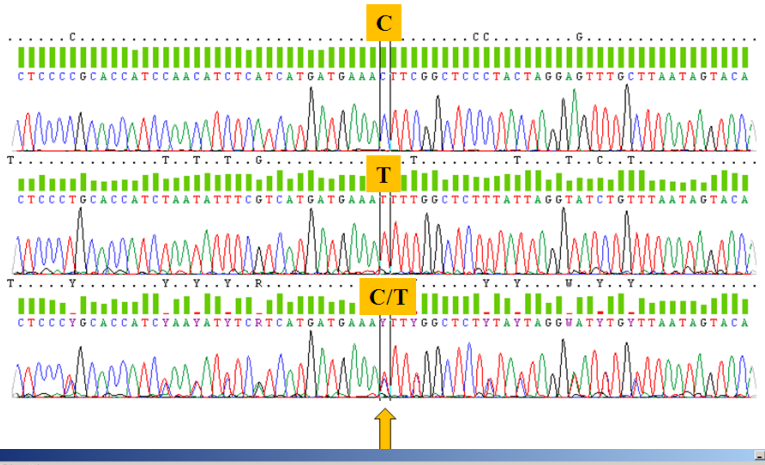
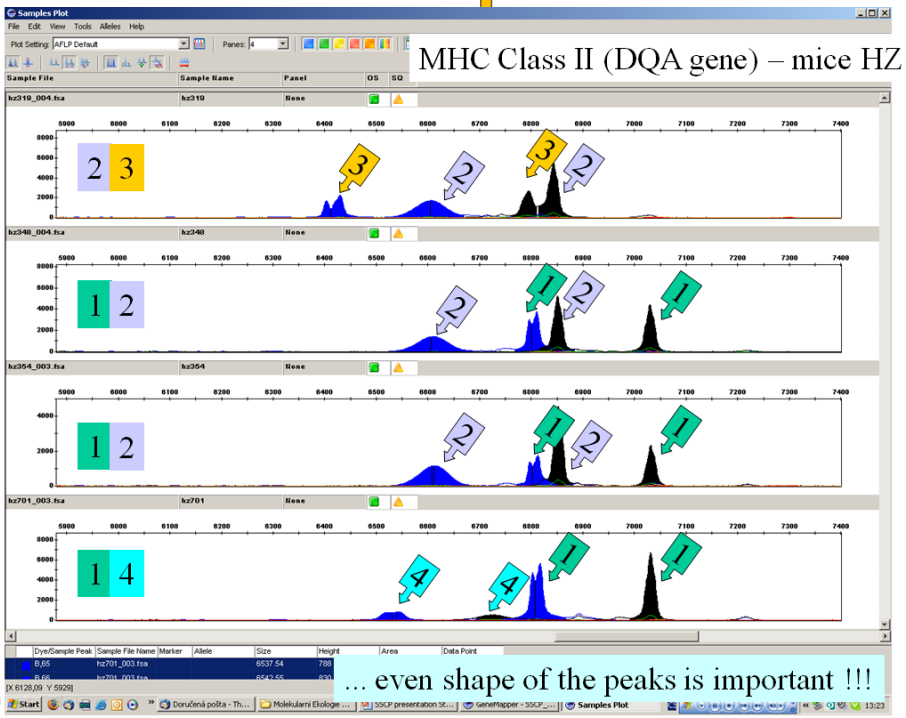
SNPs genotyping - sekvenování?
Je drahé a nejasné u heterozygotů



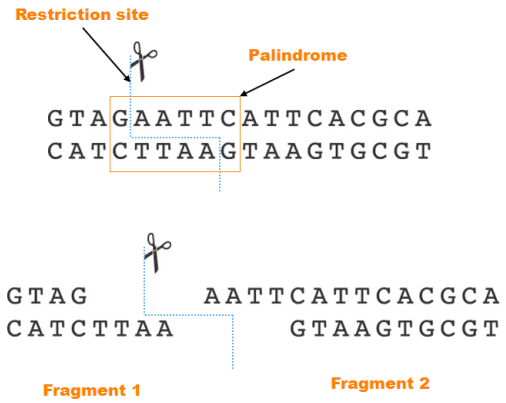


SNP genotyping - old standards

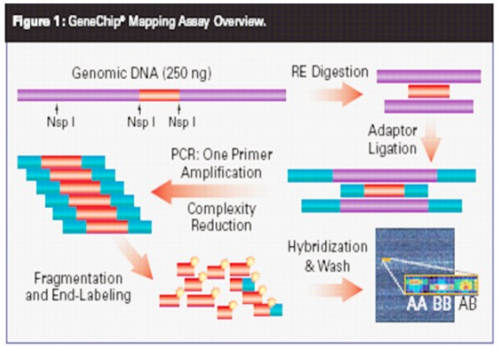
PCR-RFLP
(restriction fragments length polymorphism)

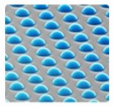
Enzyme Site Recognition

- Each enzyme digests (cuts) DNA at a specific sequence = restriction site
- Enzymes recognize 4- or 6- base pair, palindromic sequences (eg GAATTC)

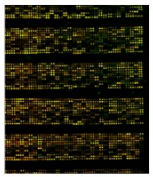


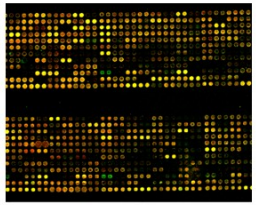
Detekce: Affymetrix, Illumina





BeadArray
(Illumina)





10 – 500 tisíc SNP znaků najednou – „chip technology“

Typy genetických markerů

	Single locus	Codominant	PCR assay	Overall variability
Nuclear multilocus				
Nuclear single locus				
Alozymy	Yes	Yes	No	Low-medium
Mikrosatelity	Yes	Yes	Yes	High
SINE (LINE)	Yes	Yes	Yes	Low
SNPs (sekvence)	Yes	Yes	Yes	Low-high

Multi-locus genetic markers

- Mnoho znaků náhodně rozmístěných v genomu – **celogenomový scan**

➢ ***minisatellite DNA fingerprinting***

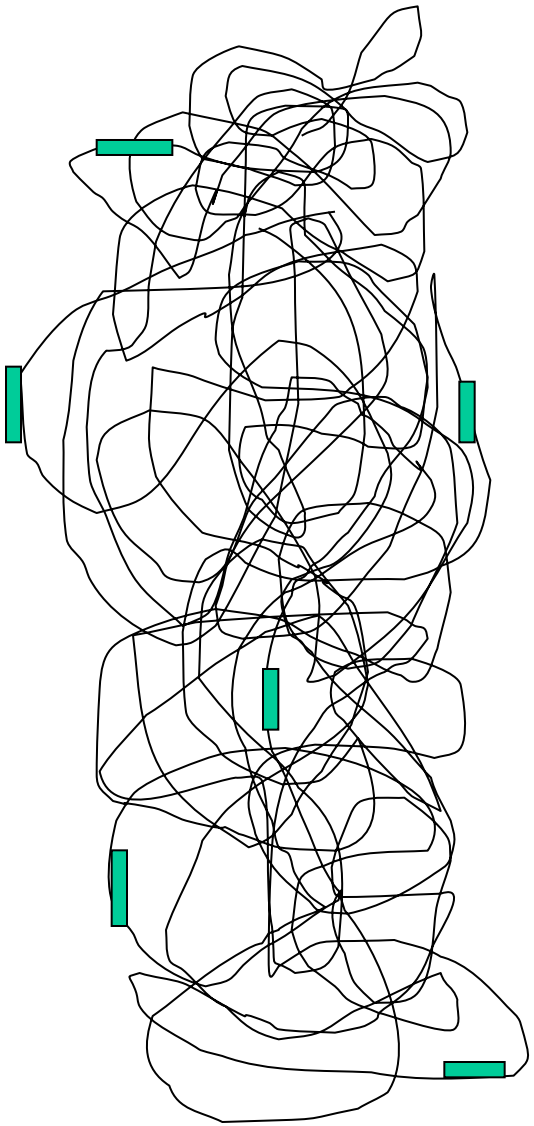
➢ ***RAPD*** (randomly amplified polymorphic DNA)

➢ ***AFLP*** (amplified fragment length polymorphism)

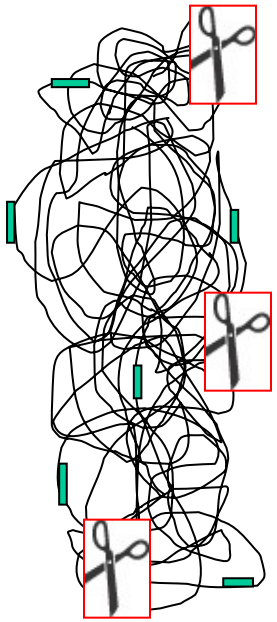
- presence vs. absence **restrikčního místa** (AFLP) **či místa pro dosednutí primerů** (RAPD) = **dominantní znaky** (neodliší heterozygota – proužek na gelu buď je nebo není)

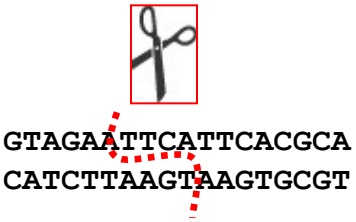
- není nutno znát předem genom studovaného druhu (tj. primery)

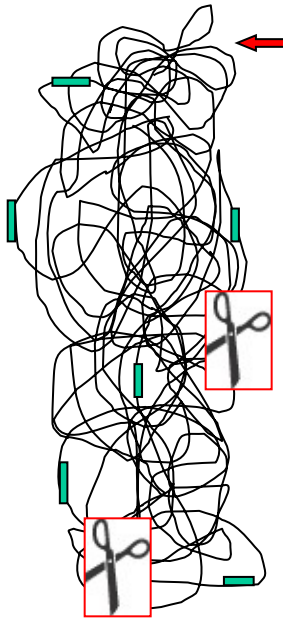
Př.: chromozóm 1



Každý jedinec má jedinečný genom







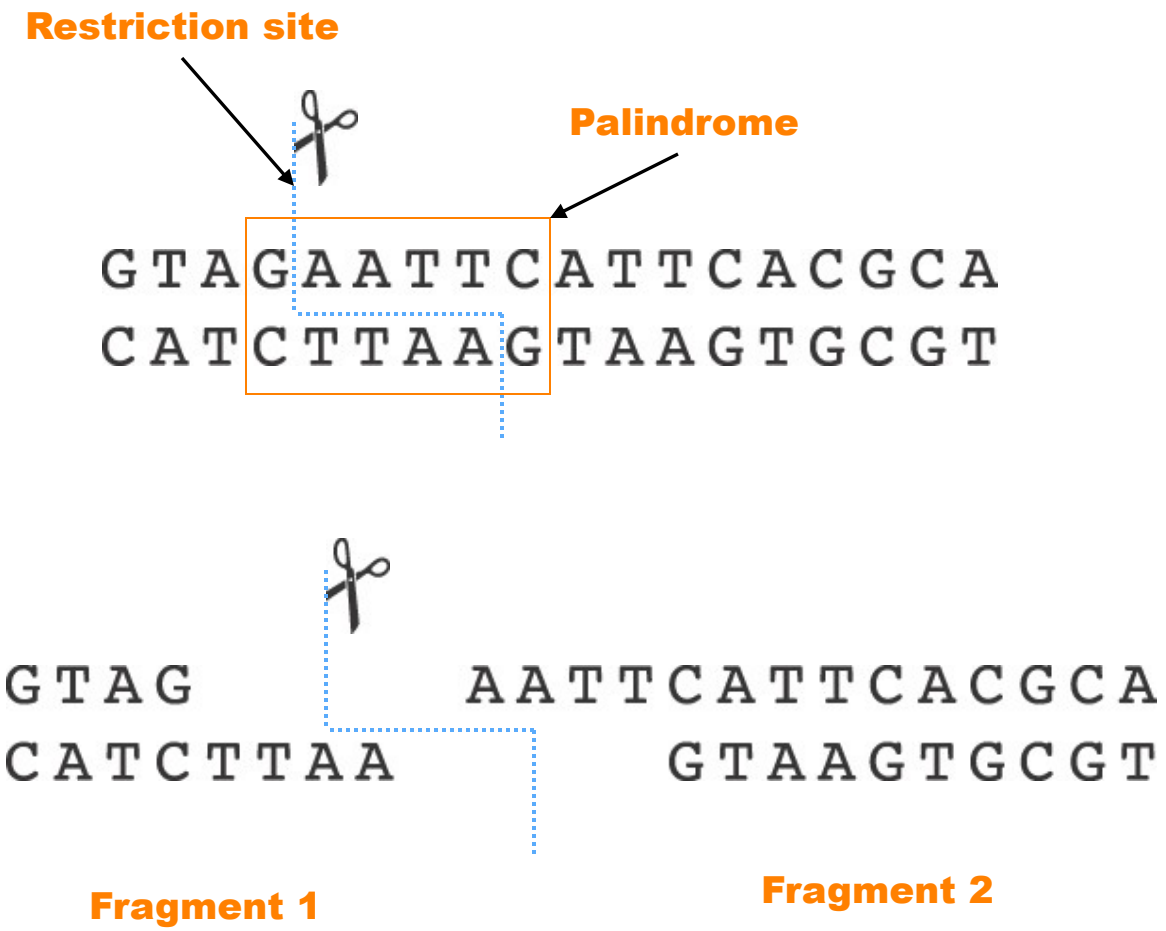
Záměna v restrikčním místě = zde ke štěpení nedojde

GTAGAATgCATTCACGCA
CATCTTAcGTAAGTGCGT

1. Ztráta nebo nabytí restrikčního místa

Enzyme Site Recognition

- **Each enzyme digests (cuts) DNA at a specific sequence = restriction site**
- **Enzymes recognize 4- or 6- base pair, palindromic sequences (eg GAATTC)**

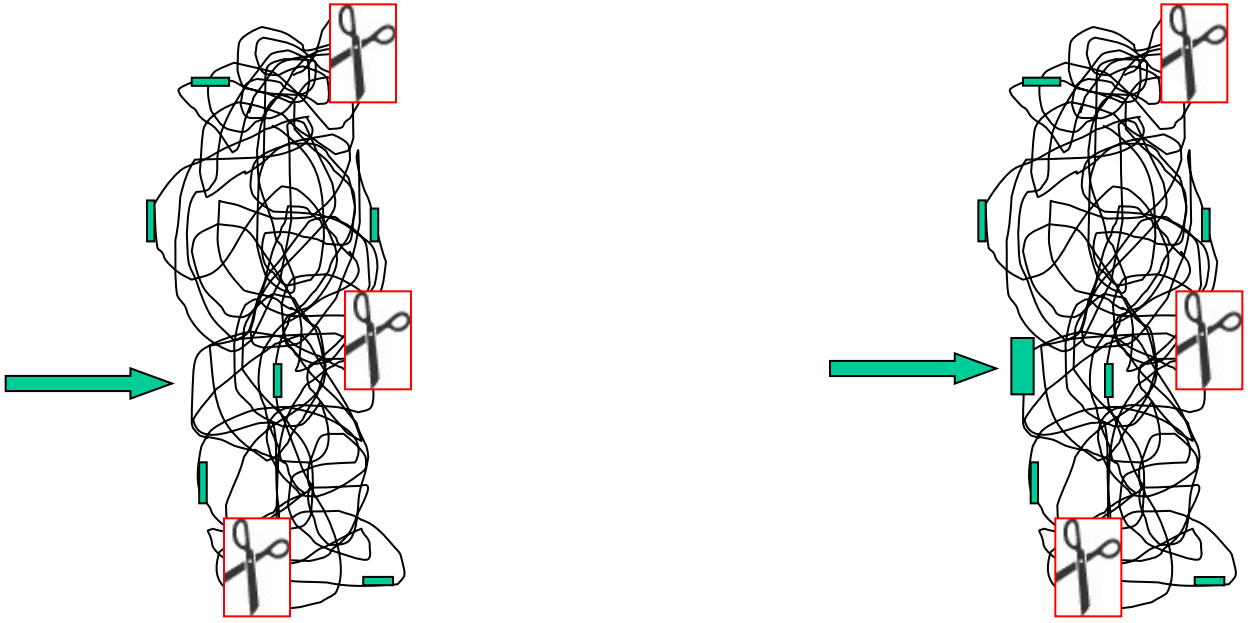


Common Restriction Enzymes

EcoRI
- *Eschericha coli*
- 5 prime overhang

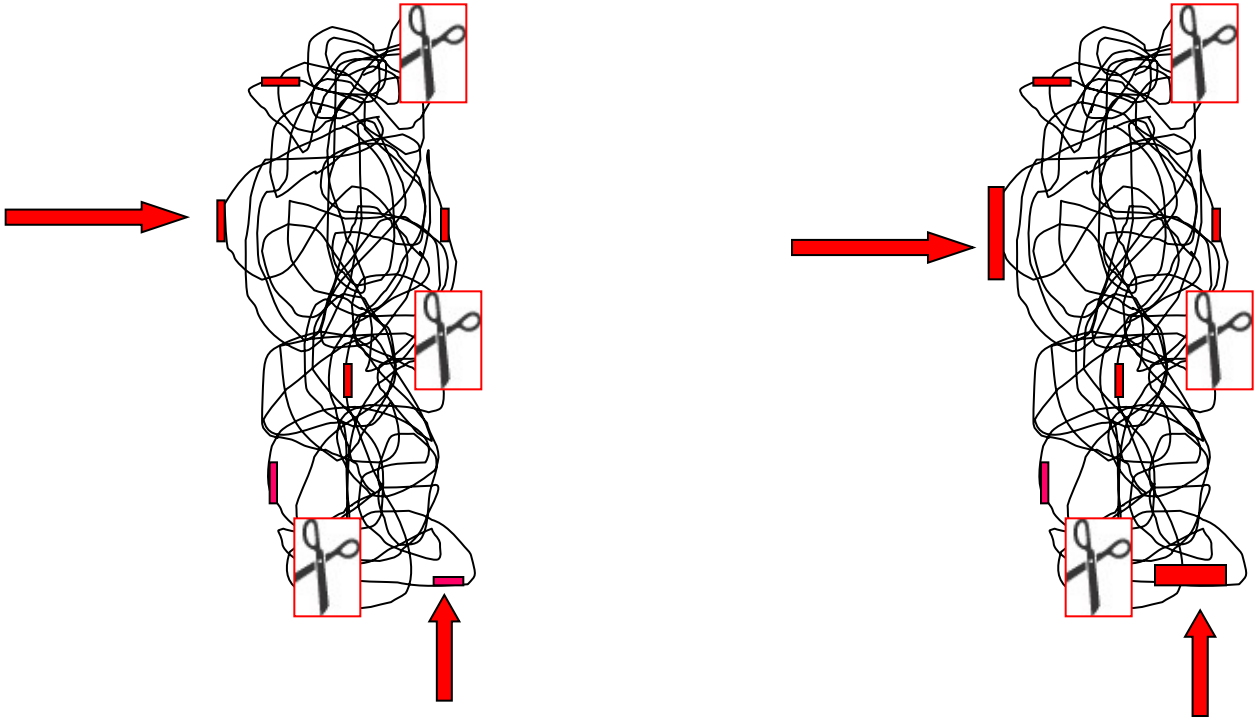
PstI
- *Providencia stuartii*
- 3 prime overhang

Každý jedinec má jedinečný genom



2. Ztráta nebo nabytí SINE (např. *Alu* sekvence) nebo LINE

Každý jedinec má jedinečný genom



3. Vysoká mutační rychlost minisatelitů a mikrosatelitů – rozdíly v počtu repeticí, tj. v délce daného úseku

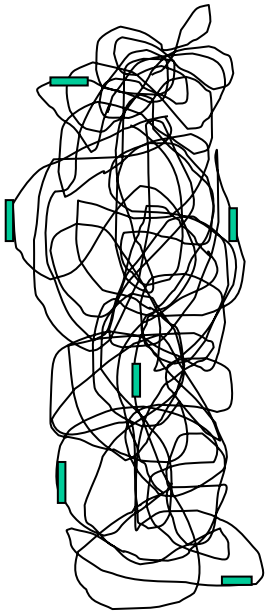
Repetitivní DNA

DNA	Typical sequence length (bp)	Location
Satellites (>10^6 repeats/genome)	5-100	Tandem arrays, scattered throughout the genome
Minisatellites (>10^3 loci/genome)	20-300	Tandem arrays up to 5 kb in length, scattered throughout the genome
Microsatellites (>10^4 loci/genome)	1-6	Tandem arrays up to a few 100 bp in length, scattered throughout the genome
Telomeres	4-8	Tandem arrays up to 1kb in legth, at the ends of each chromosome
SINEs (>10^5/genome)	50-500 (100-300)	Interspersed throughout the genome
LINEs (>10^3/genome)	1-5 k	Interspersed throughout the genome

(Minisatellite) DNA fingerprinting
(Jeffreys et al. 1985)

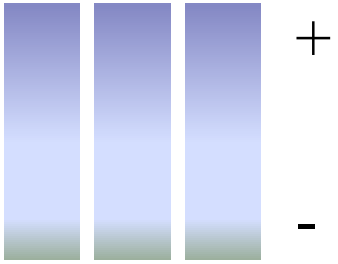
- první celogenomový screening

- restrikční štěpení kompletní DNA – sekvenčně specifické restrikční endonukleázy

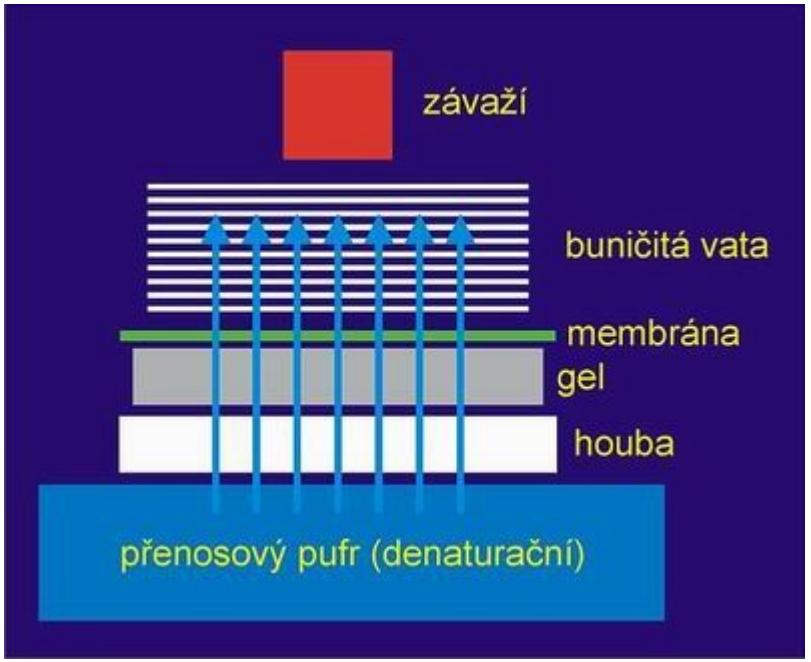


Minisatellite DNA fingerprinting

- elektroforéza rozštěpené DNA
- Southern blotting – přenesení DNA na membránu

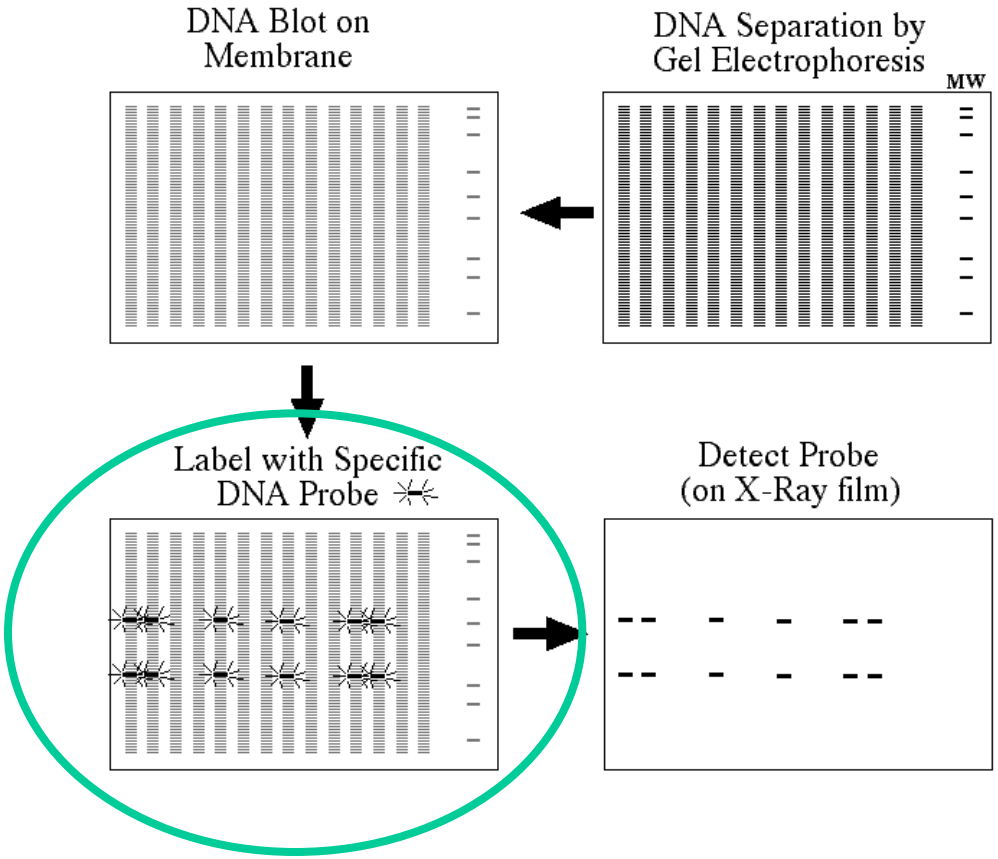


„smear“



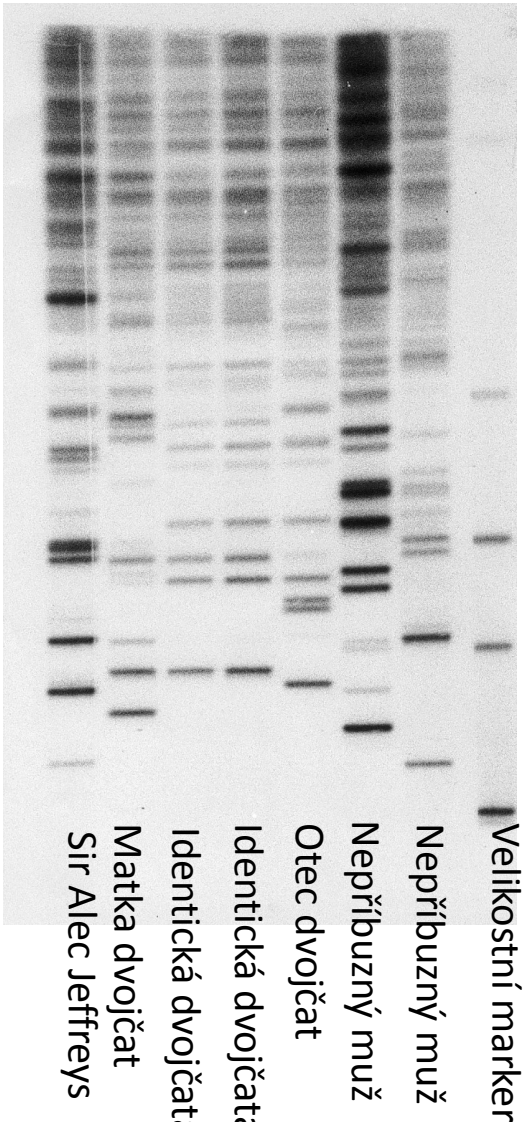
Minisatellite DNA fingerprinting

- elektroforéza
- Southern blotting – přenesení DNA na membránu
- hybridizace se značenou sondou (nejčastěji radioaktivní značení), tj. specifickou sekvencí odpovídající danému minisatelitu (popř. SINE)



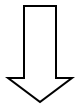
Minisatellite DNA fingerprinting

- elektroforéza
- Southern blotting – přenesení DNA na membránu
- hybridizace se značenou sondou, tj. specifickou sekvencí odpovídající danému minisatelitu
- zásadní objevy např. EPC u ptáků
- v posledních 10-15 letech – přesun k PCR-based metodám

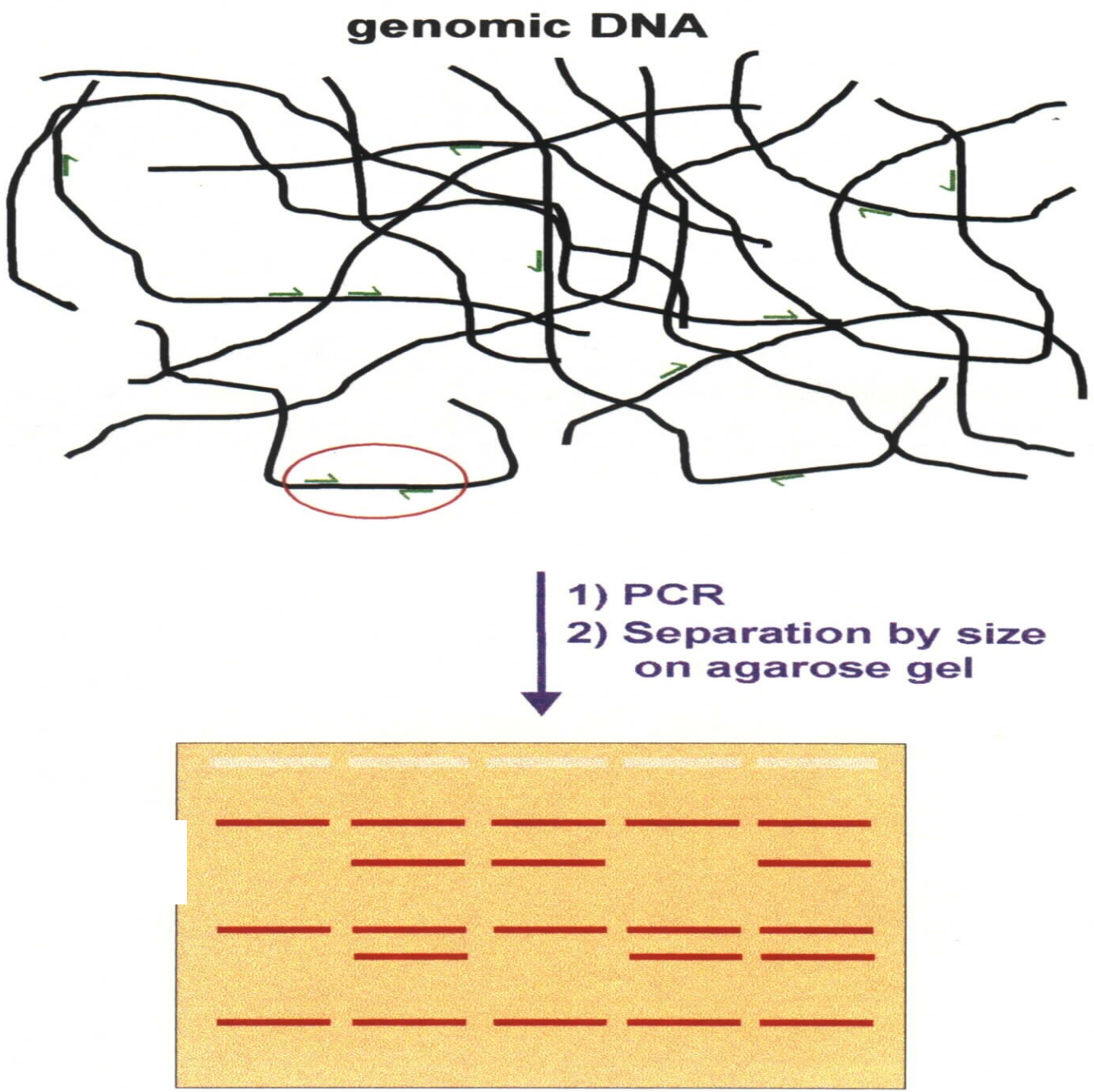


RAPD (randomly amplified polymorphic DNA)

Krátké náhodné oligonukleotidy
(~ 10 bp) jako primery



PCR za málo specifických podmínek


genomic DNA
1) PCR
2) Separation by size
on agarose gel

Variabilní DNA detekovaná metodou RAPD je důsledkem ztráty RAPD lokusů v důsledku:

a) Změna sekvence v místě nasedání primeru

b) Delece místa nasedání primeru

c) Velká inzerce mezi dvěma místy nasedání primeru

RAPD - review

Krátké náhodné oligonukleotidy
(~ 10 bp) jako primery

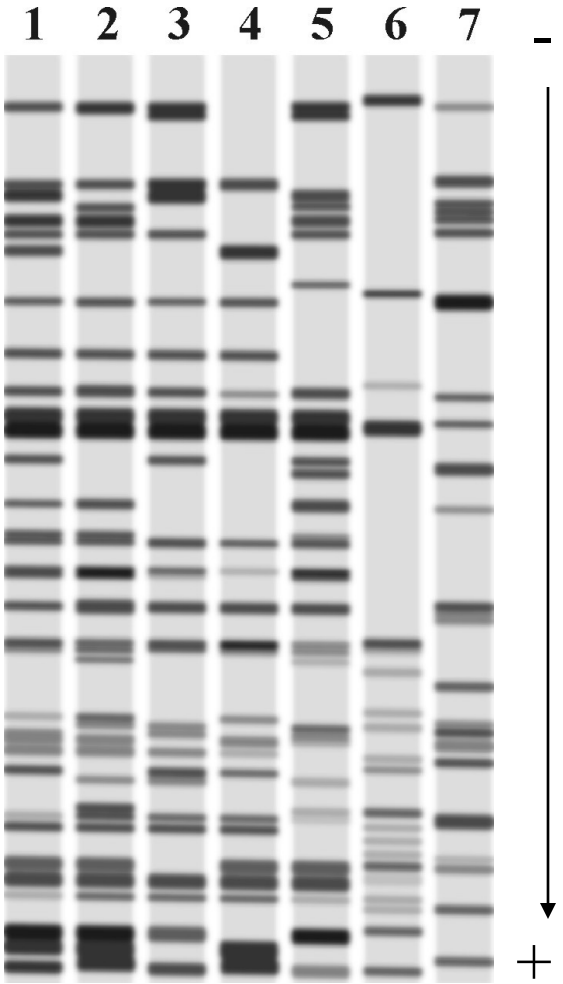
⇩

PCR za málo specifických podmínek

⇩

Detekce PCR produktů elektroforézou

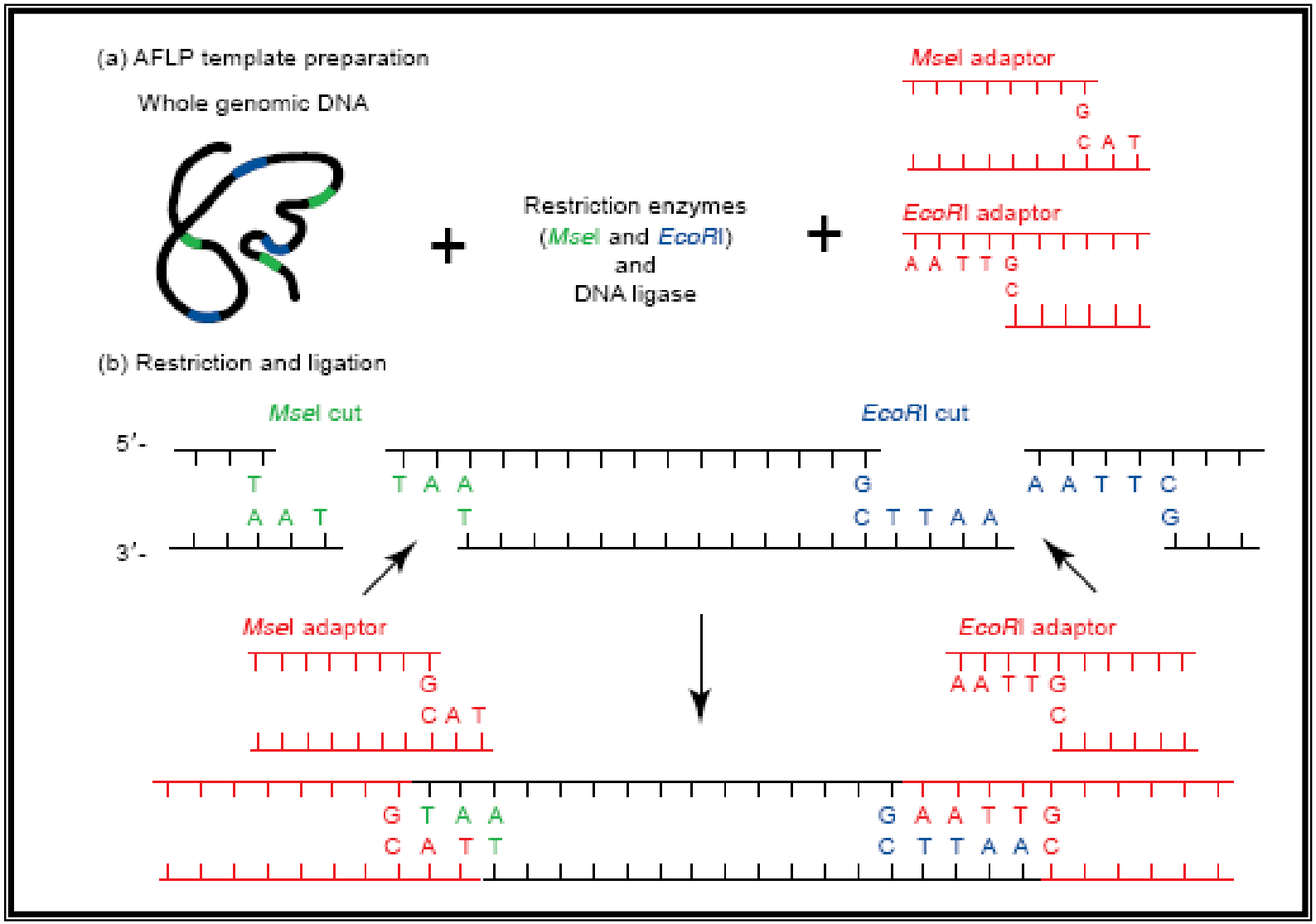
Nízká opakovatelnost v důsledku mnoha faktorů ovlivňujících PCR – dnes již není akceptována jako metoda např. pro studium populační struktury



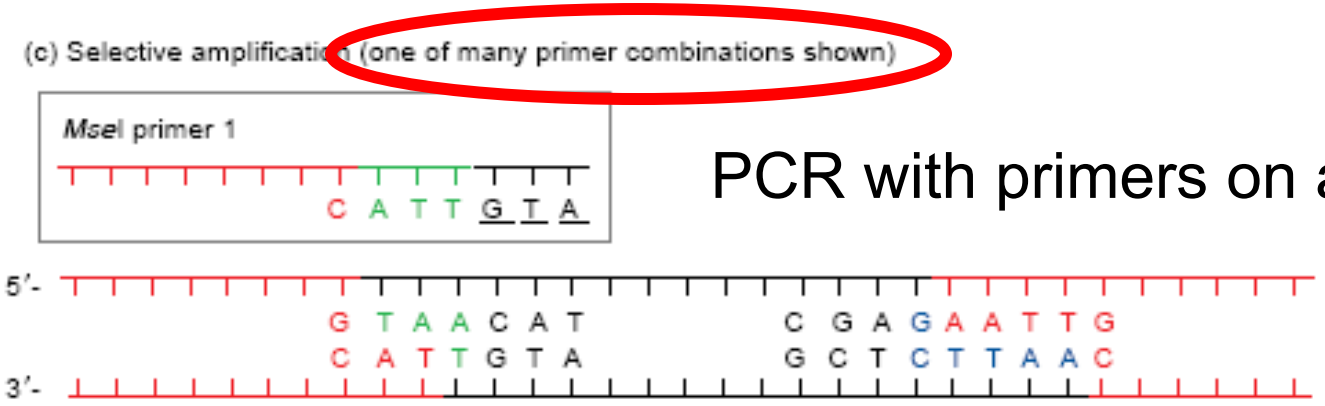
AFLP (amplified fragments length polymorphism)

- levná, jednoduchá, rychlá a spolehlivá metoda na generování stovek informativních genetických markerů
- současný screening mnoha různých DNA oblastí distribuovaných náhodně v genomu
- lépe reprodukovatelná než RAPD – obsahuje krok se specifickou PCR
- „genome scan“ – hledání asociací s fenotypovými znaky

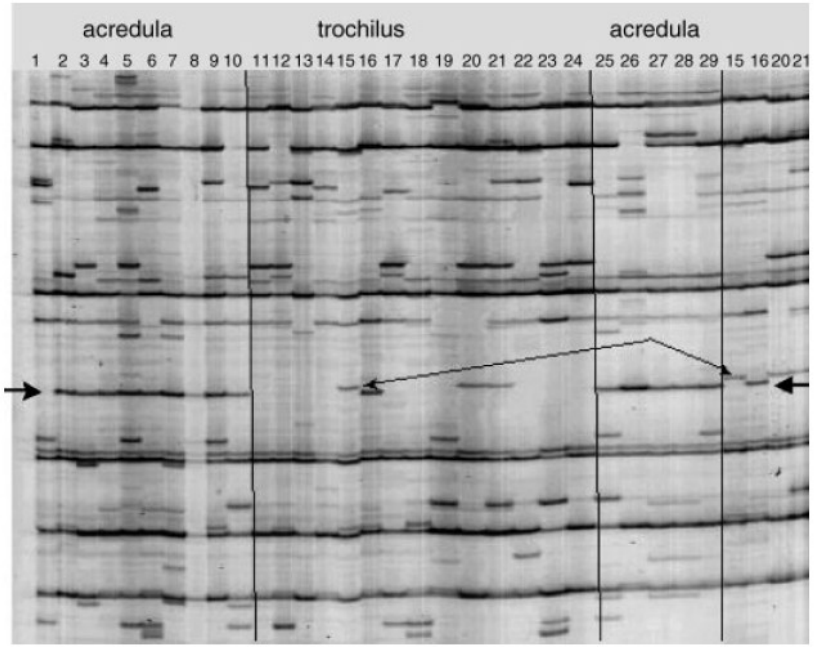
Princip AFLP metody („generating AFLP markers")



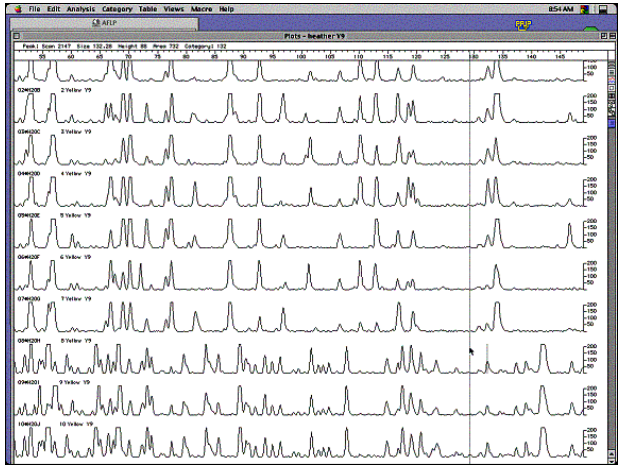
Generating AFLP markers



PCR with primers on adaptors



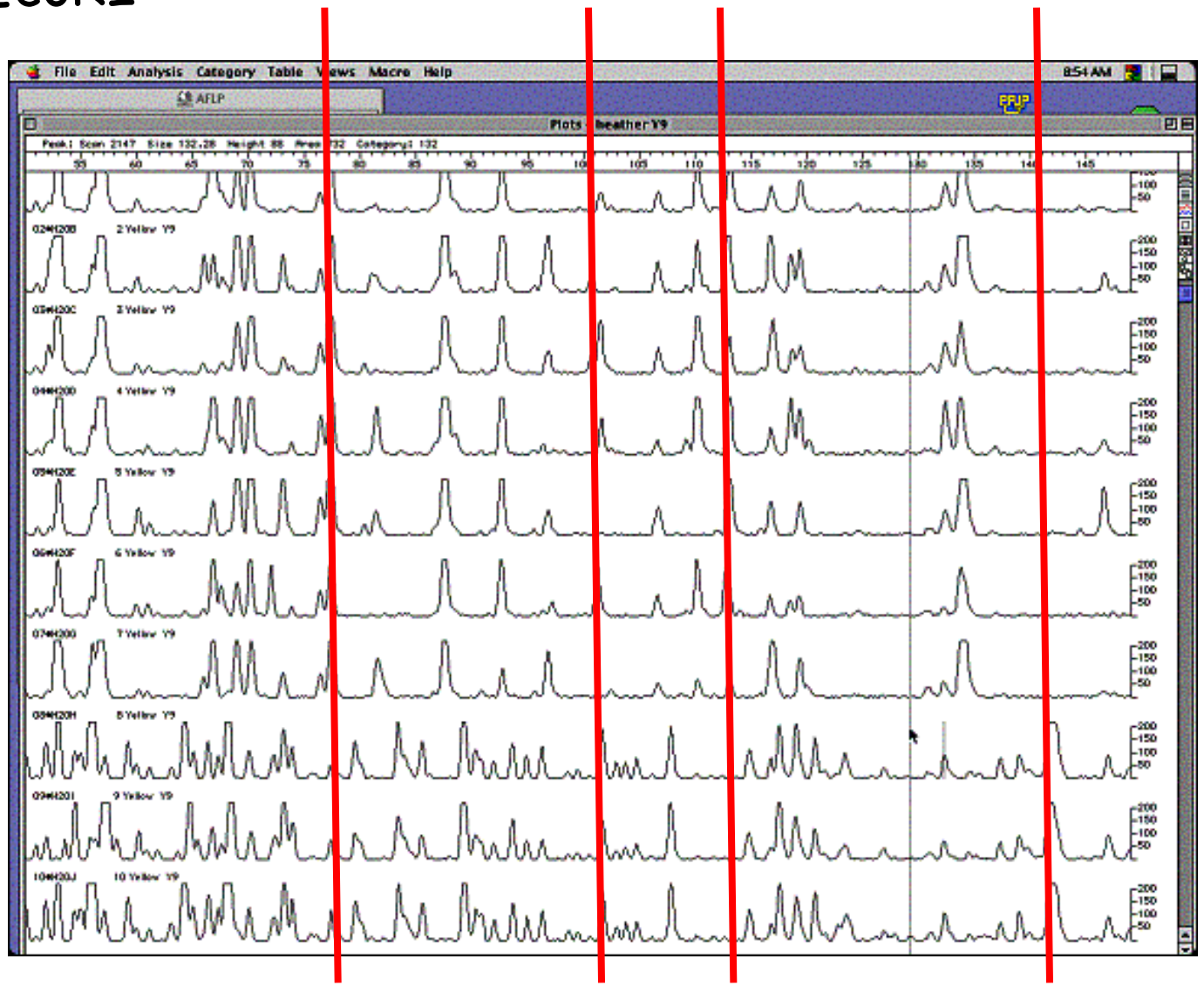
multi-locus genotype



„capillary version“

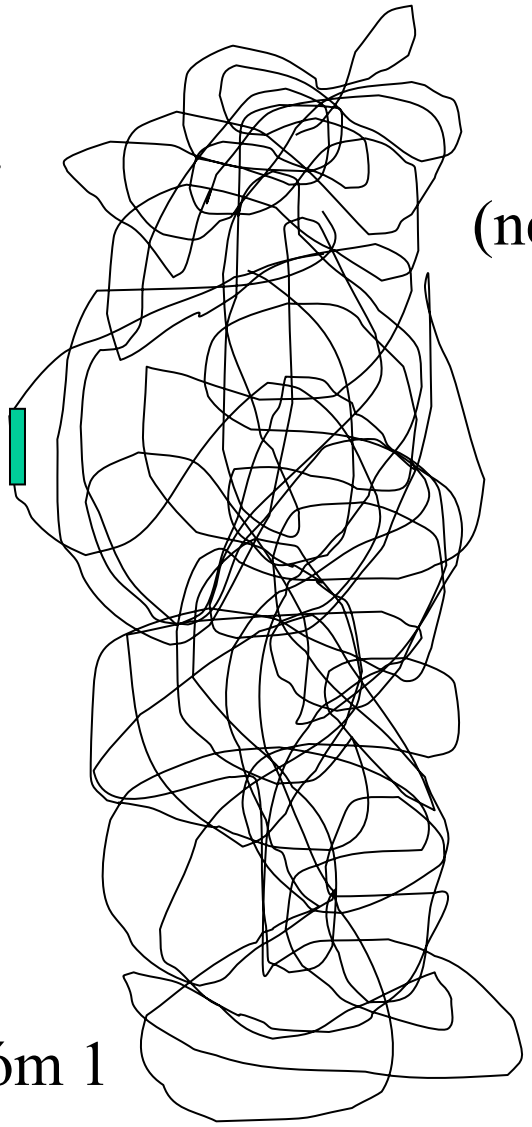
Ex.:
Combination
MseI + EcoRI

Automatizované čtení elektroforetogramu podle zadaných kritérií (např. pozice a minimální výška píku)

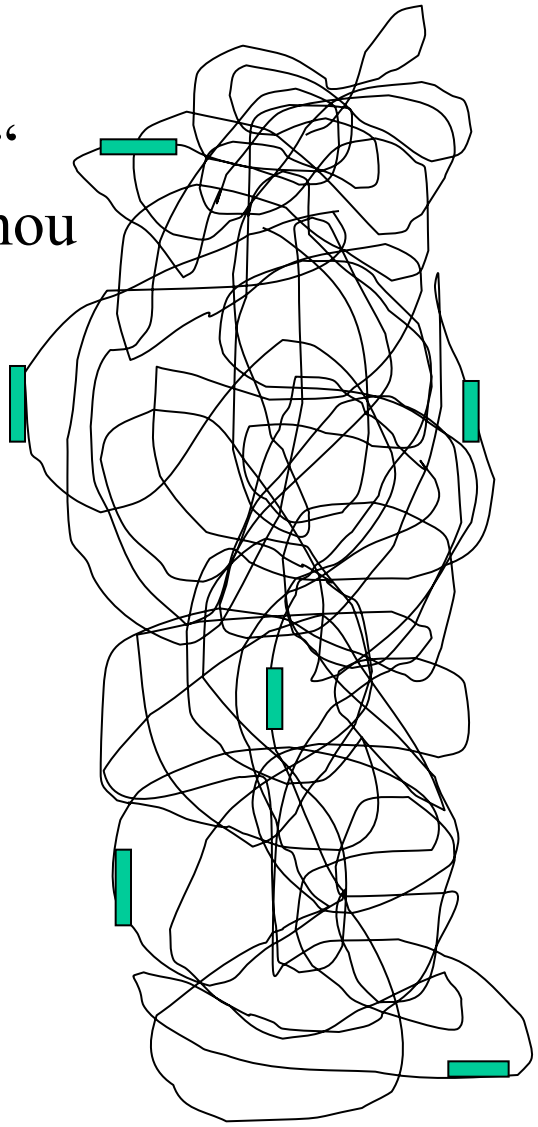


Typy genetických markerů

„single-locus“
(PCR)



„multi-locus“
(neznáme přesnou
lokalizaci
v genomu)



Př.: chromozóm 1

Budoucnost genetických metod v zoologickém výzkumu

1. Nové postupy při sekvenování DNA („genomics")

Molecular Ecology Resources (2008) 8, 3–17 doi: 10.1111/j.1471-8286.2007.02019.x

TECHNICAL REVIEW

Sequencing breakthroughs for genomic ecology and evolutionary biology

MATTHEW E. HUDSON
Department of Crop Sciences, University of Illinois, Urbana, 334 NSRC, 1101 W. Peabody Blvd., IL 61801, USA

4-kapilární sekvenátor

=

96 x 500 bp/12 hodin

=

cca 100 000 bp/den

Next-generation sequencing

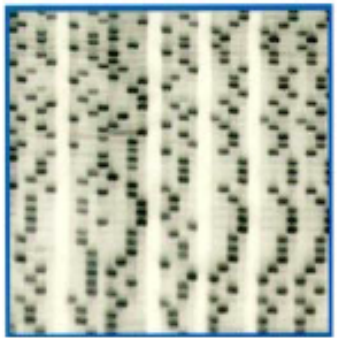
=

cca 1 000 000 000 bp/den

electrophoresis

Evoluce Sangerova sekvenování

Pre-1992
"old fashioned way"



S35 ddNTPs
Gels
Manual loading
Manual base calling

1992-1999
ABI 373/377

Fluorescent ddNTPs*
Gels
Manual loading
Automated base calling*

1999
ABI 3700

Fluorescent ddNTPs
Capillaries*
Robotic loading*
Automated base calling
Breaks down frequently

2003
ABI 3730XL

Fluorescent ddNTPs
Capillaries
Robotic loading
Automated base calling
Reliable*

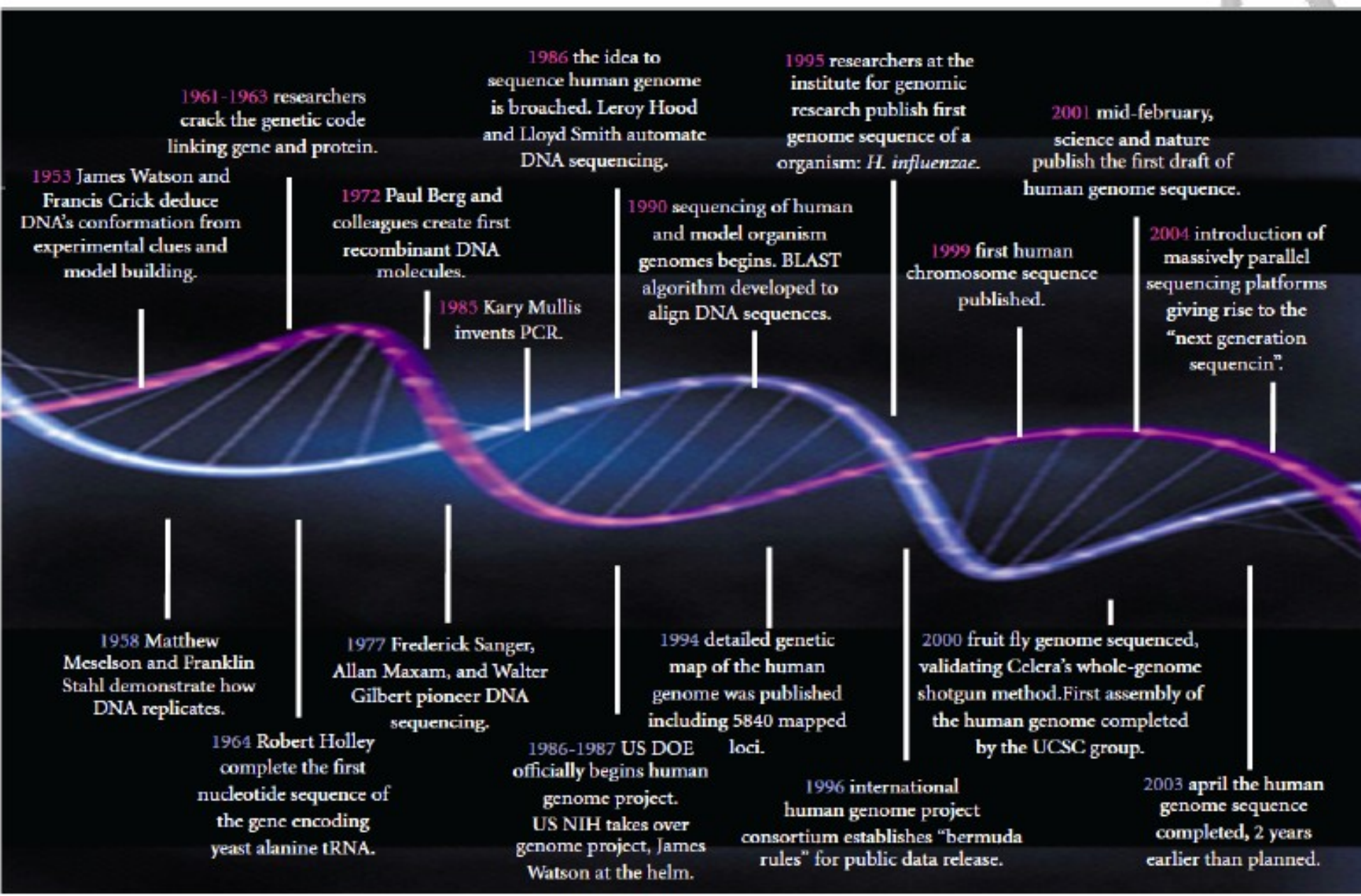
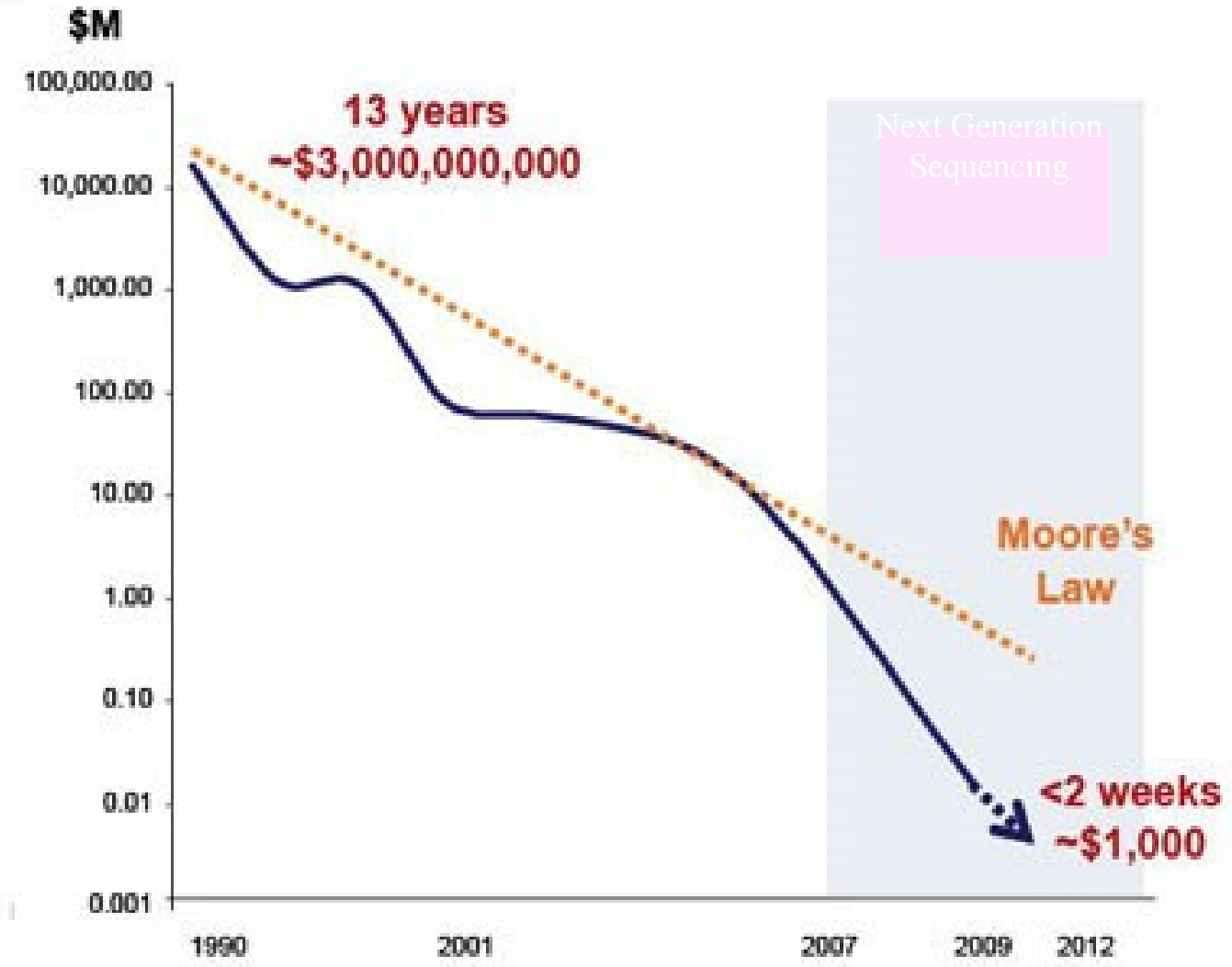


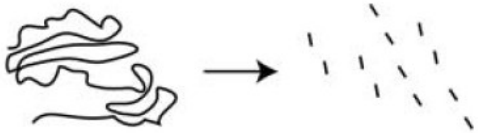
FIGURE 1: Evolution of DNA revolution.

Cost per Human Genome

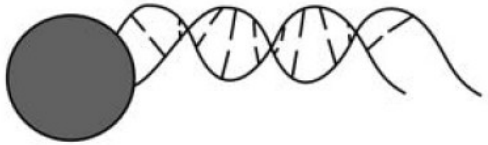


„Next generation sequencing"

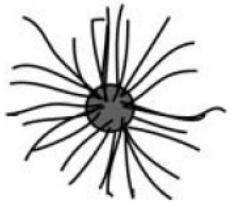
1) Randomly fragment many molecules of target DNA



2) Immoblize individual DNA molecules on solid support



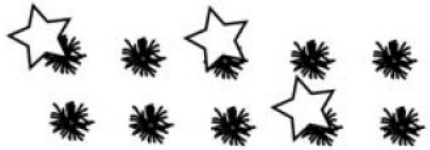
3) Amplify DNA in clonal 'polymerase colony'



„polonies"
(polymerase colonies)

4) Sequence DNA by adding liquid reagents to immoblized DNA colonies

5) Interrogate sequence incorporation *in situ* after each cycle using fluorescence scanning or chemiluminescence



... commercially available since August 2007

Available next-generation sequencing platforms

- **Roche 454**
- **Illumina/Solexa**
- ABI SOLiD
- ABI IonTorrent
- Polonator
- HeliScope
- …

454 pyrosequencing

- emulzní techniky amplifikace
  pikolitrové objemy
- simultánní sekvenování
  na destičce z optických vláken
  detekce pyrofosfátů uvolňovaných při inkorporaci bazí
- První generace GS20
  → 200 000 reakcí najednou
  (zhruba 20 milionů bp)
  dnes FLX → 400 000 reakcí najednou
  eukaryotní genom za týden!!!
- Délka jednotlivých sekvencí 100 – 400 (800 bp)

Molecular Ecology (2008) 17, 1629–1635

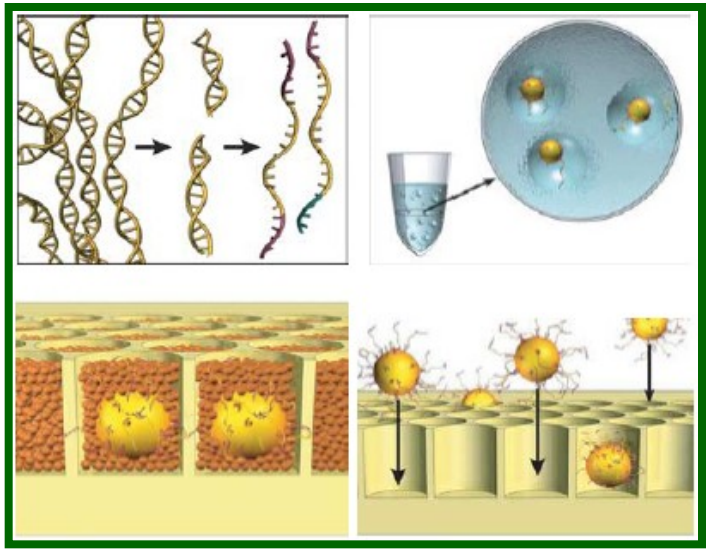
NEWS AND VIEWS

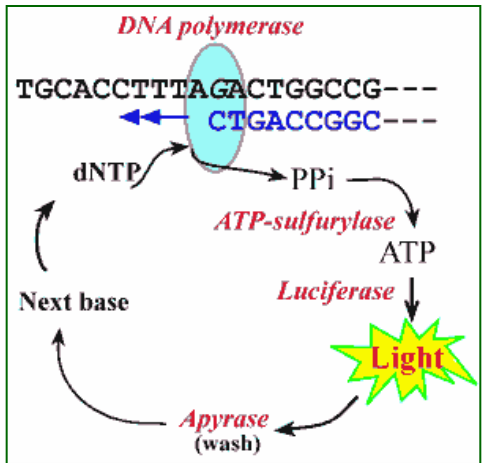
PERSPECTIVE

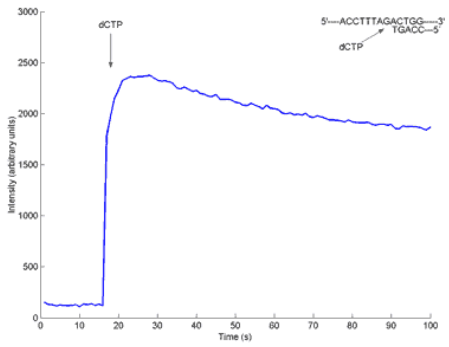
Sequencing goes 454 and takes large-scale genomics into the wild

HANS ELLEGREN
Department of Evolutionary Biology, Uppsala University, Norbyvägen 18D, SE-75236 Uppsala, Sweden

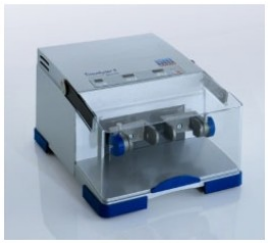
1 600 000 well plate







Pracovní postup



1

DNA Library Preparation

1. DNA Fragmentation (Nebulization)
2. DNA Fragment Size Selection
3. DNA Sample Quality Assessment (Nebulized or LMW DNA Sample)
4. Fragment End Polishing
5. Adaptor Ligation
6. Small Fragment Removal
7. Library Immobilization
8. Fill-In Reaction
9. Single-Stranded DNA Library Isolation
10. DNA Library Quality Assessment and Quantitation

Time: 11 - 72 h

General Laboratory 1

2

Emulsion-Based Clonal Amplification (emPCR)

1. Preparation of the Live and Mock Amplification Mixes
2. DNA Library Capture
3. Emulsification

Controlled Room

4. Amplification
5. Bead Recovery
6. DNA Library Bead Enrichment
7. Sequencing Primer Annealing

Time: 11 - 13 h

Amplicon Room

3

Sequencing / Genome Sequencer FLX Operation

1. The Pre-Wash
2. PicoTiterPlate Device Preparation
3. The Sequencing Run

Time: 11.5 h

General Laboratory 2

4

Data Processing and Analysis

1. Data Processing
   a) Image Processing
   b) Signal Processing
2. Data Analysis
   a) Assembly
   b) Mapping
   c) Amplicon Variant Analysis

Time: variable

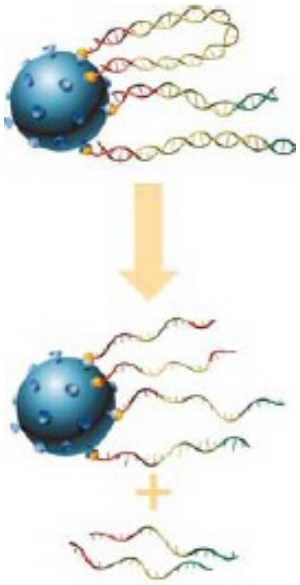
1. Příprava jednořetězcové DNA knihovny (ssDNA library preparation)

1 DNA Fragmentation (Nebulization):

5 Adaptor Ligation:

7 Library Immobilization:

9 ssDNA Library Isolation:



Adaptor A + **Adaptor B**

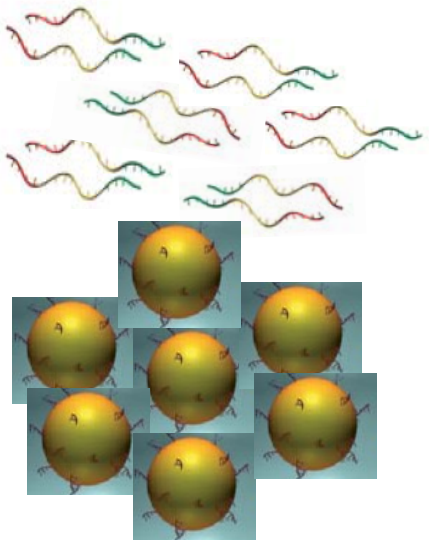
-Slouží jako vazebné místo primerů pro následnou PCR amplifikaci a sekvenování

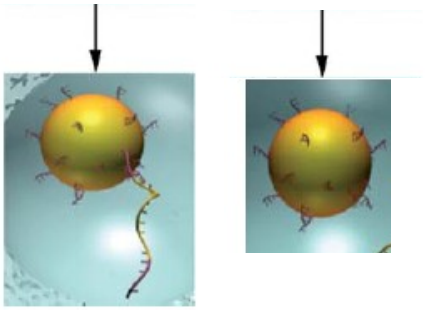
-Slouží k uchycení na kuličky (na adaptor B je připojen biotin)

2. Namnožení každé jednotlivé molekuly pomocí emulzní PCR (emPCR)

1 DNA Library Capture:

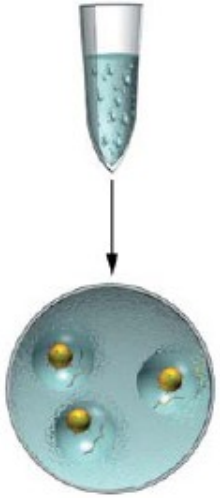
- poměry nastavit tak aby 1kulička ≤ 1 molekula DNA



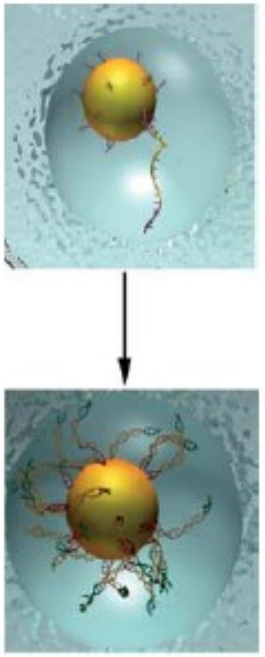


2 Preparation of the Amplific. Mixes

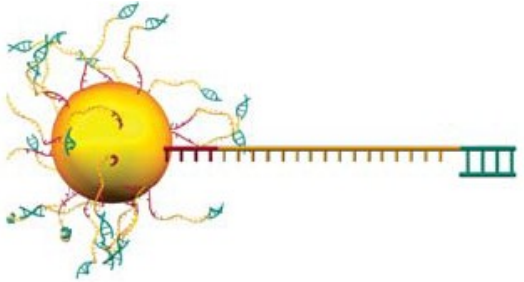
3 Emulsification:



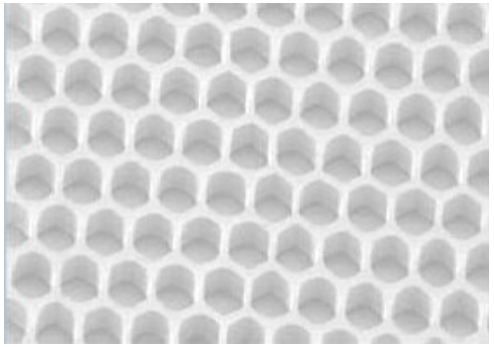
4 emPCR Amplification:



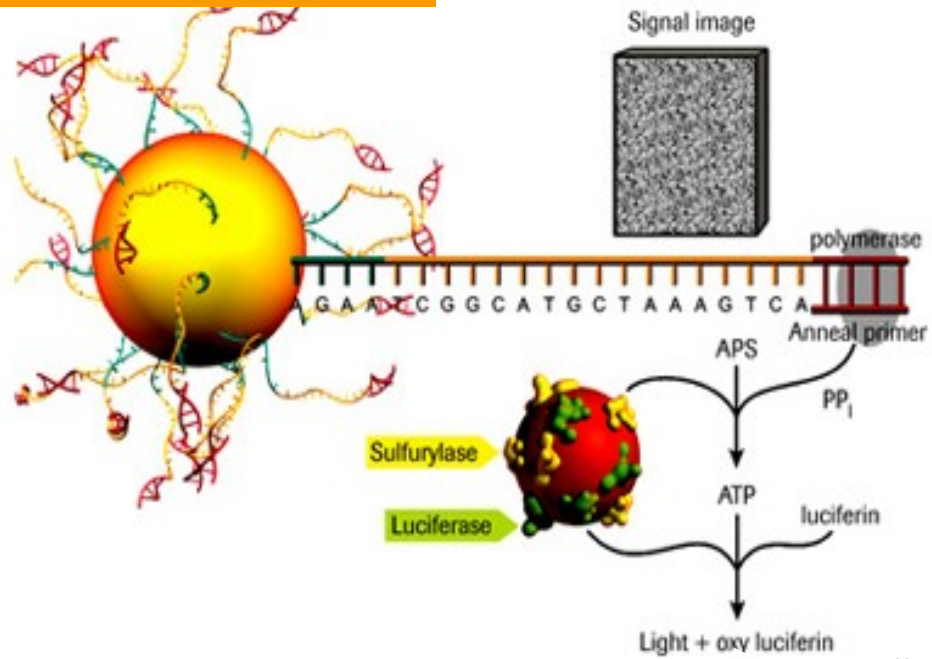
7 Sequencing Primer Annealing:



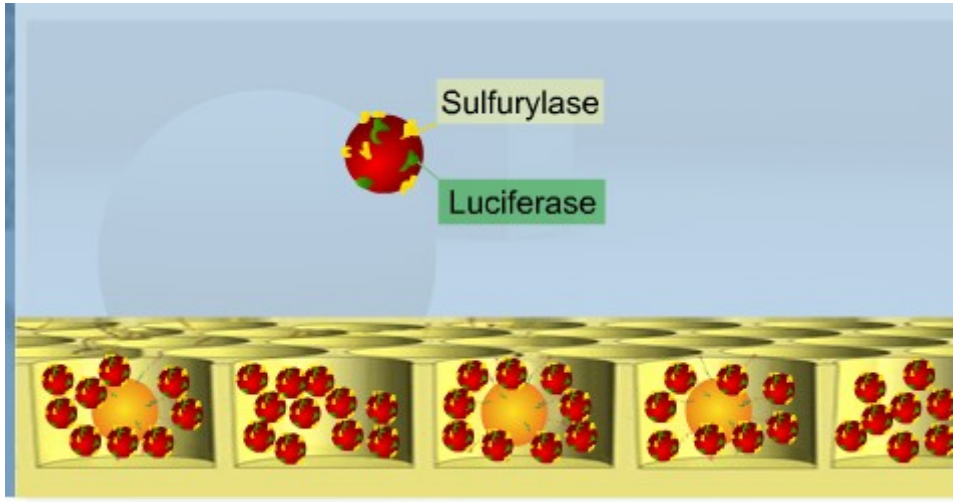
3. Pyrosekvenování („sequencing by synthesis“)

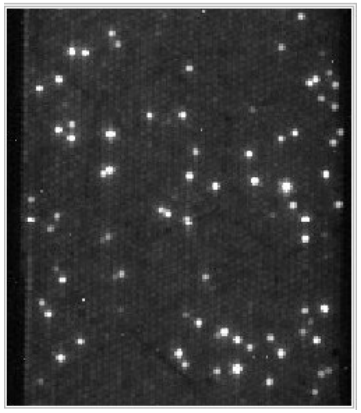


pikotitrační destička



Na jedné desticče 400 000 až 1milión jamek

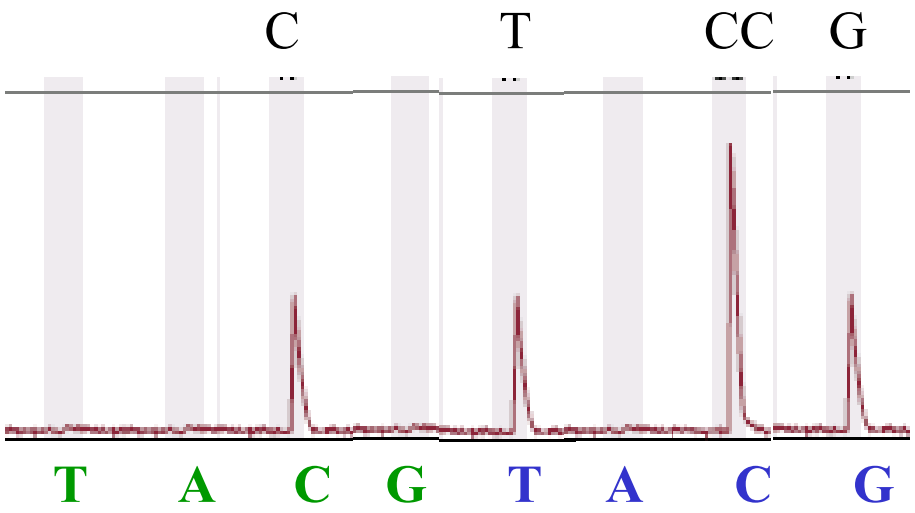




3. Pyrosekvenovani – detekce signálu

- postupně se přidávají nukleotidy v definovaném pořadí: např. TACG TACG TACG
- po přidání každého nukleotidu a detekci signálu se nukleotid odmyje a přidá se další odmyje

DNA sekvence: **C T C C G**



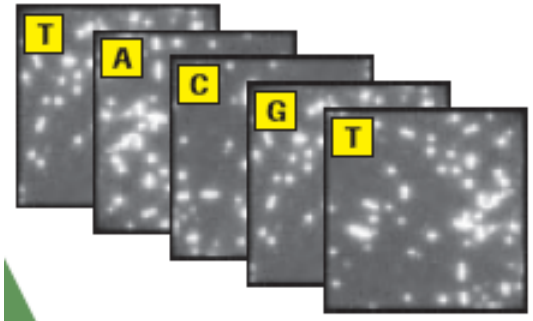
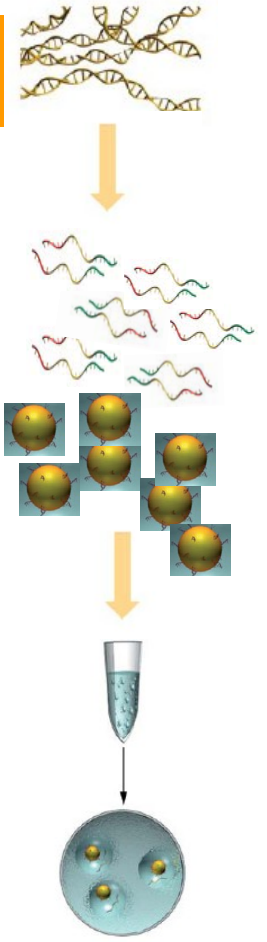


Image Files:
12-15 gigabytes
per run

Problém!!!! Homoplymery např. AAAAAAAAAA

High-throughput – paralelní sekvenování



1 běh (run) = 1 destička:

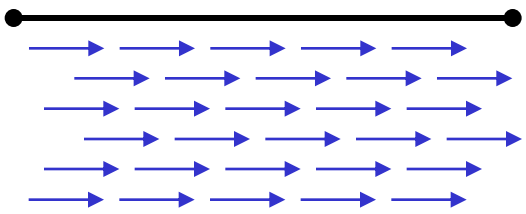
- 400 000/ 1milión jamek (reads)
- v každé 240 / 400 bp (read length)
- 7.5 / 10 hod

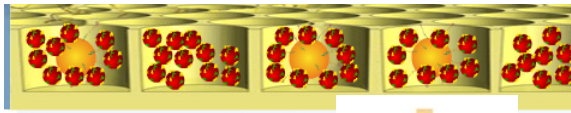
→ 100 Mb / 400 Mb na jednu destičku

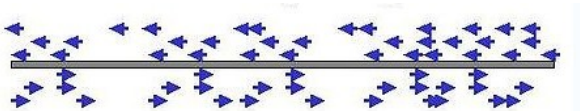
→ cena??? 150-350 000 Kč ???? (verze Junior – od 15 tisíc)

!!! Samozřejmě nestačí mít každou bázi osekvenovanou 1x !!!

- Pospojování (reads assembly) do souvislé sekvence
- Nepřesnosti – pokrytí (coverage)

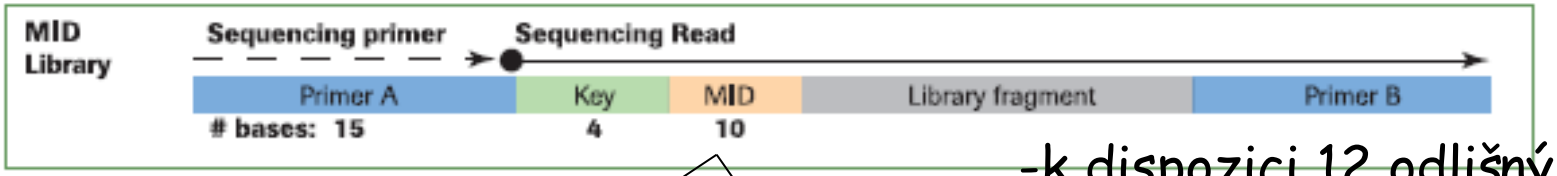






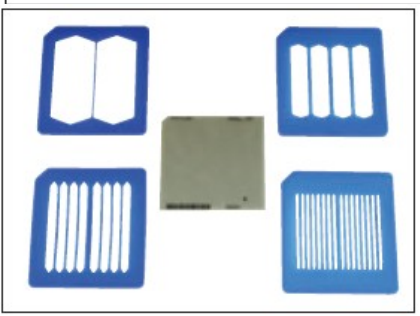
Kapacita destičky 400 Mb:

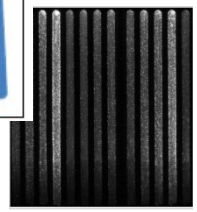
Mus:	2700 Mb	→ 7 run 1x coverage
Caenorhabditis:	100 Mb	→ 1 run 4x coverage
E. coli:	5 Mb	→ 1 run 80x coverage
mitoch. Mus:	0.016 Mb	→ 1 run 25000x coverage
HIV:	0.01 Mb	→ 1 run 40000x coverage

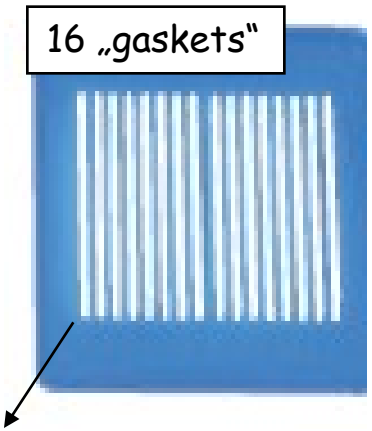


-k dispozici 12 odlišných MID („multiplexing")

1. CCCCCCCCCC
2. GGGGGGGGG
.
.
.
12. CCCCCAAAG







12 MID
X
16 gaskets
=
max. 192 vzorků

V každém max. 12 vzorků
(každý označen svým MID)

454 Genome Sequencers

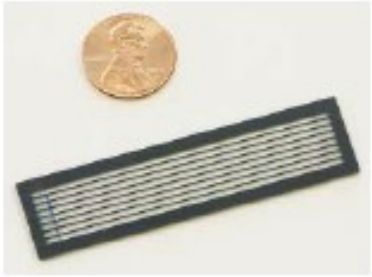
FLX System

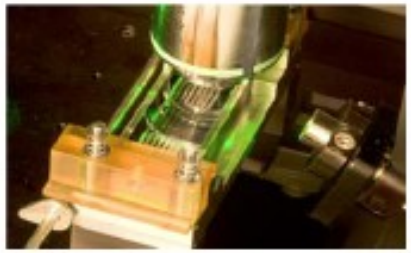
- 1 million of reads/run
- 400-650 bp/read
- 2 přístroje v ČR

GS Junior

- 0.1 millions of reads/run
- 400 bp/read

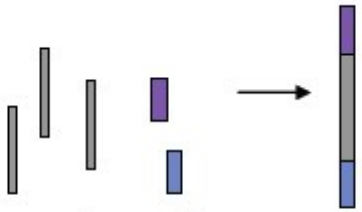
Illumina Genome Analyzer
Introduction to the Technology





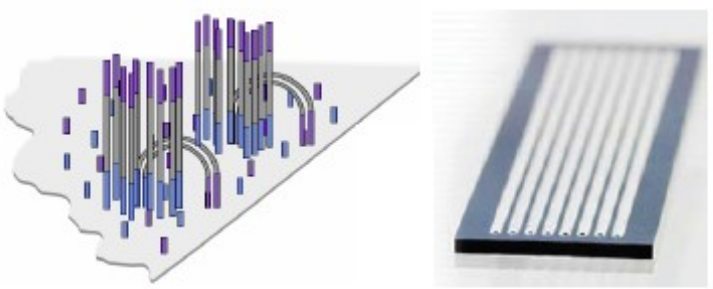
Illumina Sequencing pipeline

1. Sample Prep
(1-5 days)



Ligate adapters

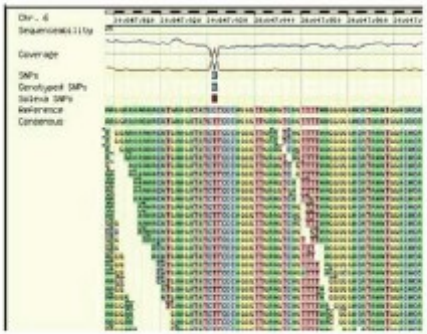
2. Cluster generation on flow cell
(1.5 day)



Clonal Single molecular Array

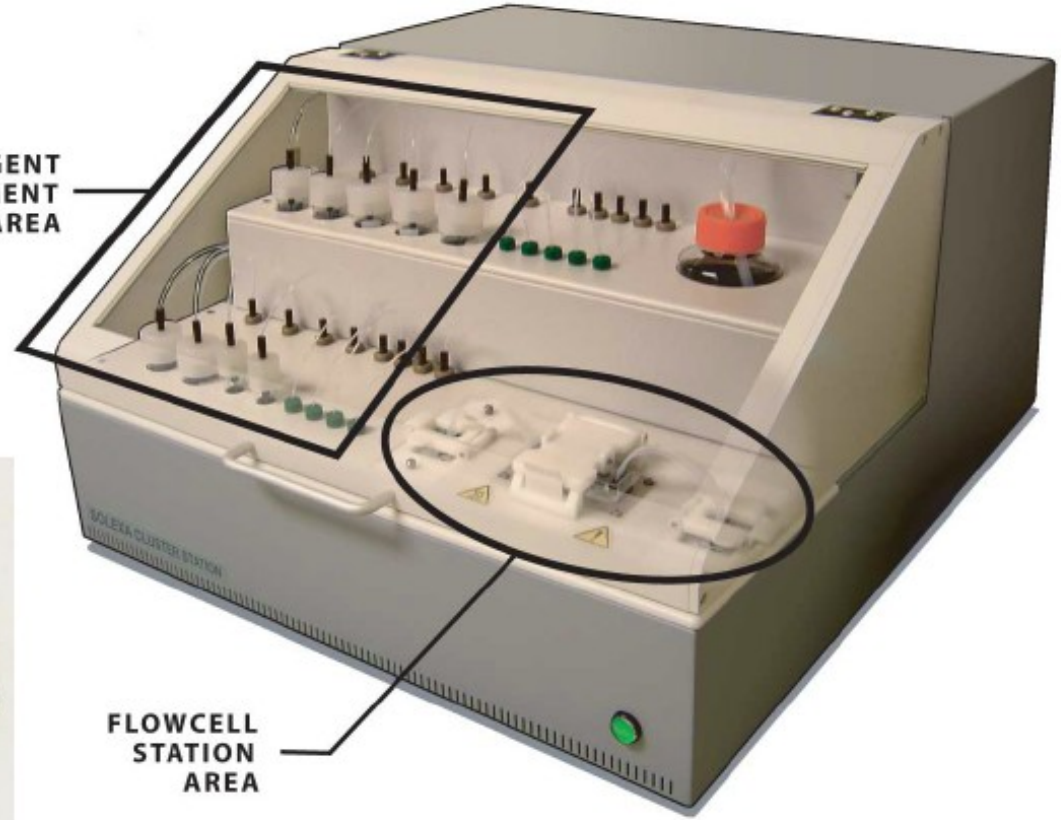
3. Sequencing and imaging
(2-3 days)

4. Data Analysis
(days-months)

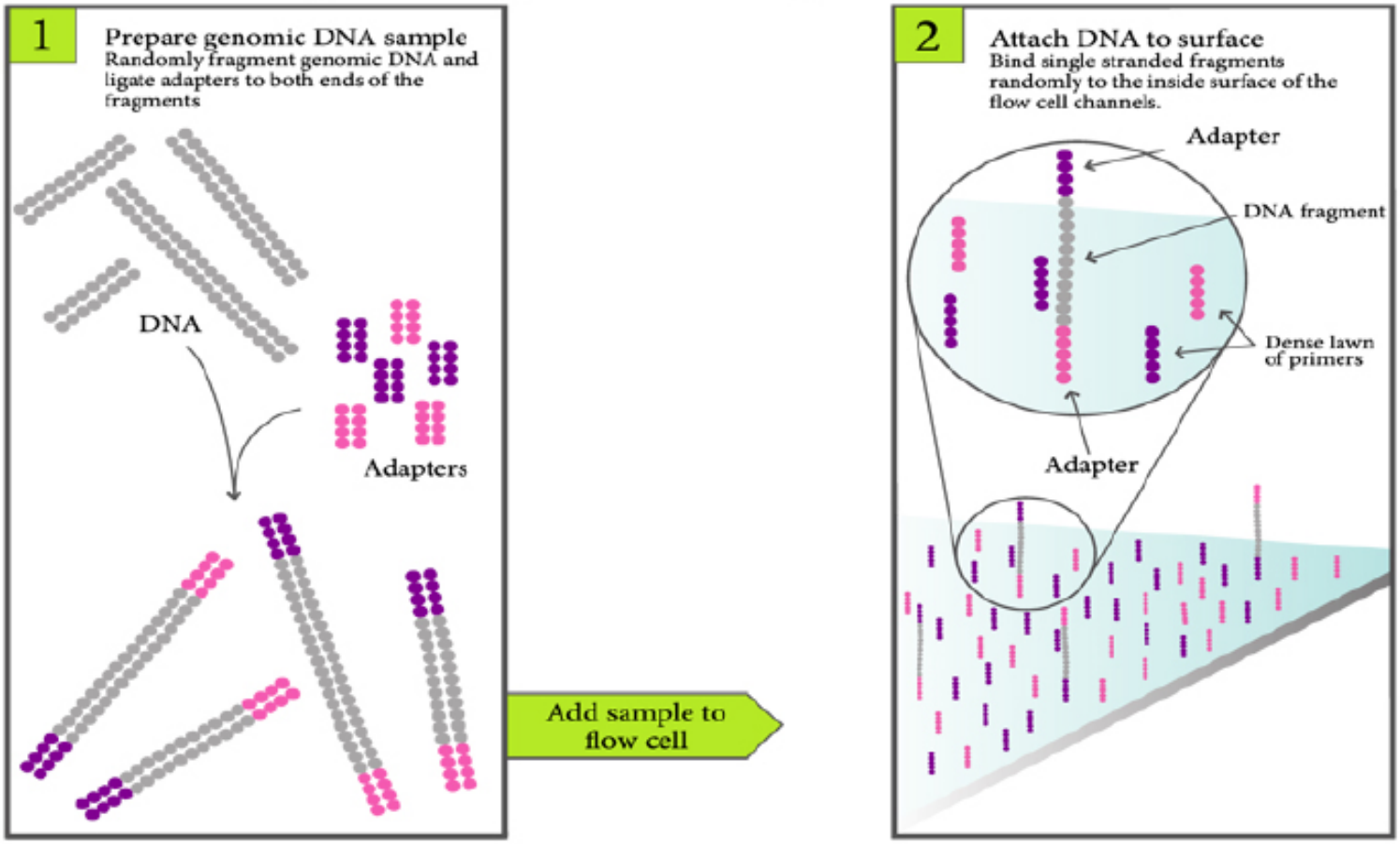


Cluster Generation

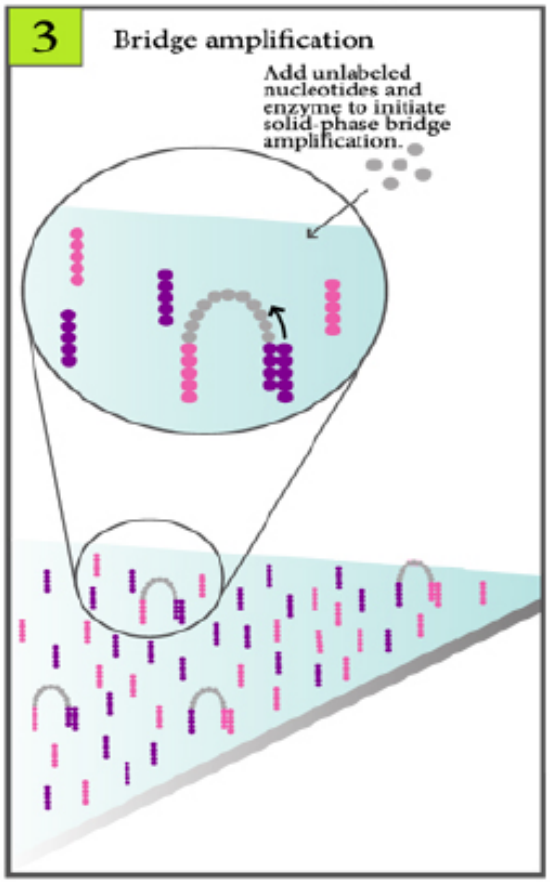
8 channels (lanes)

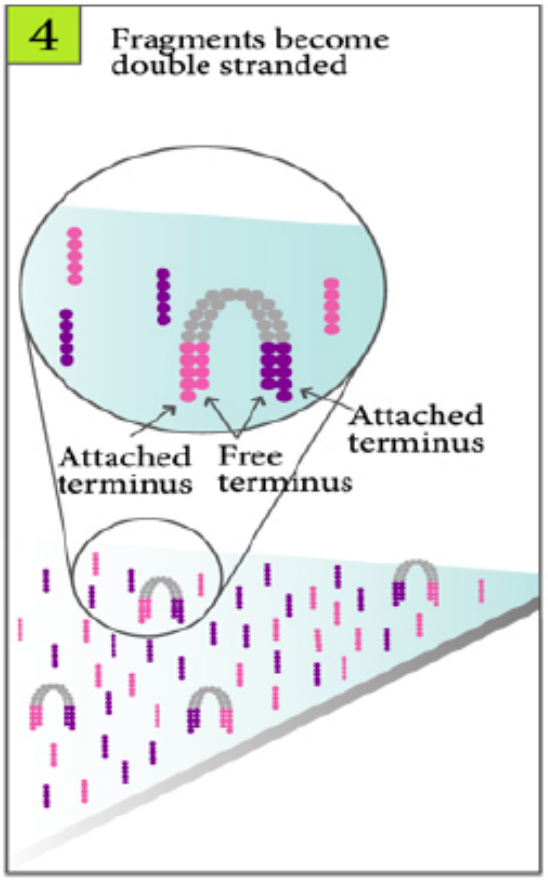


Attach DNA to flow cell

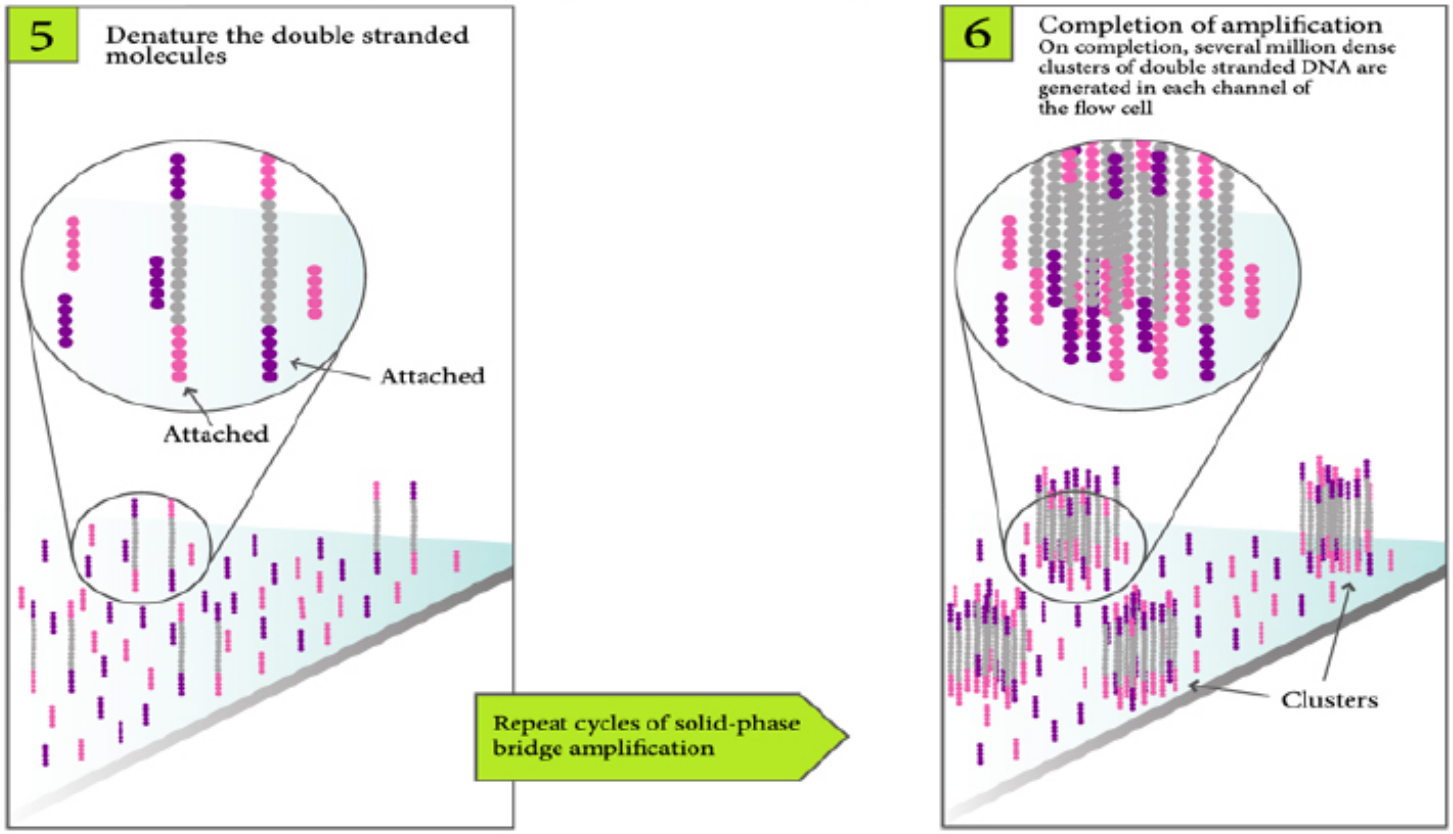


Bridge Amplification



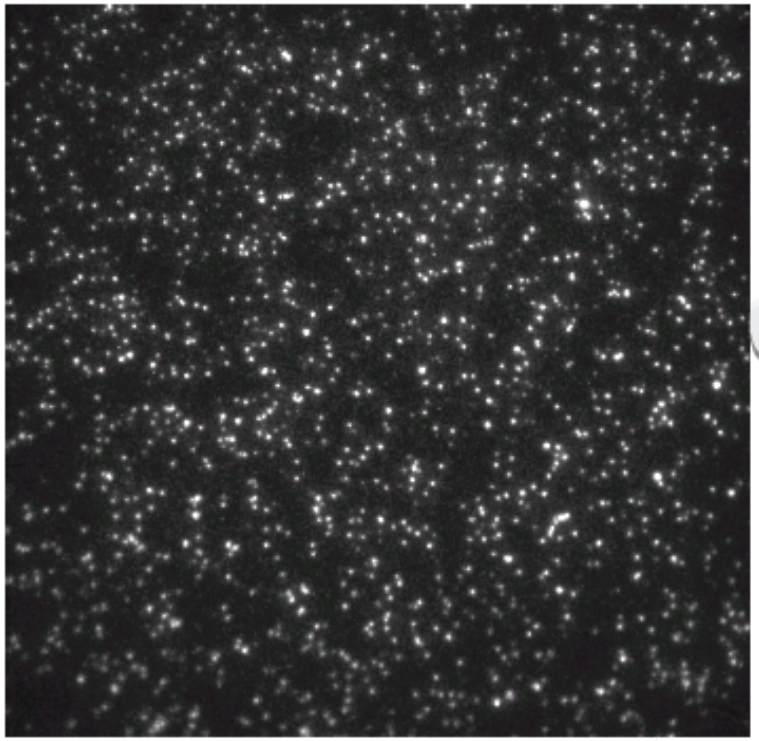


Cluster Generation



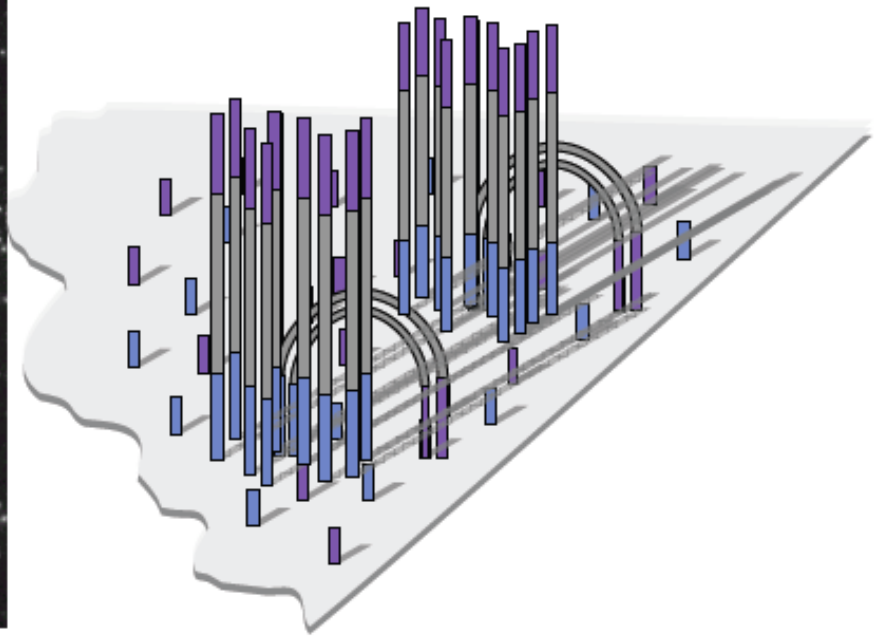
Clonal Single molecular Array

Clonal Single molecule Array



100um

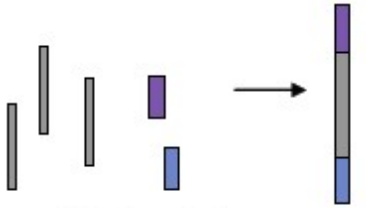
Random array of clusters



~1000 molecules per ~ 1 um cluster
~20-30,000 clusters per tile
~40 M clusters per flowcell

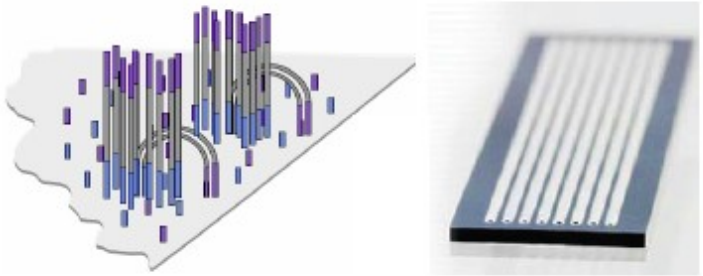
Illumina Sequencing pipeline

1. Sample Prep (1-5 days)



Ligate adapters

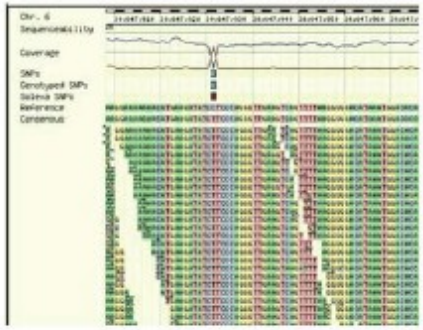
2. Cluster generation on flow cell (1.5 day)



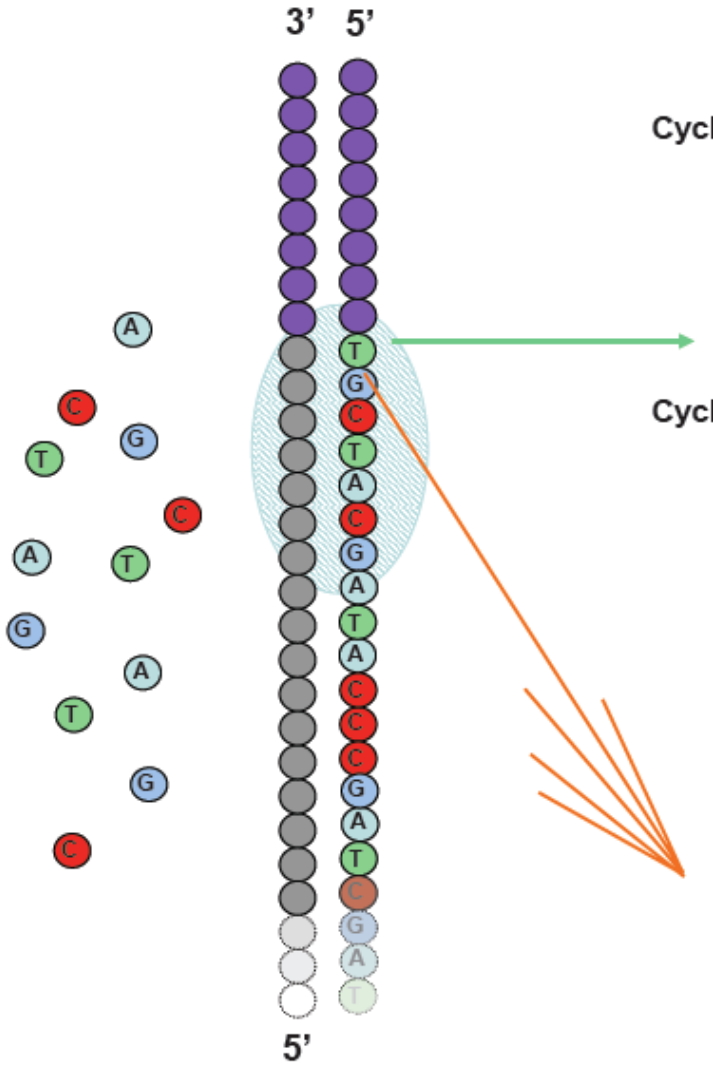
Clonal Single molecular Array

3. Sequencing and imaging (2-3 days)

4. Data Analysis (days-months)



Sequencing By Synthesis (SBS)



Cycle 1: Add sequencing reagents

First base incorporated

Remove unincorporated bases

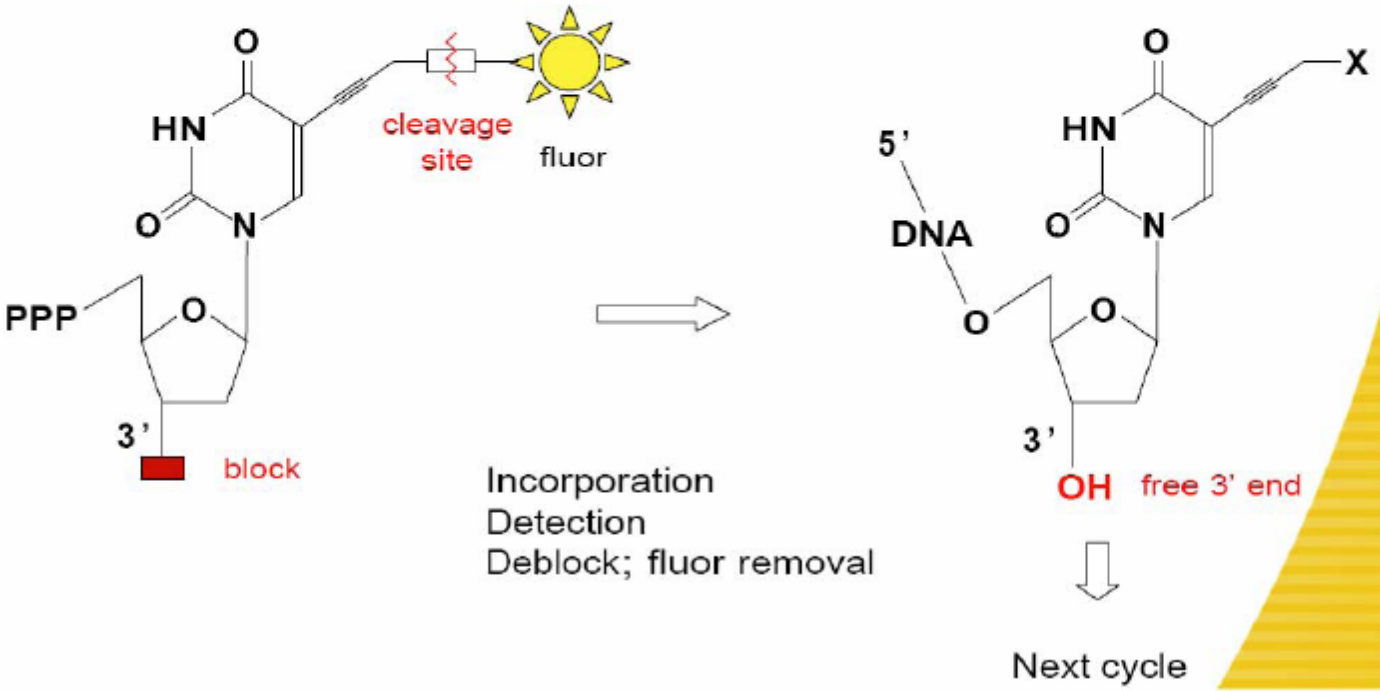
Detect signal

Cycle 2-n: Add sequencing reagents and repeat

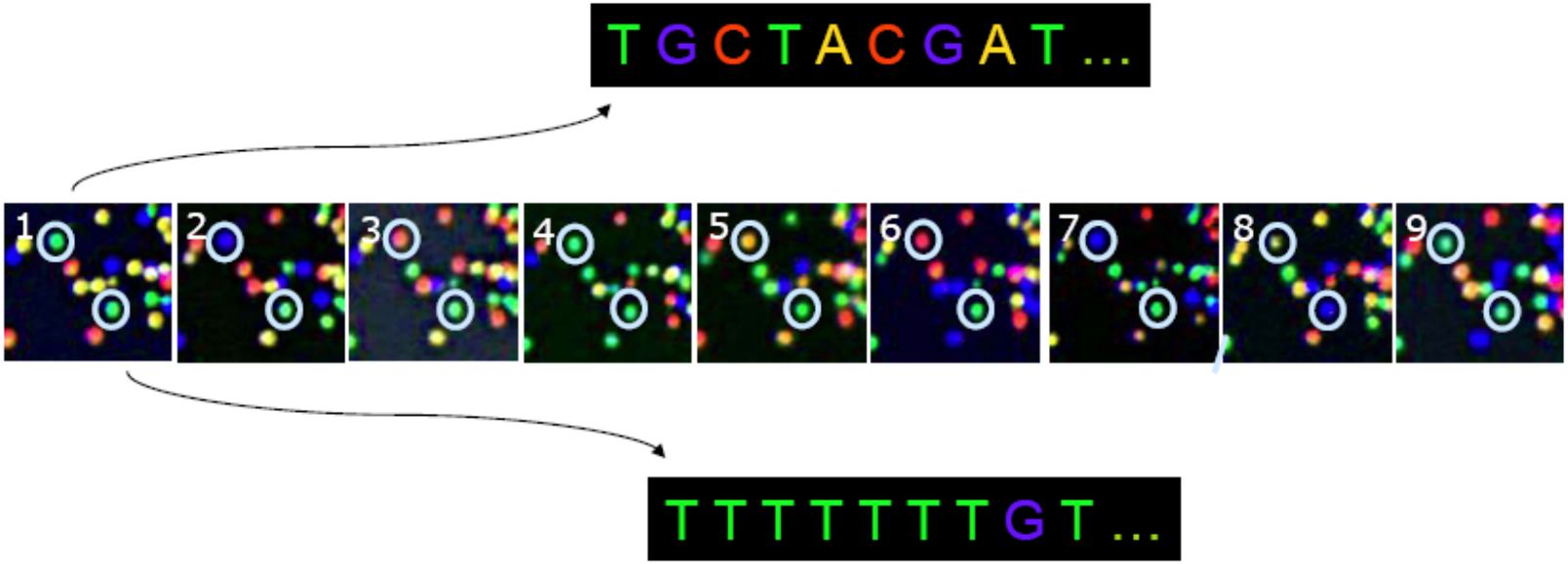
Reversible Terminator Chemistry

Solexa

- All 4 labelled nucleotides in 1 reaction
- Higher accuracy
- No problems with homopolymer repeats

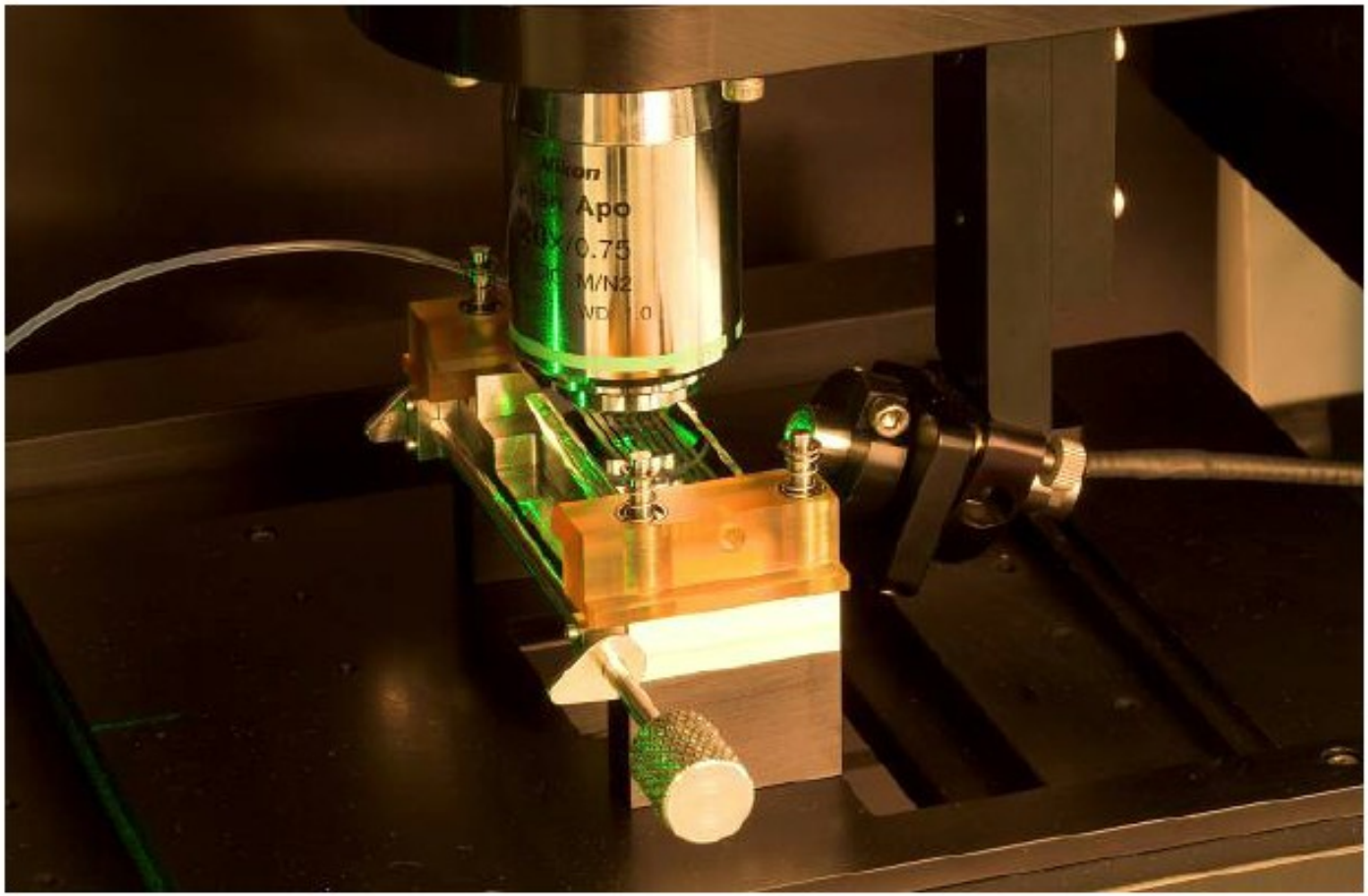


Base Calling From Images

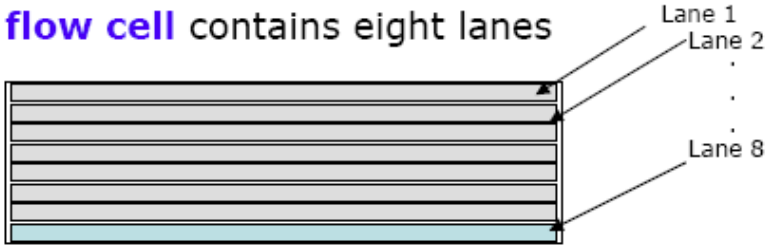


The identity of each base of a cluster is read off from sequential images

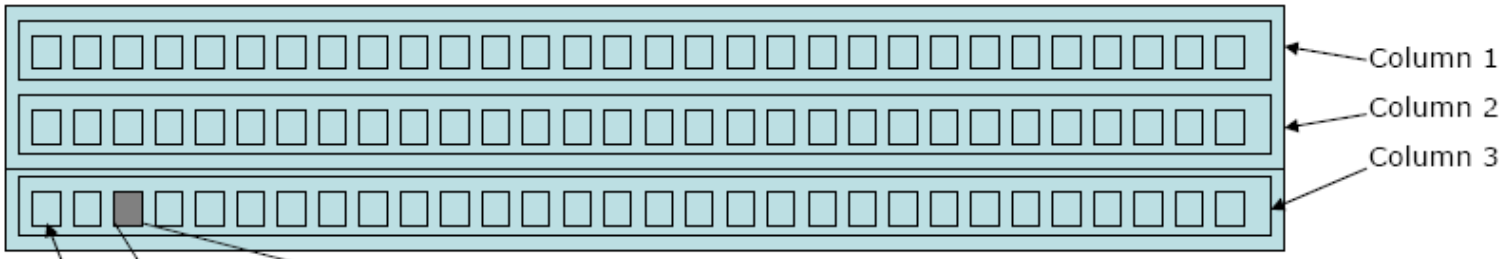
Flowcell imaging



A **flow cell** contains eight lanes

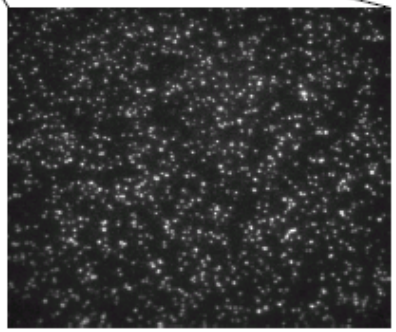


Each **lane/channel** contains **three columns** of tiles



Each **column** contains **100 tiles**

Tile



20K-30K Clusters

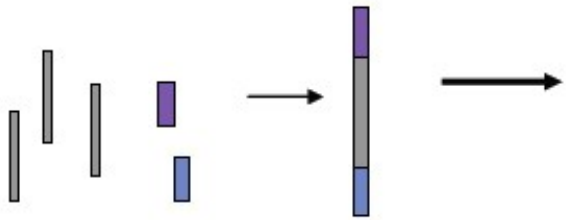
350 X 350 µm

Each tile is imaged four times per cycle – one image per base.

345,600 images for a 36-cycle run

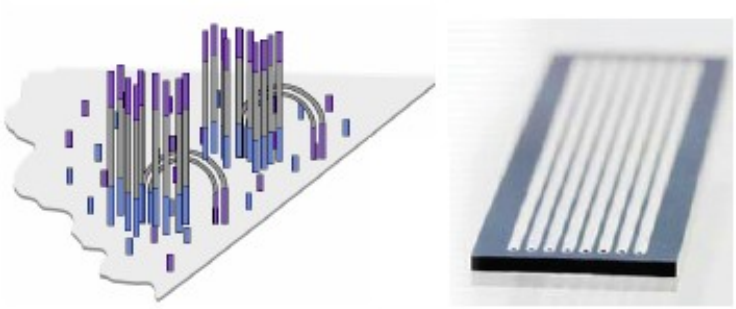
Illumina Sequencing pipeline

1. Sample Prep
(1-5 days)



Ligate adapters

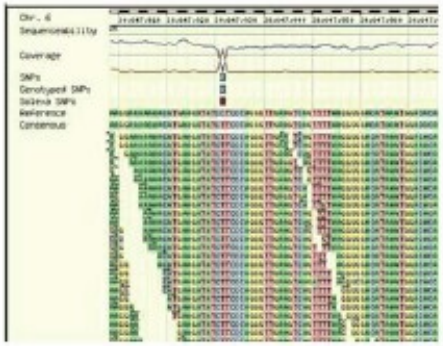
2. Cluster generation on flow cell
(1.5 day)



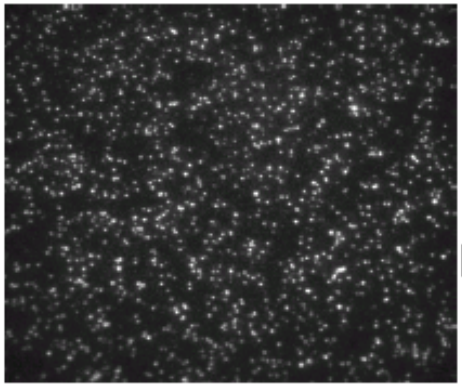
Clonal Single molecular Array

3. Sequencing and imaging
(2-3 days)

4. Data Analysis
(days-months)

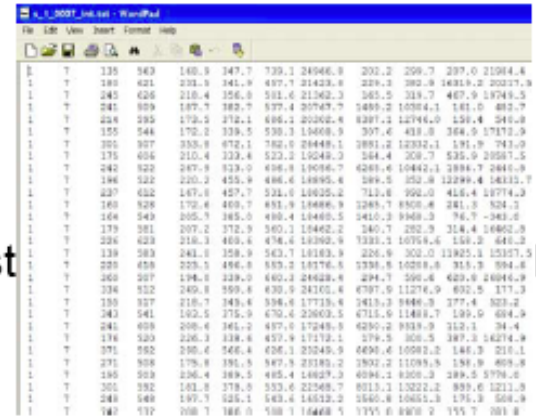


Data Analysis Pipeline



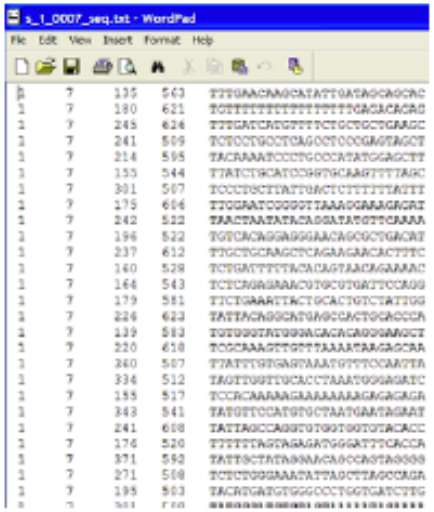
tiff image files
(345,600)

Firecrest



intensity files

Bustard



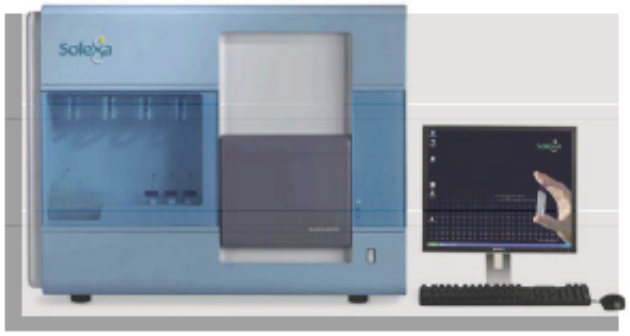
Sequence files

Eland

Alignment to Genome

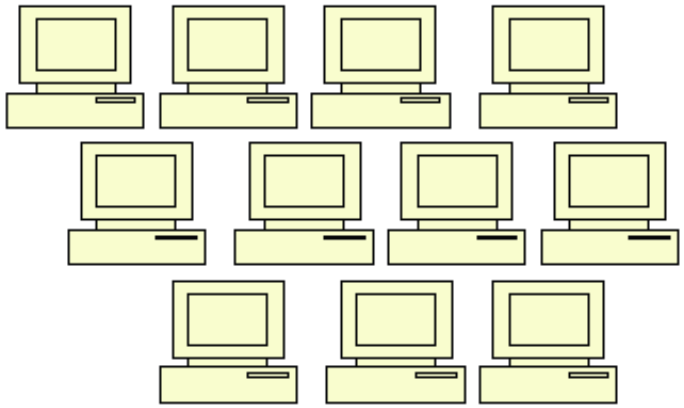
Additional
Data Analysis

Data Analysis Pipeline



rsync

Computer Cluster



Imaging
Base calling
Sequence alignment

(10-12hrs)

All this generates a lot of Data!
1.5 TB data/run

- 1 Gig of Space
  - 125,000 pages of text
  - 11 CDs of Music
  - 4000 (1024x768) JPEG images
  - 40,000 pages of PDF
- 1 TB of space
  - 220 Million pages of text
  - 300 hours of video
  - 4,000,000 JPEG images
  - 1,000 copies of the Encyclopedia Britannica
  - 1/10 of the printed Library of Congress

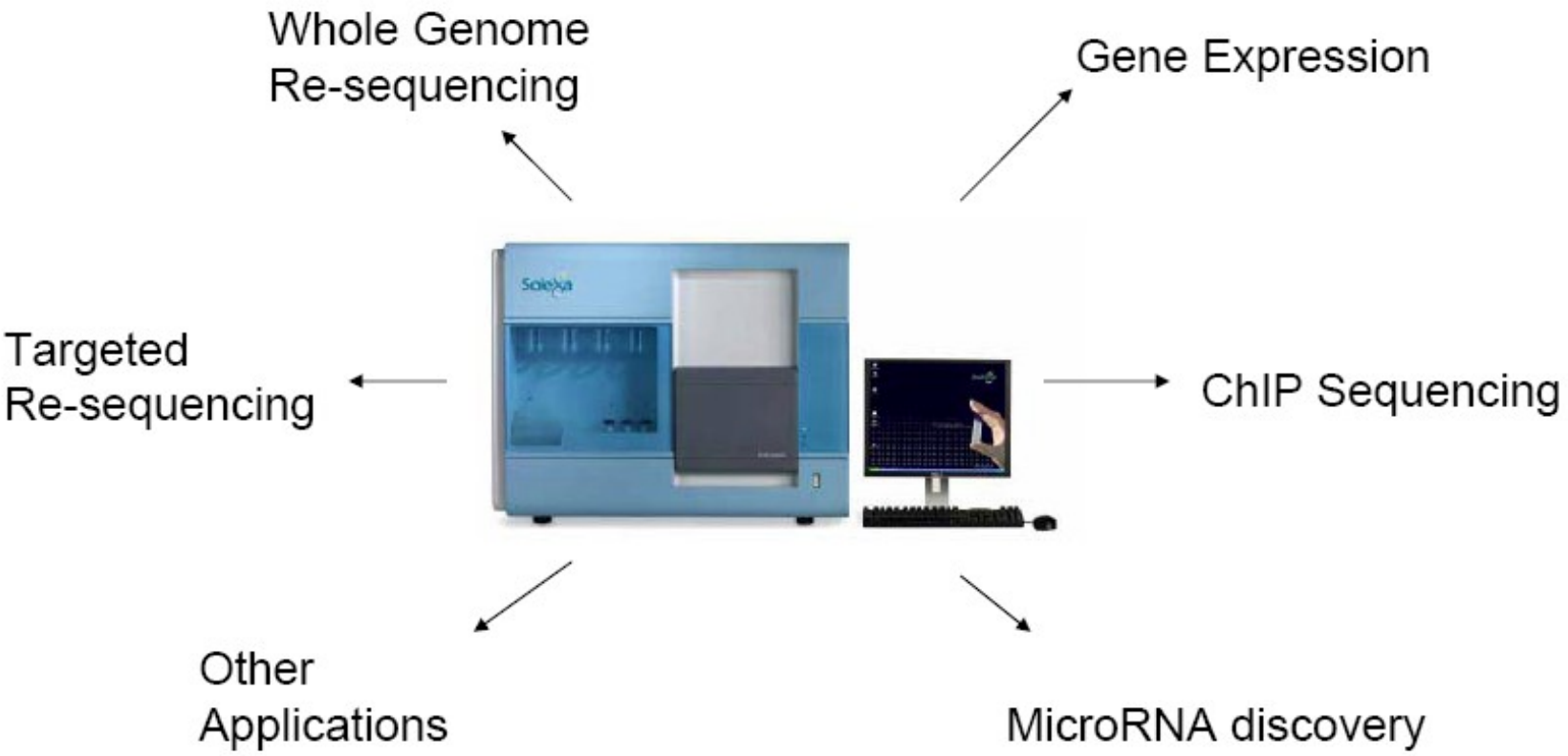
Illumina sequencers

Illumina MiSeq
4 millions reads/run
150 bp/read

Illumina GAIIx
300 millions reads/run
150 bp/read

Illumina HighSeq
1500 – 3000 millions reads/run
100 bp/read

Applications of the Technology



SOLiD

(sequencing by Oligonucleotide Ligation and

… a další (každého půlroku nová technologie – bouřlivý rozvoj !!!)

Přehled současných metod NGS

Platform	Year	Sequencing Method	Amplification	Detection	Features
454	2005	Pyro-sequencing	Emulsion PCR	Light	First NGS
Illumina	2007	Synthesis	Bridge PCR	Light	90% of Market
SOLiD	2008	Ligation	Emulsion PCR	Light	Lowest Error Rate
Ion Torrent	2010	Synthesis	Emulsion PCR	Hydrogen Ion	Semiconductor Chip
Pacific Biosciences	2010	Synthesis	None = Single Molecule	Light	Anchored Polymerases
Oxford Nanopore	2012	Nanopore	None = Single Molecule	Electrical Conductivity	"Run Until" Sequencing

Výkonnost jednotlivých metod

Instrument	Run time	Millions of Reads/run	Bases / read	Yield MB/run
3730xl (capillary)	2 hrs	0.000096	650	0.06
PacBio RS	2 hrs	0.01	860 – 1,500	5-10
454 GS Jr. Titanium	10 hrs	0.1	400	50
Ion Torrent – 314 chip	2.5 hrs	0.25	200	50
454 FLX Titanium	10 hrs	1	400	400
454 FLX+	20 hrs	1	650	650
Ion Torrent – 316 chip	3 hrs	1.6	200	320
Illumina MiSeq	26 hrs	4	150+150	1200
Ion Torrent – 318 chip	4.5 hrs	4	200	800
Illumina GAIIx	14 days	300	150+150	96,000
SOLiD – 5500xl	8 days	>1,410[d]	75+35	155,100
Illumina HiSeq 1000	8.5 days	≤1500	100+100	≤300,000
Illumina HiSeq 2000	11.5 days	≤3000	100+100	≤600,000

2012. NGS Field Guide (www.molecularecologist.com)

Chybovost jednotlivých metod

Platform	Primary Errors	Single-pass Error Rate (%)	Final Error Rate (%)
3730xl (capillary)	Substitution	0.1-1	0.1-1
454	Indel	1	1
Illumina	Substitution	~0.1 (85% of reads)	~0.1 (85% of reads)
SOLiD	A-T bias	~5	≤0.1
Ion Torrent	Indel	~1	~1
PacBio RS	CG deletions	~15	≤15
Oxford Nanopore	Deletions	≥4	4

2012. NGS Field Guide (www.molecularecologist.com)

Traditional Sequencing vs. Next Generation Sequencing: Data Throughput

1 x Illumina GAII

Vs.

200+ of 3730xl

Days vs. Years

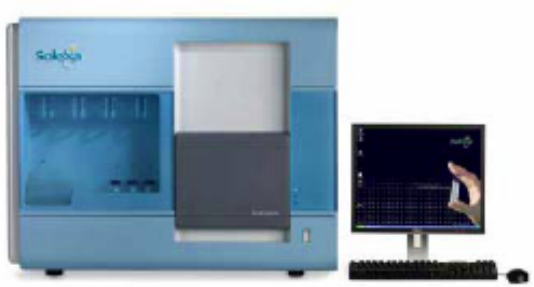
The Sequencing Landscape is Changing

Is Sanger sequencing dead? Future of sequencing centers

ABI 3730XL

- Routine sequencing
- Verify SNPs from next gen
- 1X scaffold for novel genomes

Next Gen
short read instrument
(Solexa)



"When quantity matters but length doesn't"

- Expression tags
- Chip Seq
- Re-sequencing

Next Gen
long read instrument
(454)

"When length matters"

- Novel genomes
- Metagenomics

Využití

1. Celogenomové sekvenování de novo

2. Celogenomové resekvenování

3. Sekvenování amplikonů (PCR produktů)

   + to samé i s RNA (resp. cDNA)

1. Celogenomové sekvenování de novo

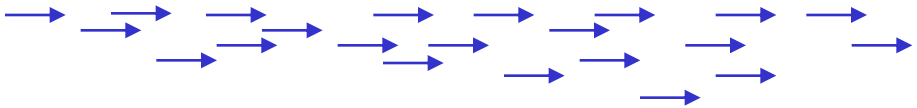
Problém: **KRÁTKÝ READ LENGTH**

- **400bp** 454 FLX Roche
- **35-75bp** Solexa, Solid
  vs **800-1000bp** Sanger

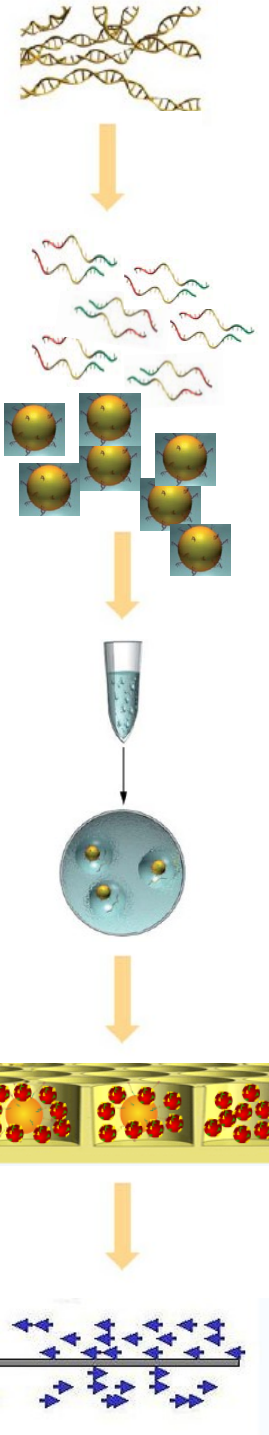
→ Uspořádání (assembly) už není problém z hlediska výpočetní kapacity

!!!!! REPETITIVNÍ OBLASTI delší než read length !!!!!

GTAAAAAAAAAAAAAAAAAAAAAC



Zvláště komplexní eukaryotické genomy – úseky souvislých oblastí přerušených mezerami



1. Celogenomové sekvenování de novo

- získání kompletní uspořádané sekvence celých velkých eukaryotních genomů pomocí next-generation sequencing de novo je problém (ale to je nakonec i u Sangera)
- viry, prokaryota, malá eukaryota, mitochondrie/plastidy/plasmidy

× Ale čo

Genetic Detection and Characterization of Lujo Virus, a New Hemorrhagic Fever–Associated Arenavirus from Southern Africa

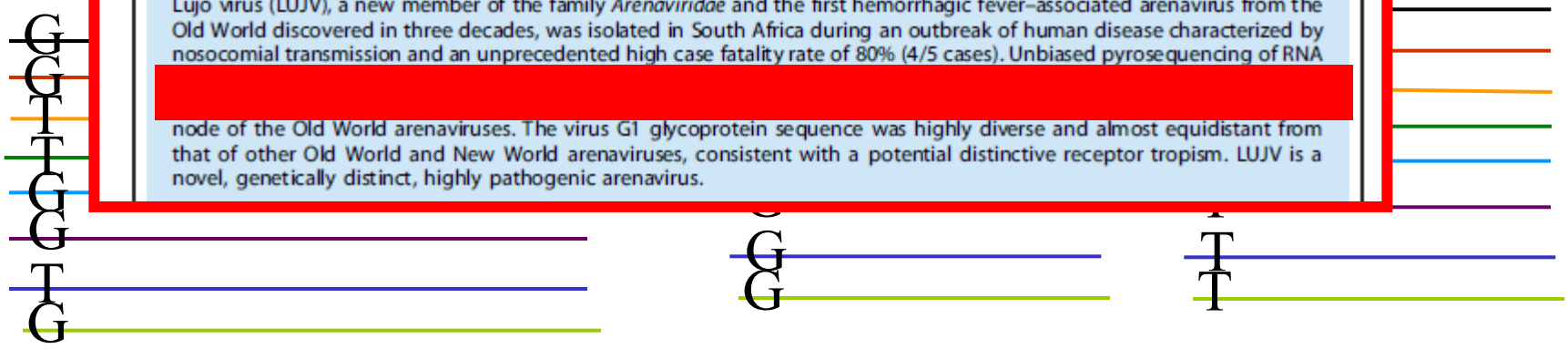
Thomas Briese[1☯*], Janusz T. Paweska[2☯], Laura K. McMullan[3], Stephen K. Hutchison[4], Craig Street[1], Gustavo Palacios[1], Marina L. Khristova[5], Jacqueline Weyer[2], Robert Swanepoel[2], Michael Egholm[4], Stuart T. Nichol[3], W. Ian Lipkin[1*]

1 Center for Infection and Immunity, Mailman School of Public Health, Columbia University, New York, New York, United States of America, 2 Special Pathogens Unit, National Institute for Communicable Diseases of the National Health Laboratory Service, Sandringham, South Africa, 3 Special Pathogens Branch, Division of Viral and Rickettsial Diseases, Centers for Disease Control and Prevention, Atlanta, Georgia, United States of America, 4 454 Life Sciences, Branford, Connecticut, United States of America, 5 Biotechnology Core Facility Branch, Centers for Disease Control and Prevention, Atlanta, Georgia, United States of America

Abstract

Lujo virus (LUJV), a new member of the family *Arenaviridae* and the first hemorrhagic fever–associated arenavirus from the Old World discovered in three decades, was isolated in South Africa during an outbreak of human disease characterized by nosocomial transmission and an unprecedented high case fatality rate of 80% (4/5 cases). Unbiased pyrosequencing of RNA

node of the Old World arenaviruses. The virus G1 glycoprotein sequence was highly diverse and almost equidistant from that of other Old World and New World arenaviruses, consistent with a potential distinctive receptor tropism. LUJV is a novel, genetically distinct, highly pathogenic arenavirus.



Cílené sekvenování

= sekvenování jen určité části genomu či vybrané skupiny genů

Restriction enzyme genome reduction (RAD-Seq)

- sekvenování náhodných oblastí genomu vybraných na základě délky po restrikčním štěpení genomové DNA. Lze kombinovat vzorky DNA z více jedinců. Identifikace polymorfních markerů.

RAD-Seq

- Štěpení genomové DNA pomocí jednoho či více restrikčních enzymů.
- Výběr restrikčních fragmentů jen určité velikosti
- Sekvenování kusů vybraných fagmentů (stačí konce fragmentů).

2. Celogenomové resekvenování

- podobné problémy jako u de novo, ale méně (větší strukturální přestavby..)

KOMPARATIVNÍ GENOMIKA
- viry, prokaryota, malá eukaryota
- mitochondrie/plastidy/plasmidy

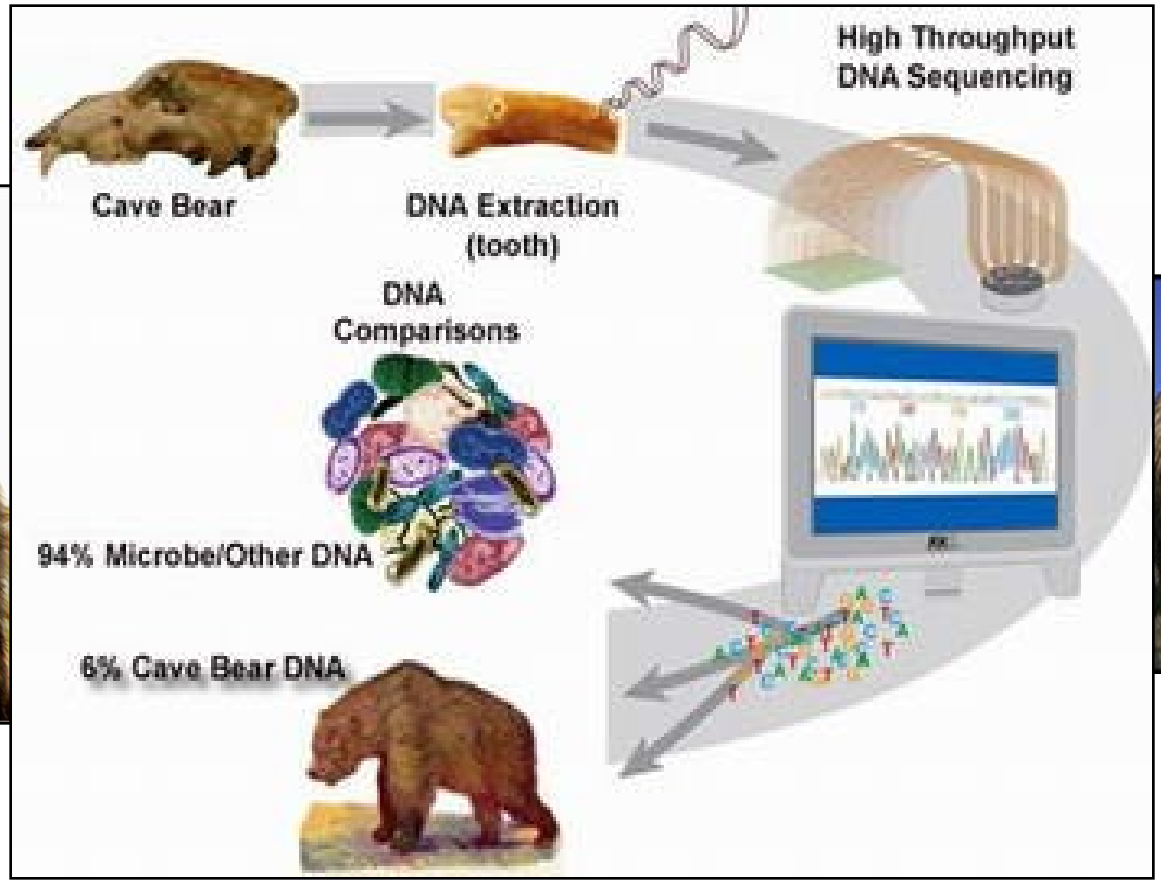
ANCIENT (mt) DNA
- různé směsné, degradované vzorky, např. fosilie

A Complete Neandertal Mitochondrial Genome Sequence Determined by High-Throughput Sequencing

Richard E. Green,[1,*] Anna-Sapfo Malaspinas,[2] Johannes Krause,[1] Adrian W. Briggs,[1] Philip L.F. Johnson,[3] Caroline Uhler,[4] Matthias Meyer,[1] Jeffrey M. Good,[1] Tomislav Maricic,[1] Udo Stenzel,[1] Kay Prüfer,[1] Michael Siebauer,[1] Hernán A. Burbano,[1] Michael Ronan,[5] Jonathan M. Rothberg,[6] Michael Egholm,[5] Pavao Rudan,[7] Dejana Brajković,[8] Željko Kučan,[7] Ivan Gušić,[7] Mårten Wikström,[9] Liisa Laakkonen,[10] Janet Kelso,[1] Montgomery Slatkin,[2] and Svante Pääbo[1]

Ancient Genomes Resurrected

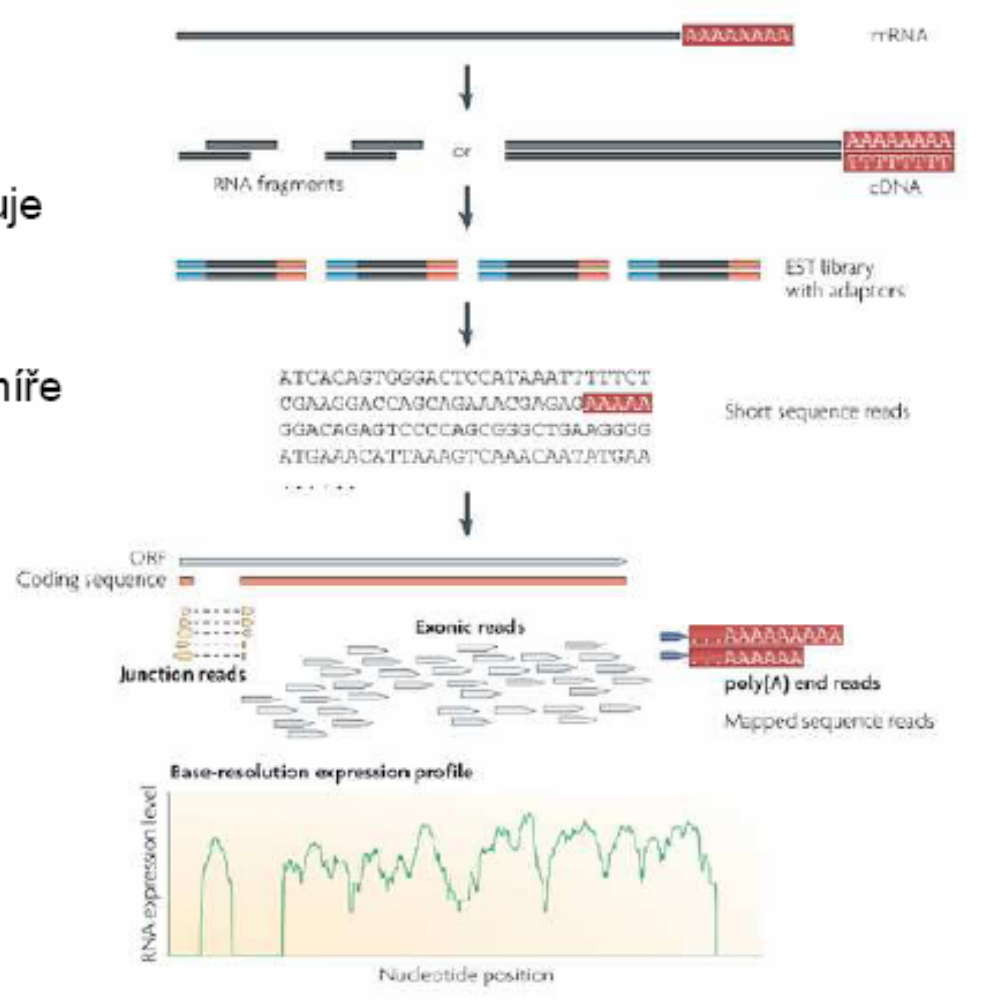
- **Degraded state of the sample → mitDNA sequencing**
- **Nuclear genomes of ancient remains: cave bear, mommoth, Neanderthal (10^6 bp)**



Problems: contamination modern humans and coisolation bacterial DNA

Sekvenování transkriptomu (RNA-Seq)

- Odpadá nutnost klonování cDNA.
- Hluboké sekvenování umožňuje identifikovat i dosud neznámé transkripty.
- Možnost získat informaci i o míře transkripce jednotlivých genů (přesnější než microarrays).
- RNA lze normalizovat – vyrovnání početnosti jednotlivých traskriptů.

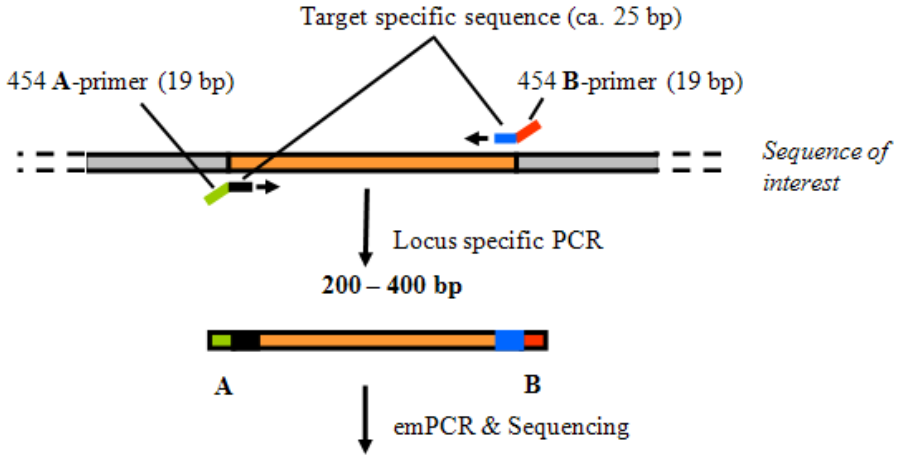


3.Sekvenování amplikonů (PCR produktů)

SMĚSNÉ VZORKY

1. Metagenomika/metatranskriptomika

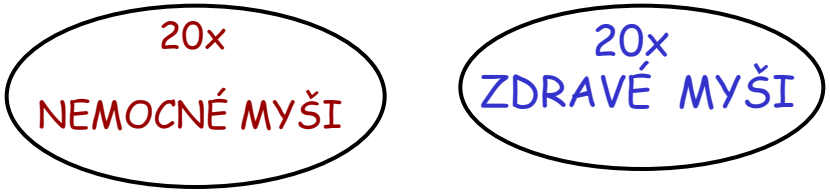
- Celé společenstvo půdních, vodních mikroorganismů, střevní mikroflóra
- PCR genu 16S (18S) rRNA
- lze i kvantifikovat



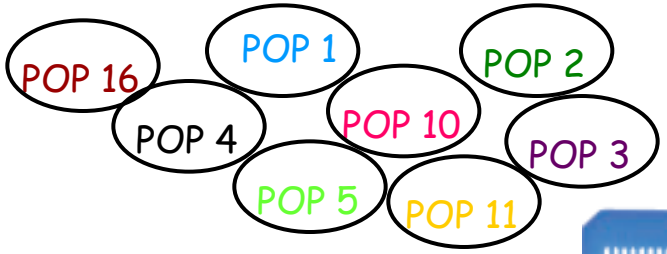
2. Složení potravy (COI barcoding)

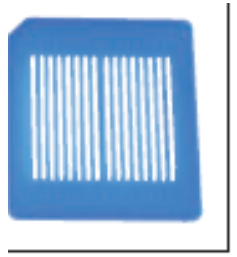
3. Populační genetika

4. Studie u kandidátních genů



1. PCR např. **imunitního genu/genů**
2. Sekvenování
3. Které varianty jsou asociovány s chorobou??

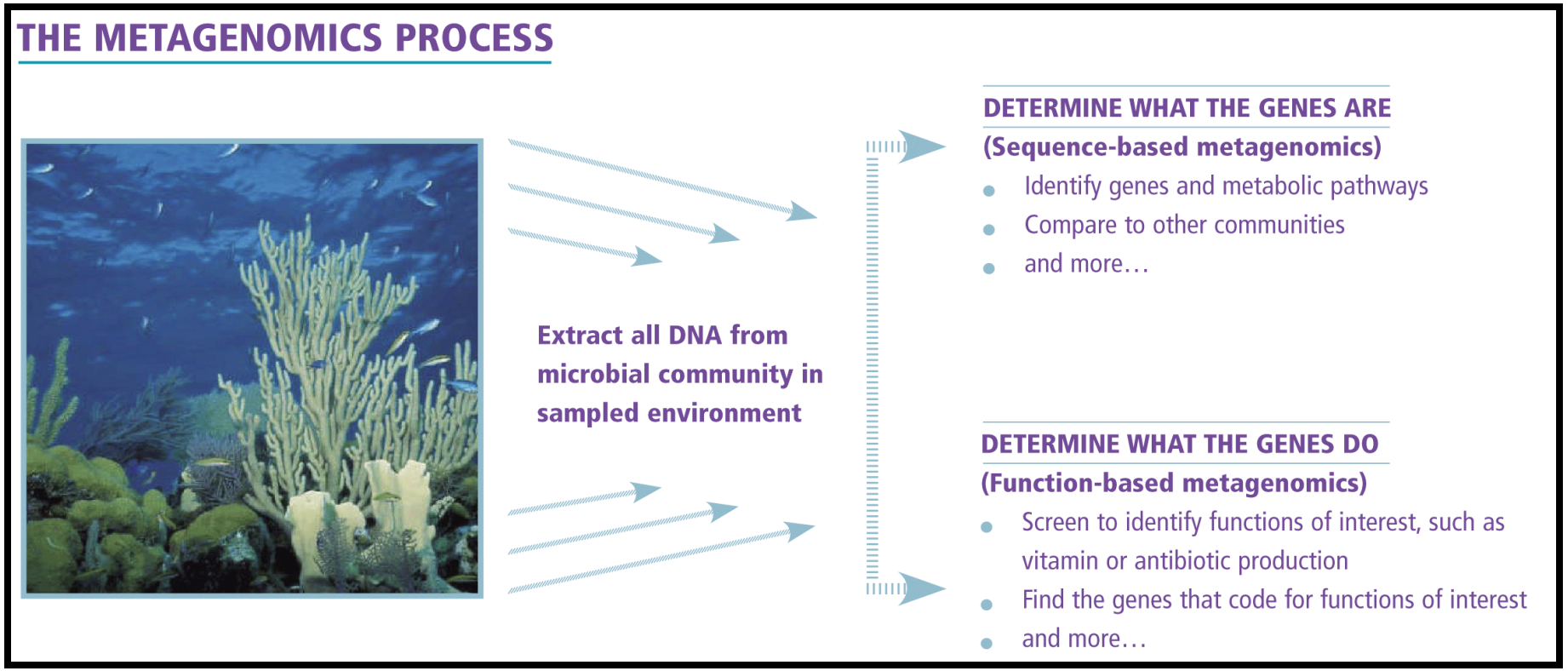




1. **PCR genu/genů**
2. Sekvenování
3. Zjištění sekvencí variant a frekvencí variant v každé populaci (záleží na pokrytí)

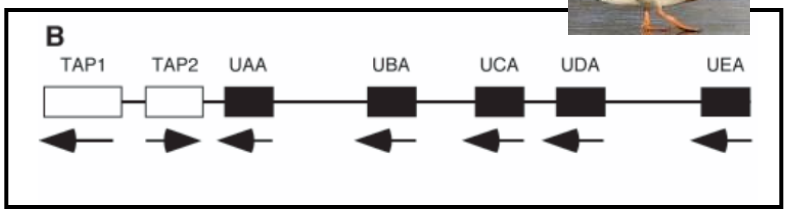
Metagenomics

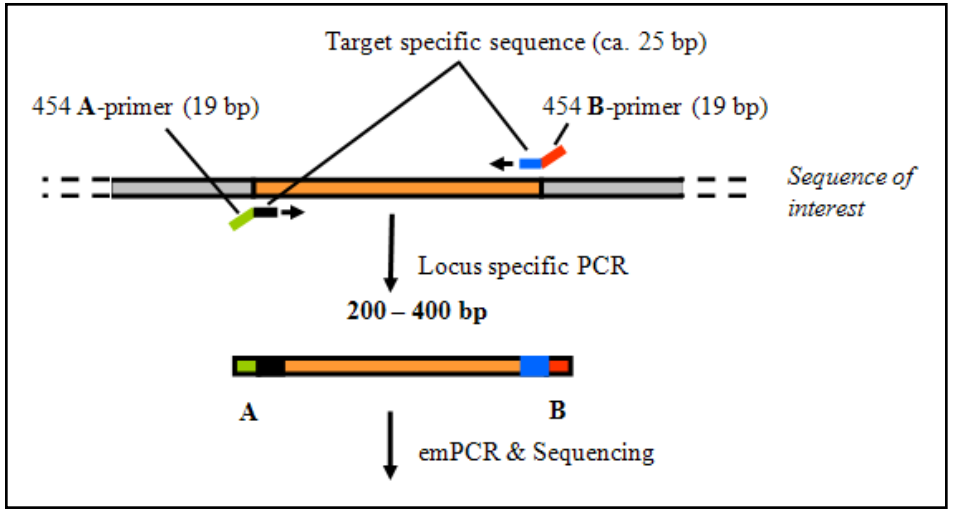
- **Characterizing the biodiversity found on Earth**
- **The growing number of sequenced genomes enables us to interpret partial sequences obtained by direct sampling of specif environmental niches.**
- **Examples: ocean, acid mine site, soil, coral reefs, human microbiome which may vary according to the health status of the individual**



3.Sekvenování amplikonů (PCR produktů)

5. Genové duplikace



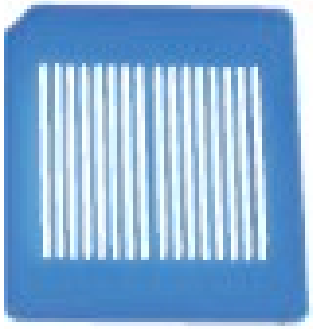


A-adaptor MID Target specific

Označí jedince

Amplifikuje všechny kopie MHC genů

Potřeba k emPCR, sekvenování..

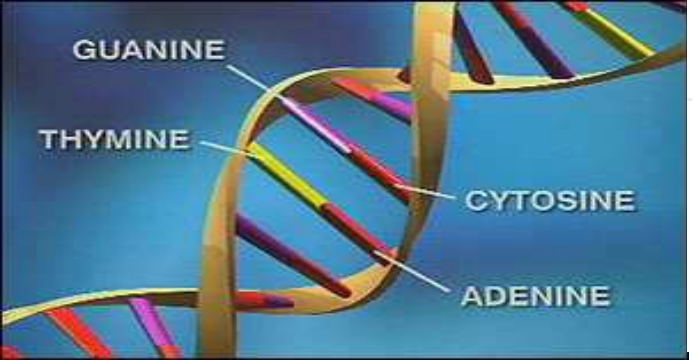


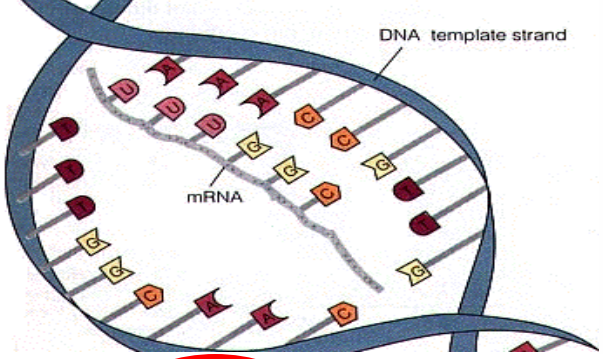
192 jedinců

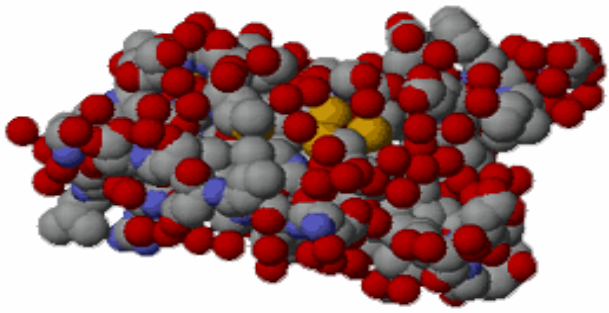
Budoucnost genetických metod
v ekologickém výzkumu

2. Analysis of expression by microarrays („transcriptomics")

Ranz JM, Machado CA: Uncovering evoutionary patterns of gene expression using microarrays. TREE, 21(1): 29-37

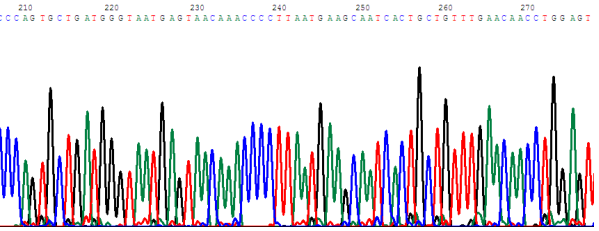


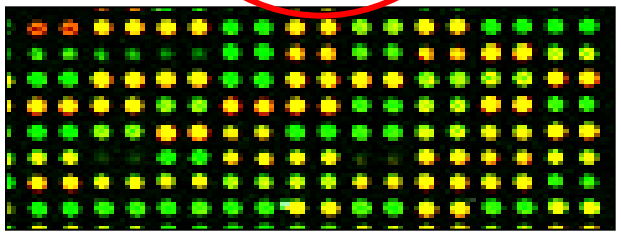


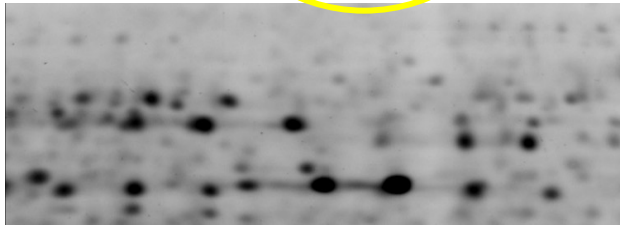


DNA → Transcription → mRNA → Translation → Proteins

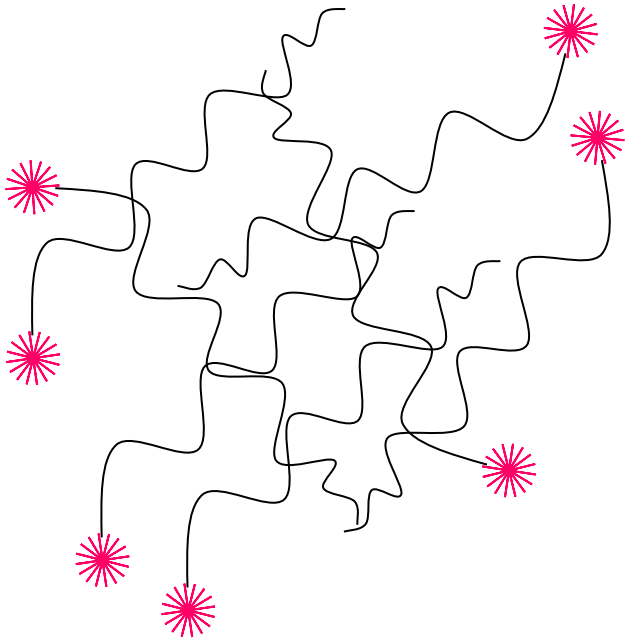
Genome		Transcriptome	Proteome
3 billion bases		20-30,000 genes	~100,000 proteins
Genomics	Functional Genomics	Transcriptomics	Proteomics

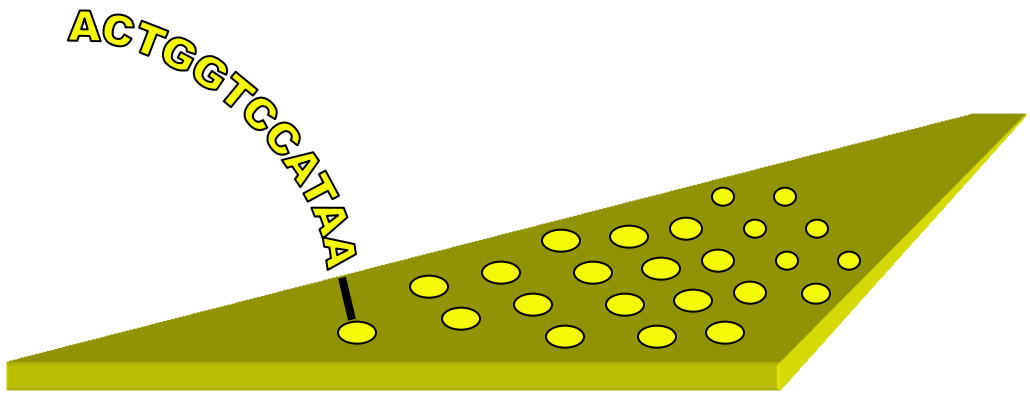






Microarray analysis of transcriptome
(~ specific DNA hybridization)





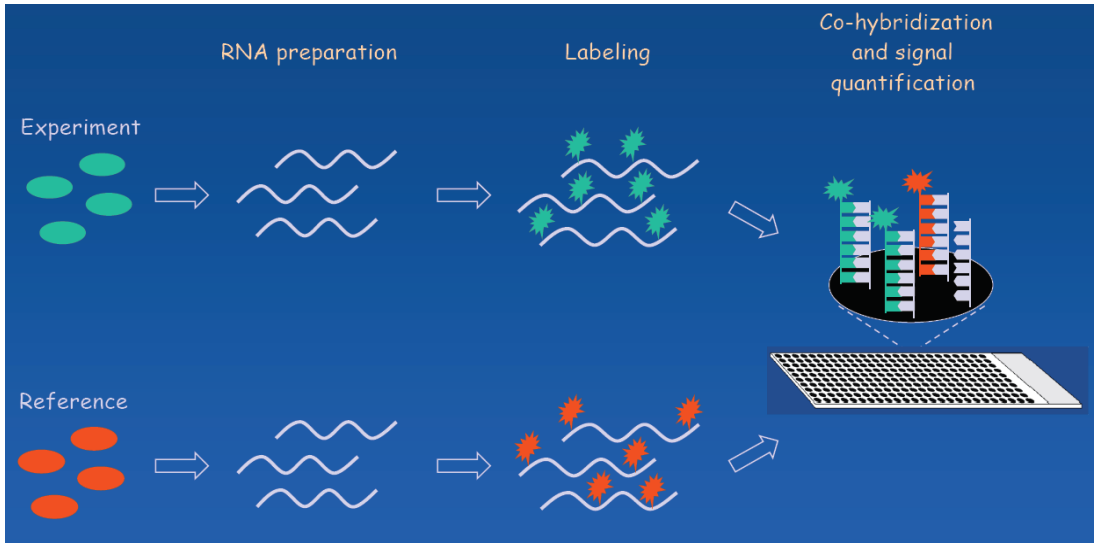
Target **(i.e. mix of transcripts in a form of cDNA)**

Probe **(i.e. synthesized oligonucleotides complementary to particular genes)**

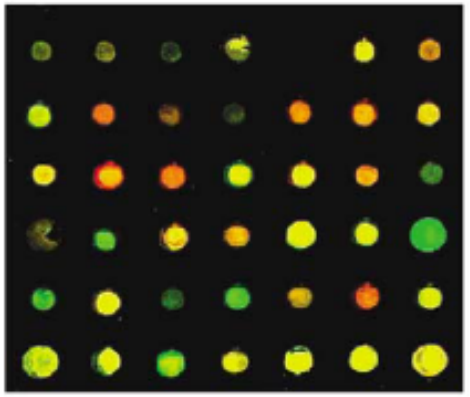
How to get a transcription profile

- vždy srovnání kontroly a „treatement“

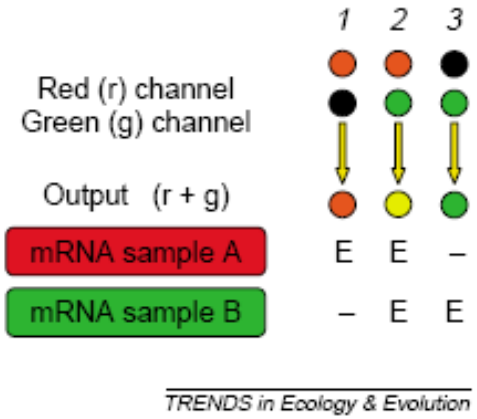
(a)



(b)



(c)



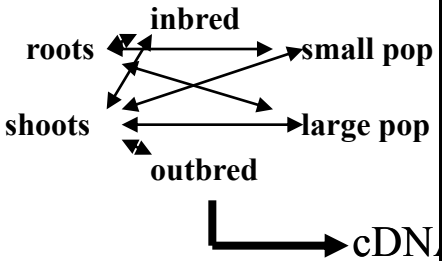
Analysis of expression l

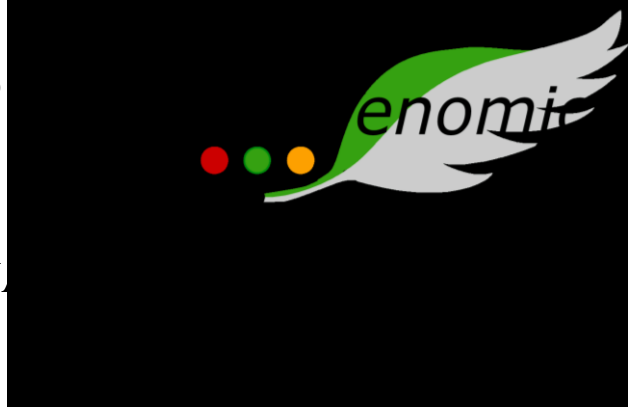
Case study: Joop Ouborg et al.

Transcriptional profiling of inbreeding depression and genetic erosion in *Scabiosa columbaria*: the balance between genetic drift and selection in the genetic erosion process.

Example:

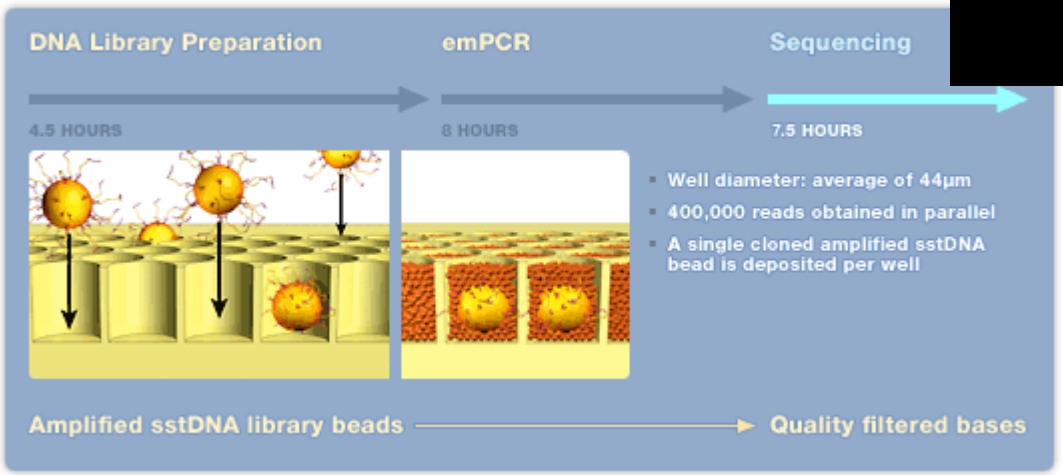
Scabiosa columbaria

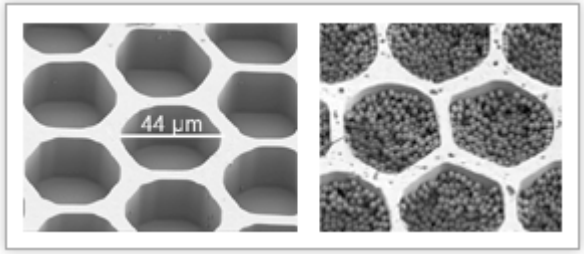


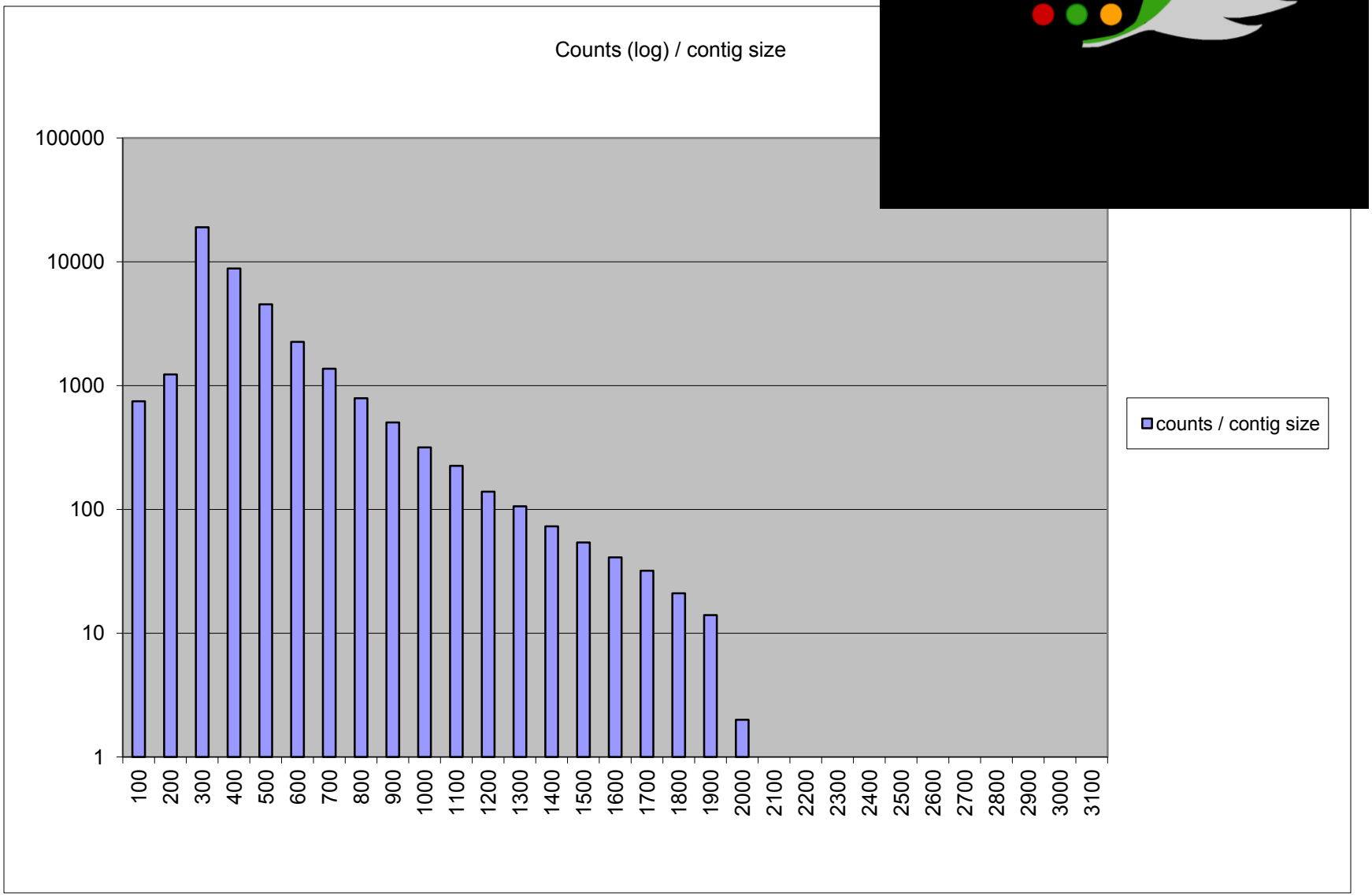


cDNA library preparation – 454 sequencing

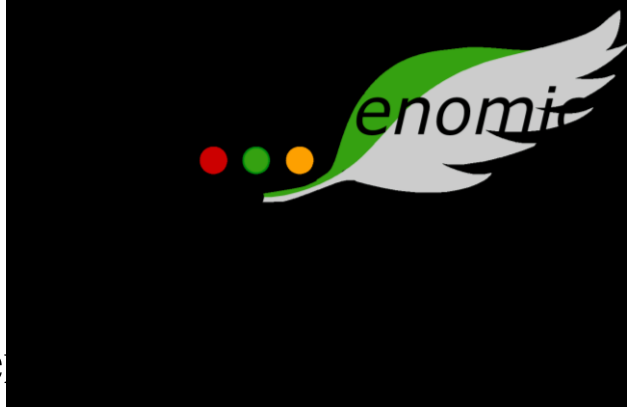
FIGURE 9







Total number of reads: **528557** Number of contigs: **40302**



In the next phase:

Annotation of these 40.000^{+} ESTs („e
sequence tags“)

Automated programs available, like **BLAST2GO (**http://www.blast2go.de/**)**:

just feed a file with the ESTs into the program, and turn it on……

1 week later you will have the results, being:

- Homology with known sequences
- Known function

The sequences may also be searched for:

EST-associated SSR markers: MISA (http://pgrc.ipk-gatersleben.de/misa/)

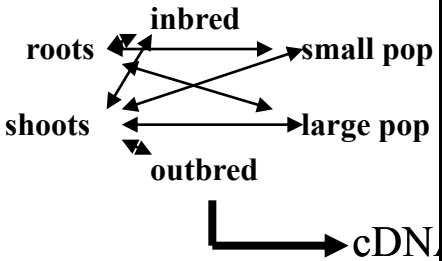
SNP markers: SNP-mining software like PolyBayes
(http://genome.wustl.edu/tools/software/polybayes.cgi)

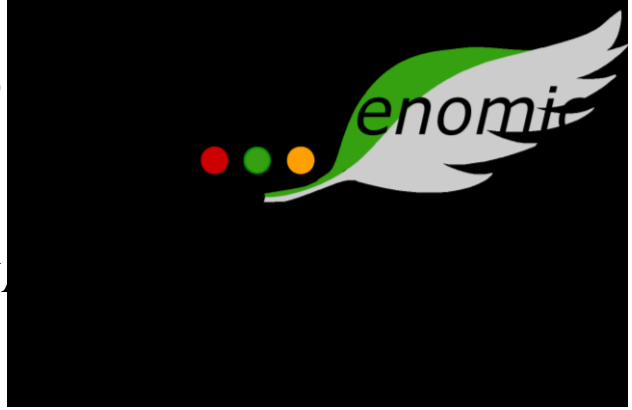
Again by using search software, freeware

ALMOST HALF OF GENES (ESTs) ARE UNKNOWN !!!

Example:

Scabiosa columbaria





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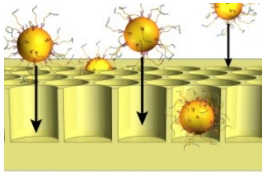


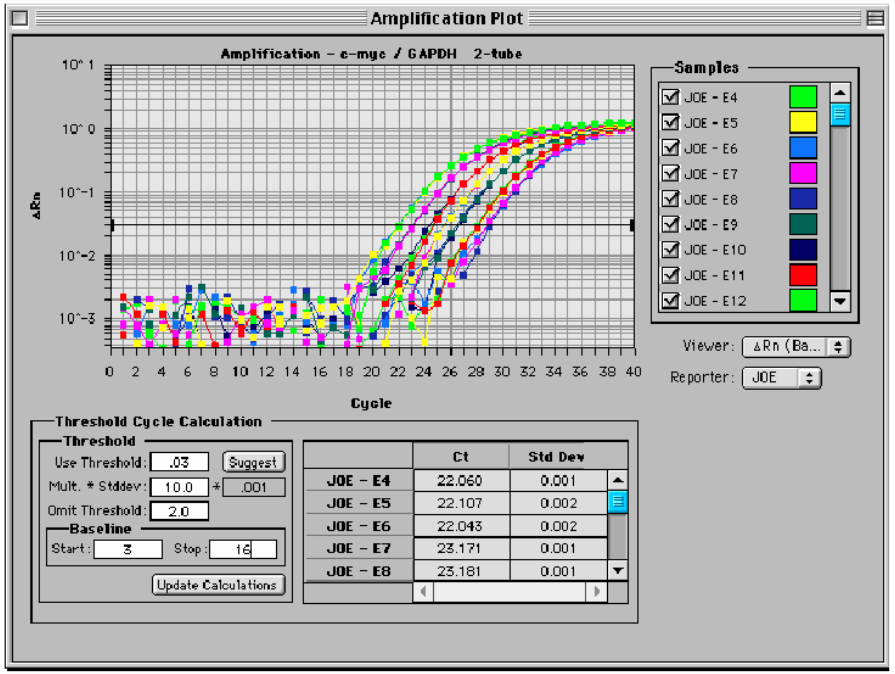
NCBI

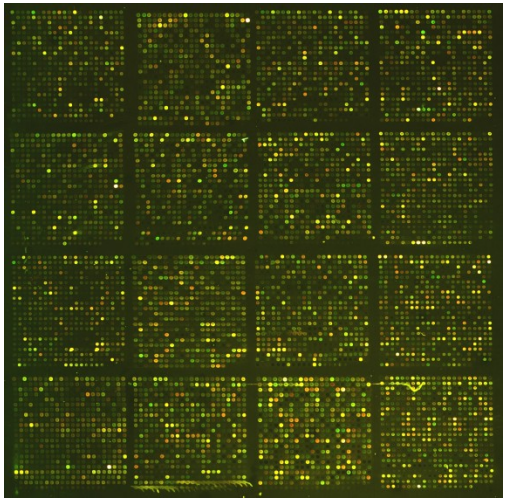
530.000 sequences in one run, leading to ~ 40.000 ESTs

Two methods of detecting transcri

1. Design of quantitative RealTime-PCR met
EST sequences

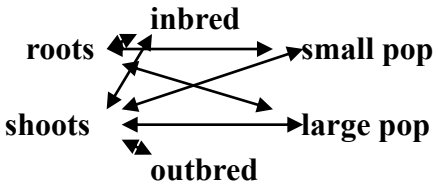
2. Design of a *Scabiosa* specific microarray



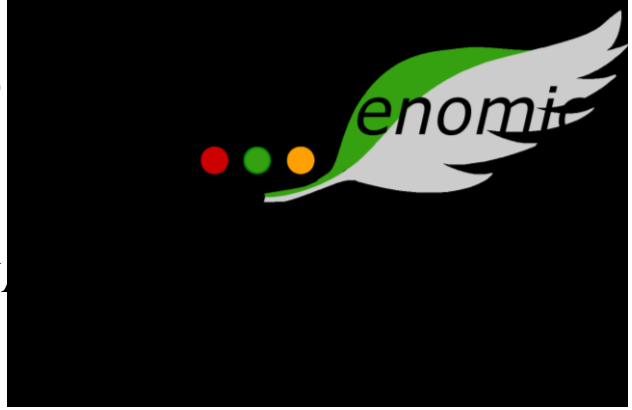


Example:

Scabiosa columbaria



cDN



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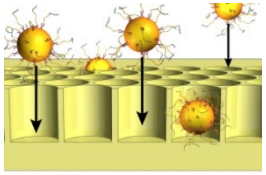

NCBI

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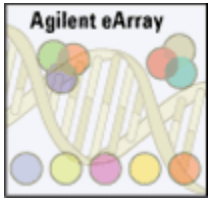
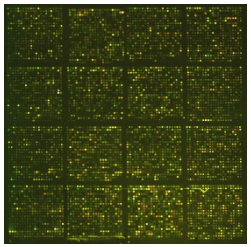
Agilent Technologies



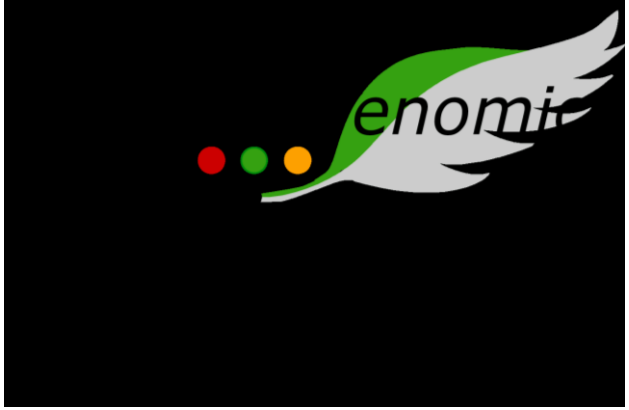


15k – 30k 60-mer microarrays

Experiment: transcriptional profiling of inbreeding depression

Expected pay-off:

- Ecogenomic approach to conservation genet
  effects of genetic erosion on functional genetic variation
- How does genetic erosion affect evolutionary potential?
- What is the **balance between genetic drift and natural selection** in effects of habitat fragmentation?
- Are there general **inbreeding depression genes**, or is inbreeding depression a random phenomenon?
- **Which genes are involved in inbreeding depression in different life history stages**, and can this explain the non-correlation of IBD between these stages?
- What are the **footprints of selection** in the genomes of individuals from small and large populations?
- What is the **selective value of variation in gene expression**?



Costs/requirements (2008/2009):

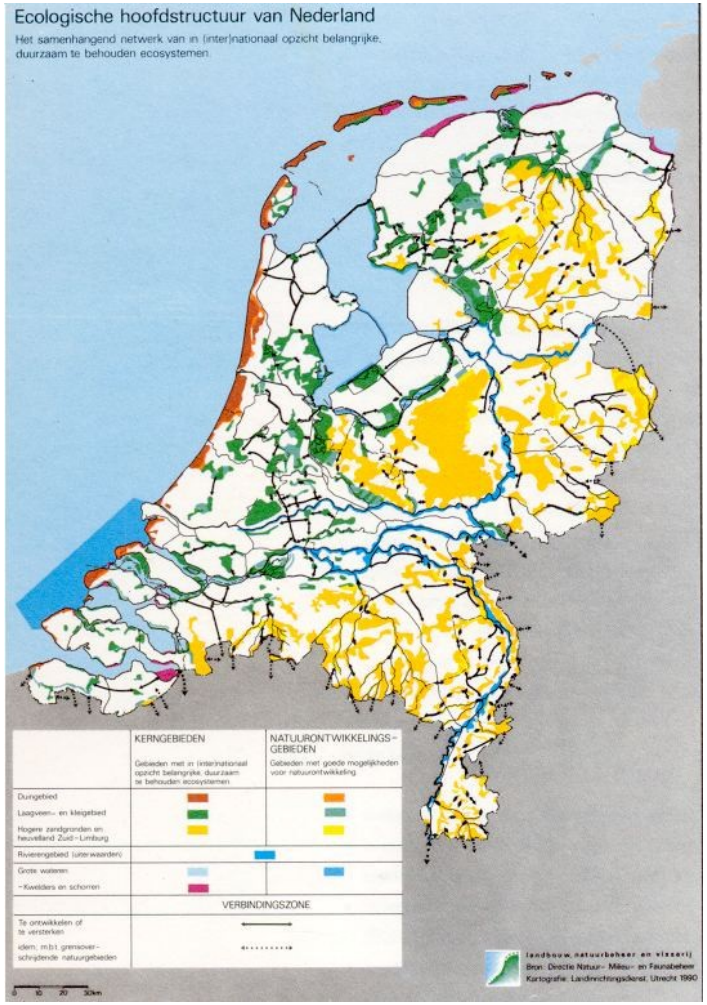
Costs are diminishing continuously

454 FLX-cDNA sequencing : 1 month, 15.000 €
(used to be
200.000 € with Sanger technology)

microarray production: 100 € per array
microarray screening: 150 € per array

cheaper options (like SOLEXA technology) are becoming available, at much lower costs

Relative costs of conservation genomics:



Projected costs (but this is almost certain a severe underestimation):

20 billion Euro

That is:

20.000.000.000 Euro

That is equivalent to 40.000.000 microarray runs……

We live in exciting times !!!