

Next-generation sequencing (NGS)

Sanger sequencing

Primer - F - AAGTCAGTCTAA**A**=0 -

Primer - F - AAGTCAGTCT**A**=0

Primer - F - AAGTCAGTCT**T**=0

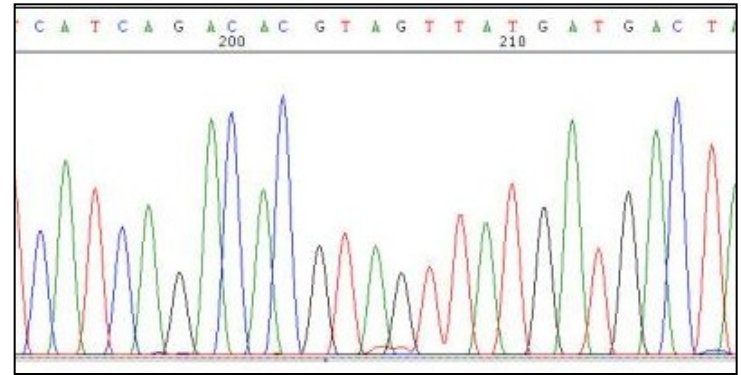
Primer - F - AAGTCAGT**C**=0

Primer - F - AAGTCAG**T**=0

Primer - F - AAGTCAG**G**=0

Primer - F - AAGTC**A**=0

Primer - F - AAGT**C**=0



krátké ----- dlouhé
(rychlé) ----- (pomalé)

+

Primer - F **AAGTCAGTCTAA**ATGCGATTGGGA Rev. Primer - R

Rev. Primer - F **TTCAGTCAGATTACGCTAACCT** Primer - R

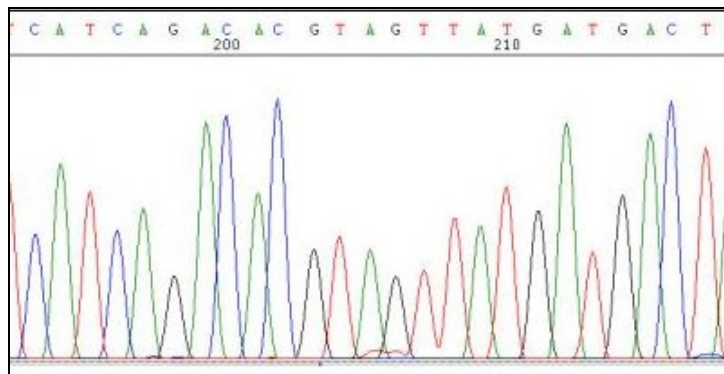
4-kapilární sekvenátor

=

96 x 500 bp/12 hodin

=

cca 100 000 bp/den



detector



laser beam



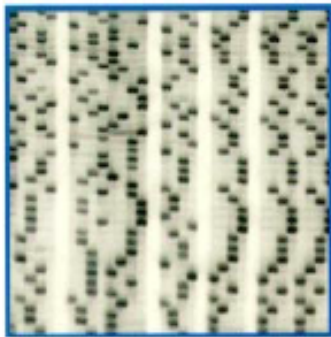
capillary
electrophoresis

+

-

Evolve 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*

96-kapilární sekvenátor

=

2304 x 500 bp/12 hodin

=

cca 2 400 000 bp/den

NGS (Illumina HiSeqX10)

=

cca 600 000 000 000 bp/den

electrophoresis

Next-generation sequencing (NGS)

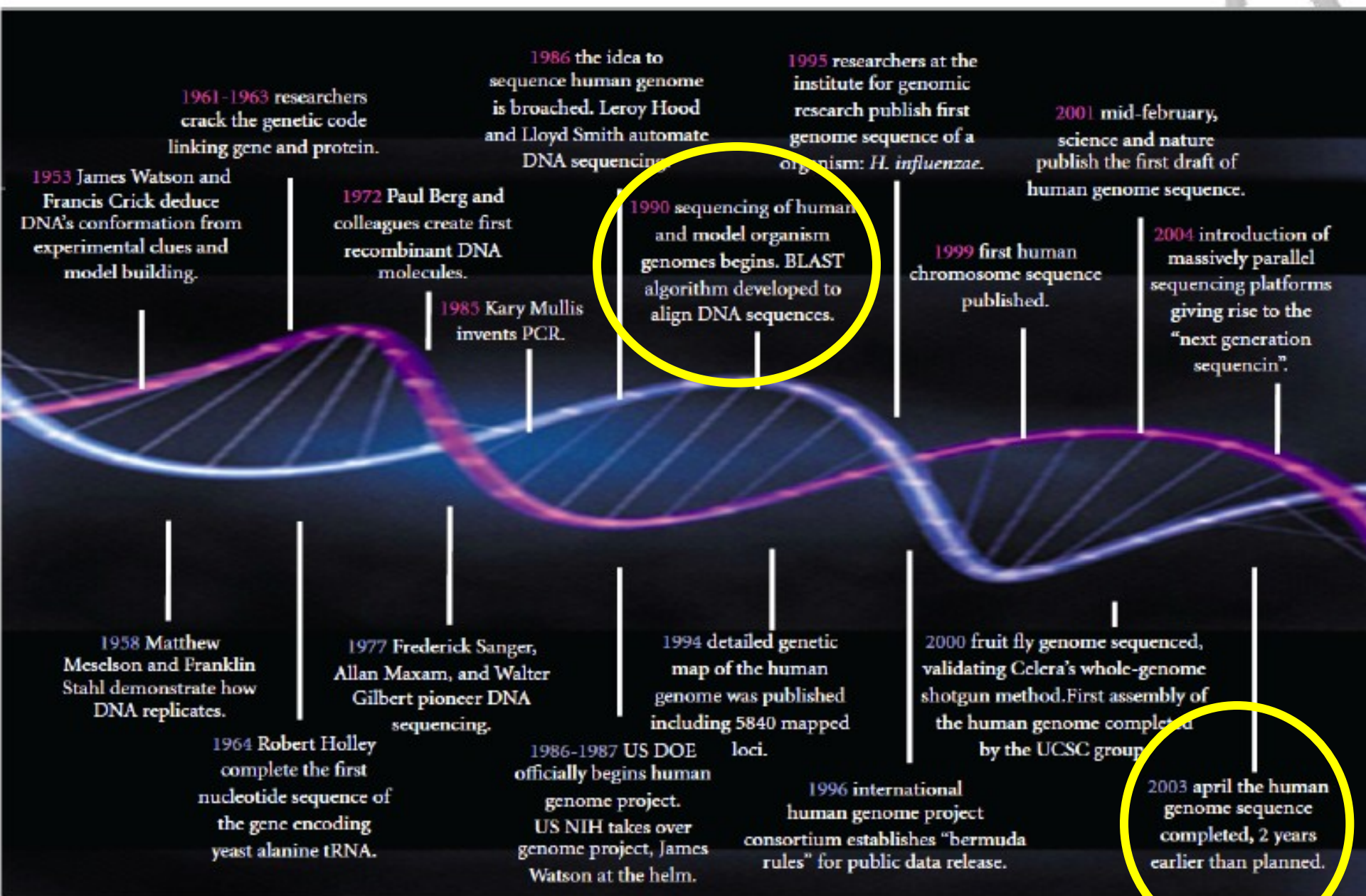
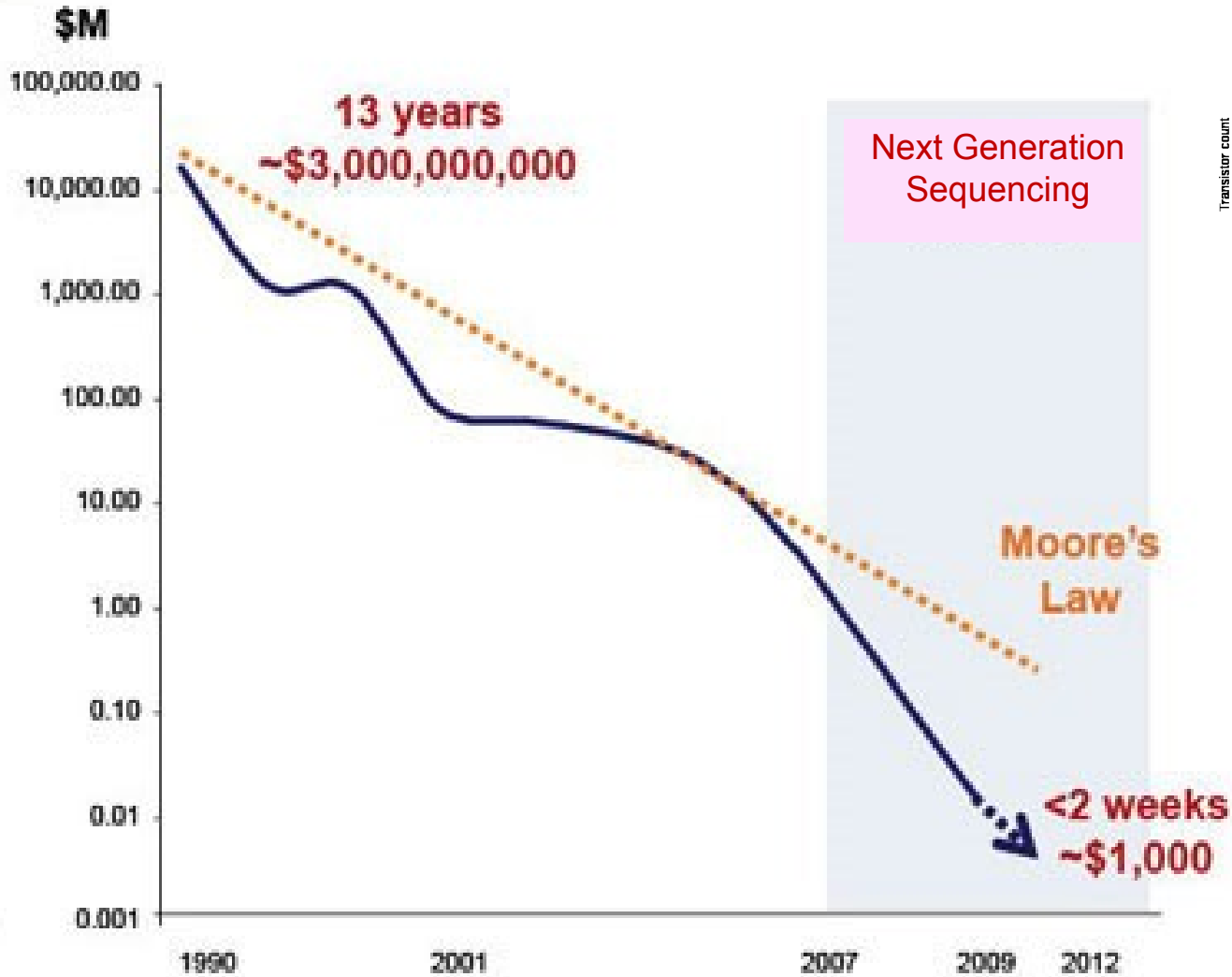
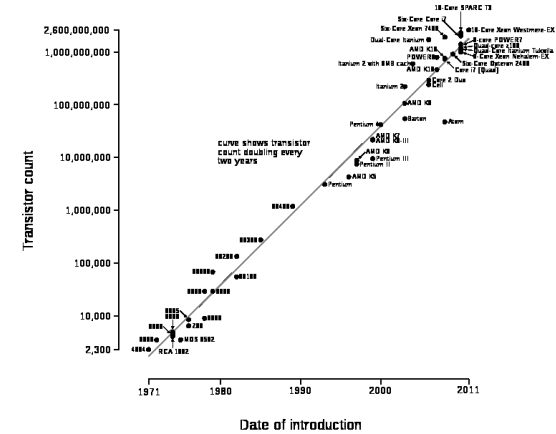


FIGURE 1: Evolution of DNA revolution.

Cost per Human Genome



Microprocessor Transistor Counts 1971-2011 & Moore's Law



Illumina HiSeqX10



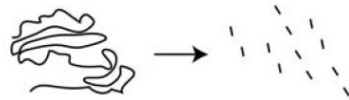
\$1 M per machine

1.8 Tbase per machine per 3 days

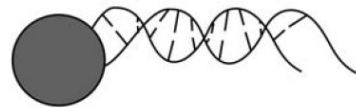
1800 human genomes per machine per year

Historie „Next generation sequencing“

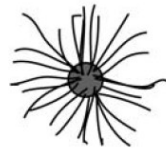
1) Randomly fragment many molecules of target DNA



2) Immobilize individual DNA molecules on solid support



3) Amplify DNA in clonal 'polymerase colony'



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



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



454 pyrosequencing ... první komerčně dostupná NGS technologie od srpna 2007

2016 – ohlášené stažení z trhu (Roche)

Široké spektrum technologií



Ale jen některé přežijí



Dnes dostupné NGS platformy

- Roche 454
- **Illumina HiSeq a MiSeq**
- ABI SOLiD
- IonTorrent (Life Technologies)
- SMRT (Pacific Biosciences)
- **Oxford Nanopore**
- ...

Illumina HiSeq/MiSeq

- v současné době nejrozšířenější typ (cca 70%) na trhu
- v horizontu následujících let její používání spíše poroste
- NextSeq, NovaSeq, etc.

https://www.youtube.com/watch?annotation_id=annotation_228575861&feature=iv&src_vid=womKfikWlxM&v=fCd6B5HRaZ8

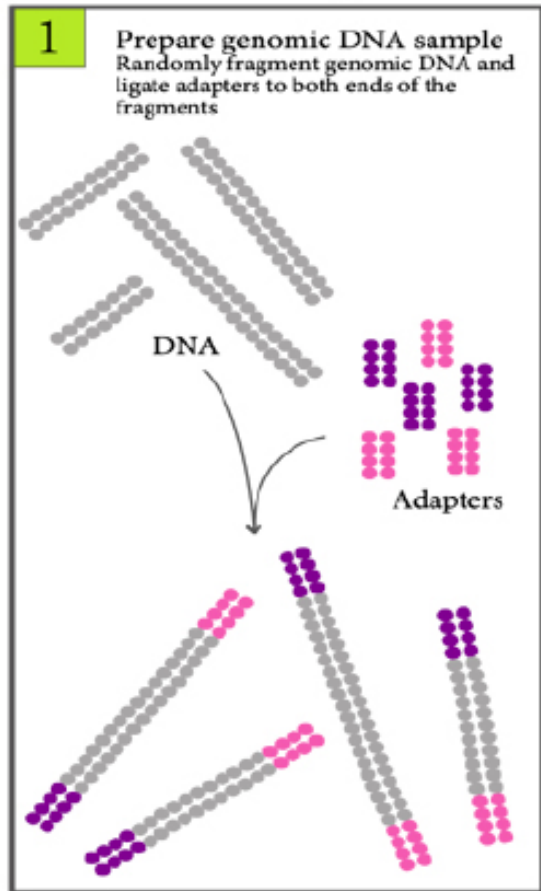
Illumina HiSeq



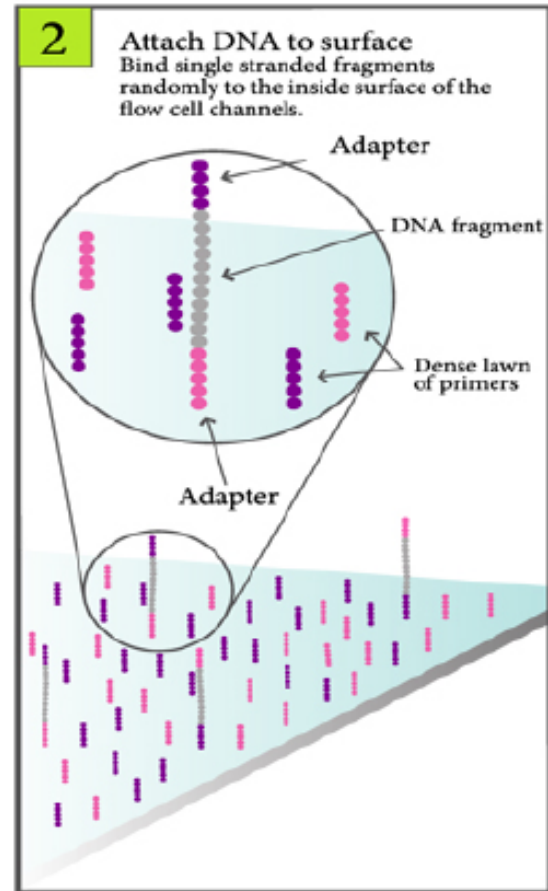
Illumina MiSeq



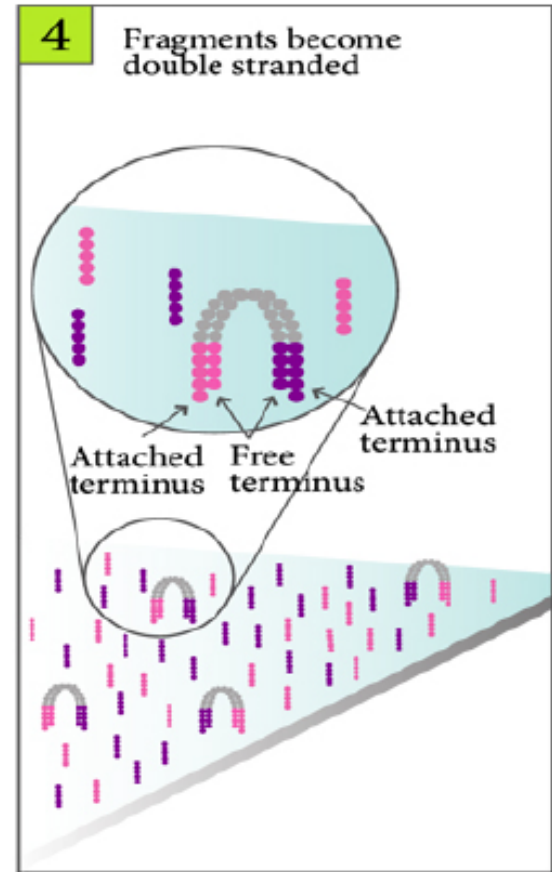
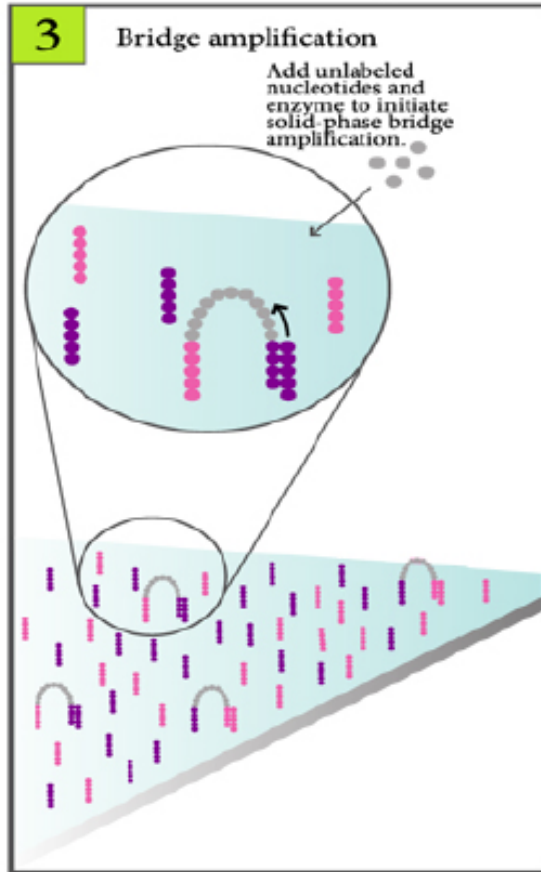
Attach DNA to flow cell



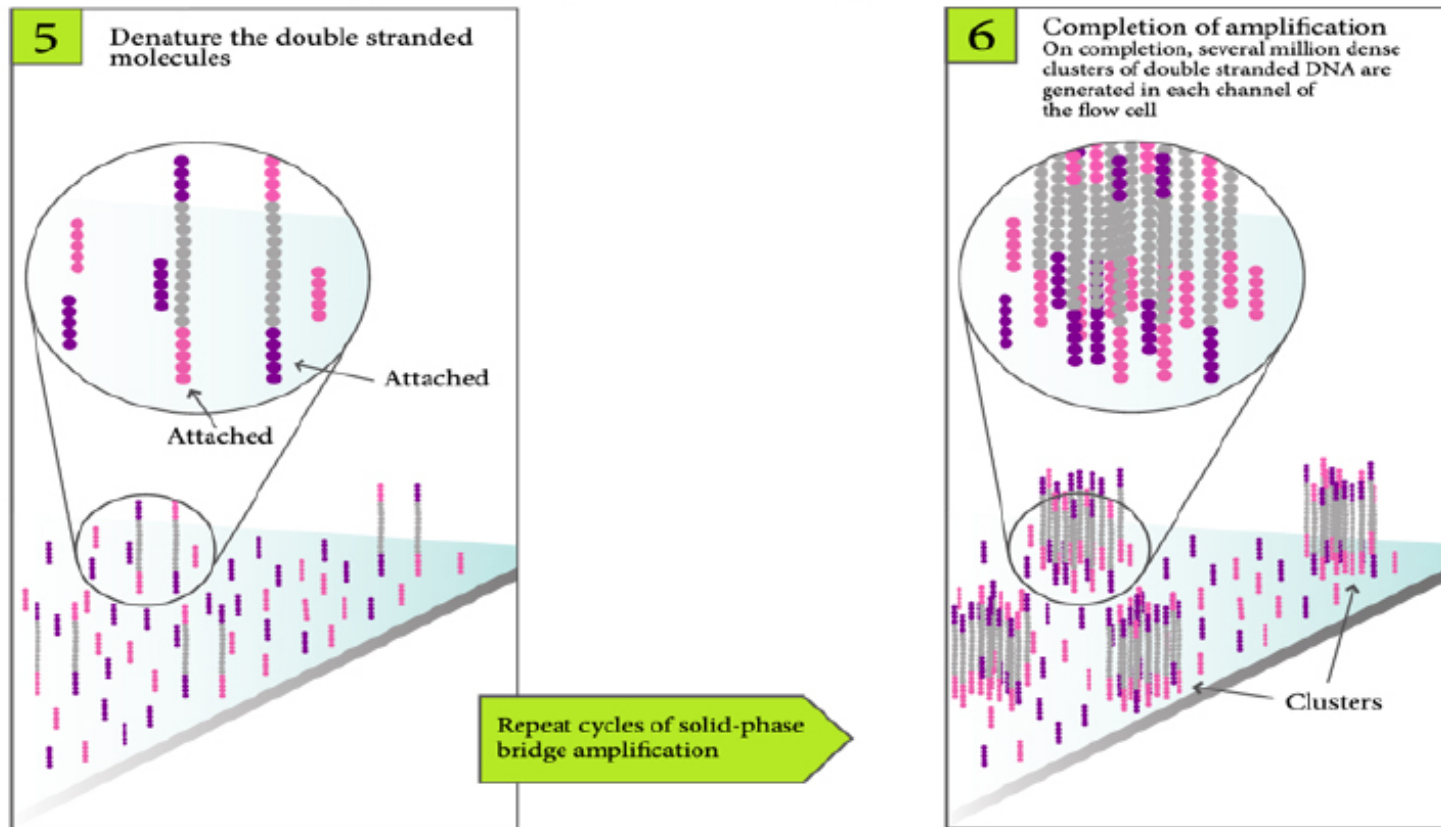
Add sample to flow cell



Bridge Amplification

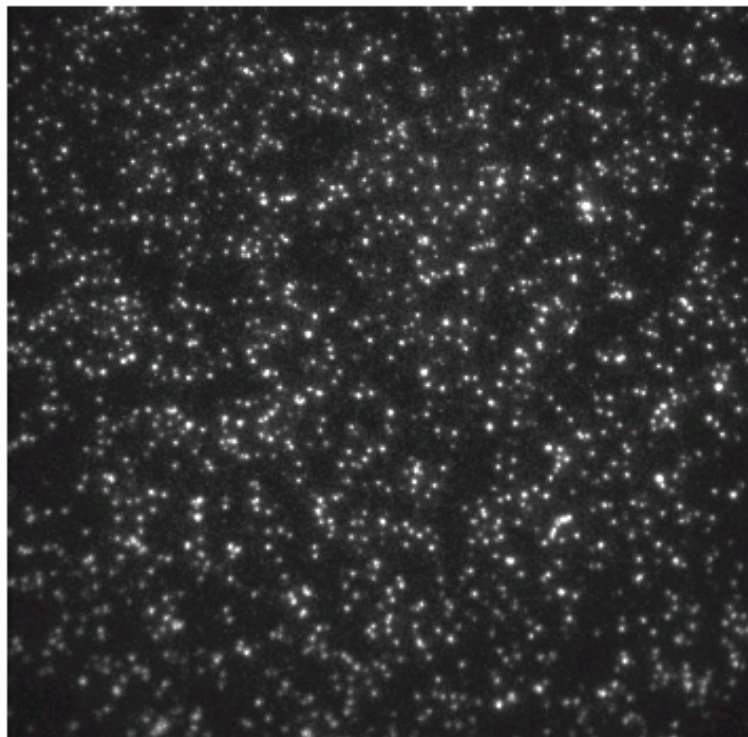


Cluster Generation



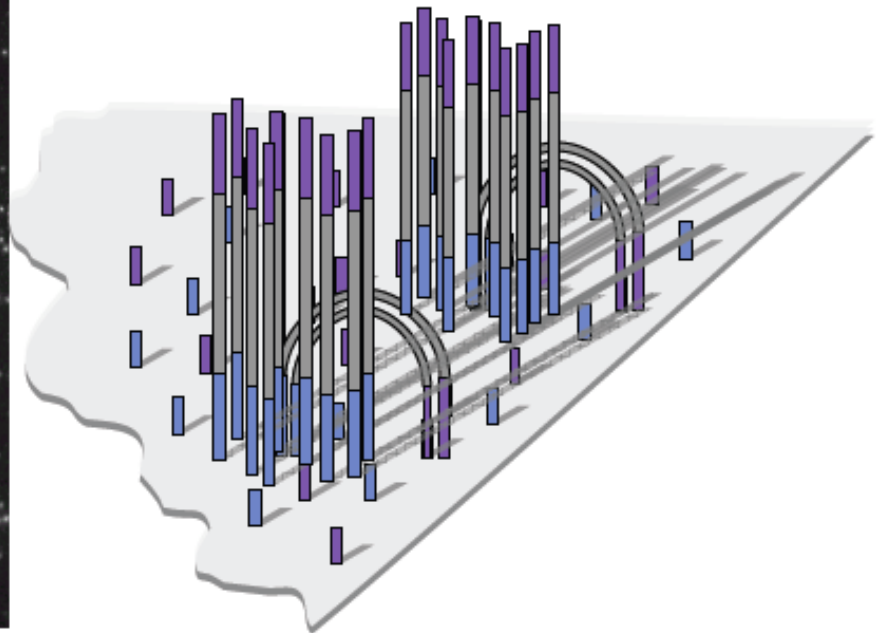
Clonal Single molecular Array

Clonal Single molecule Array



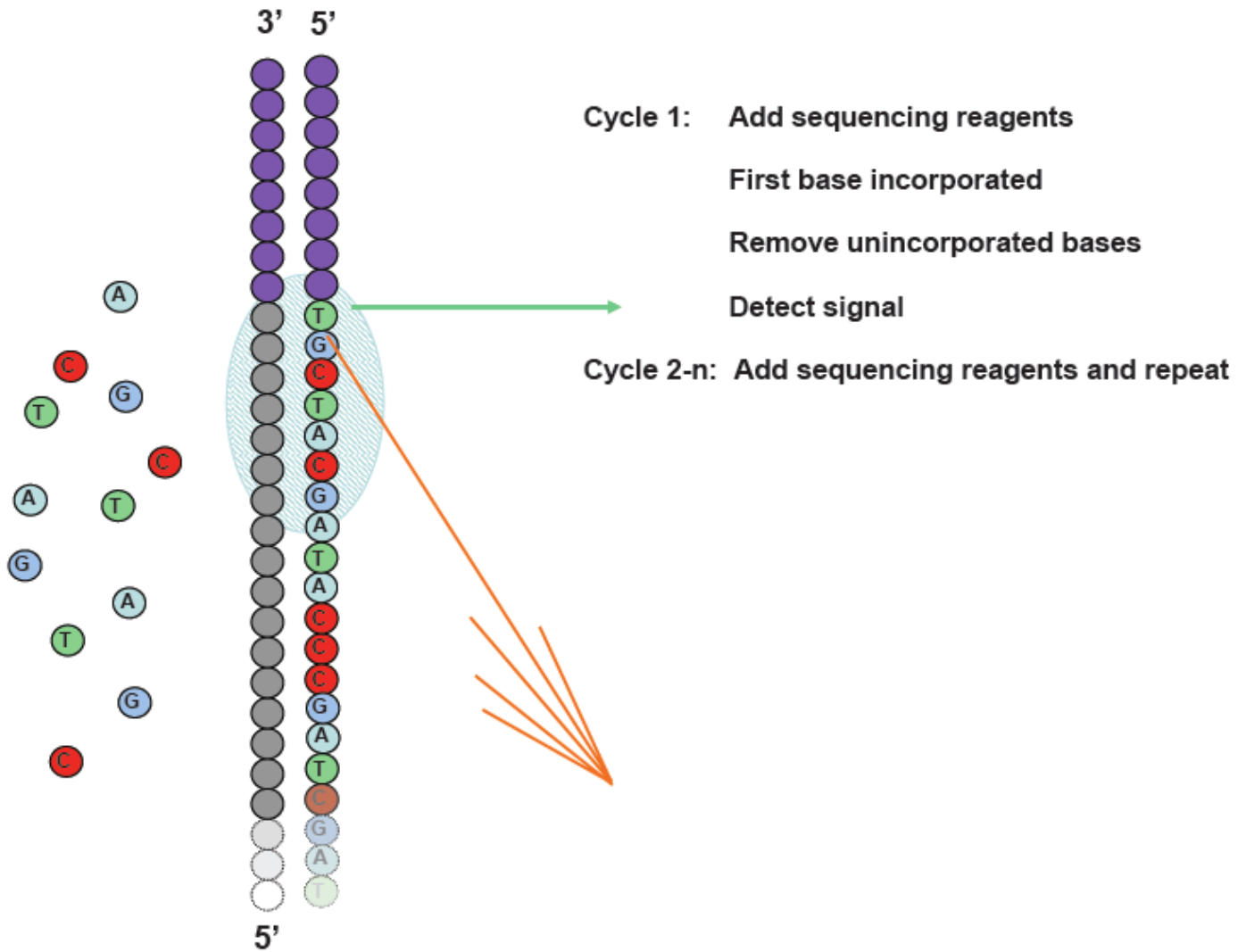
100um

Random array of clusters



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

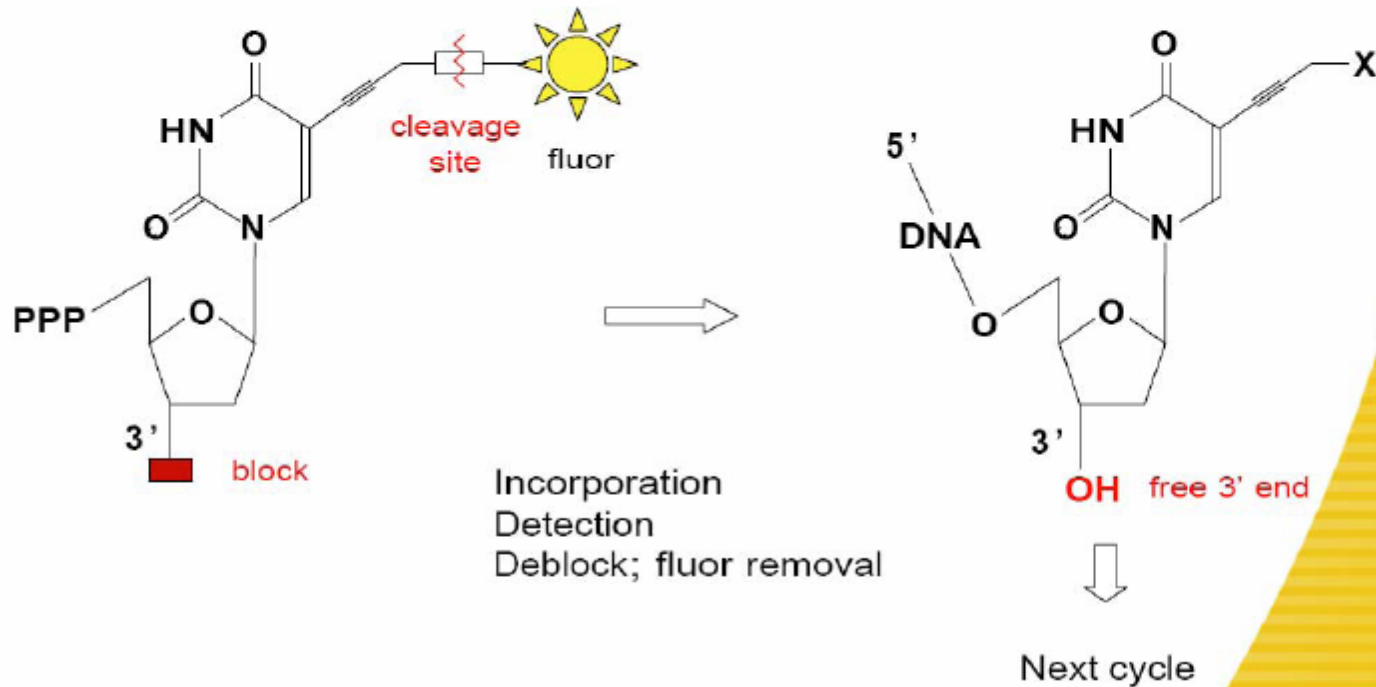
Sequencing By Synthesis (SBS)



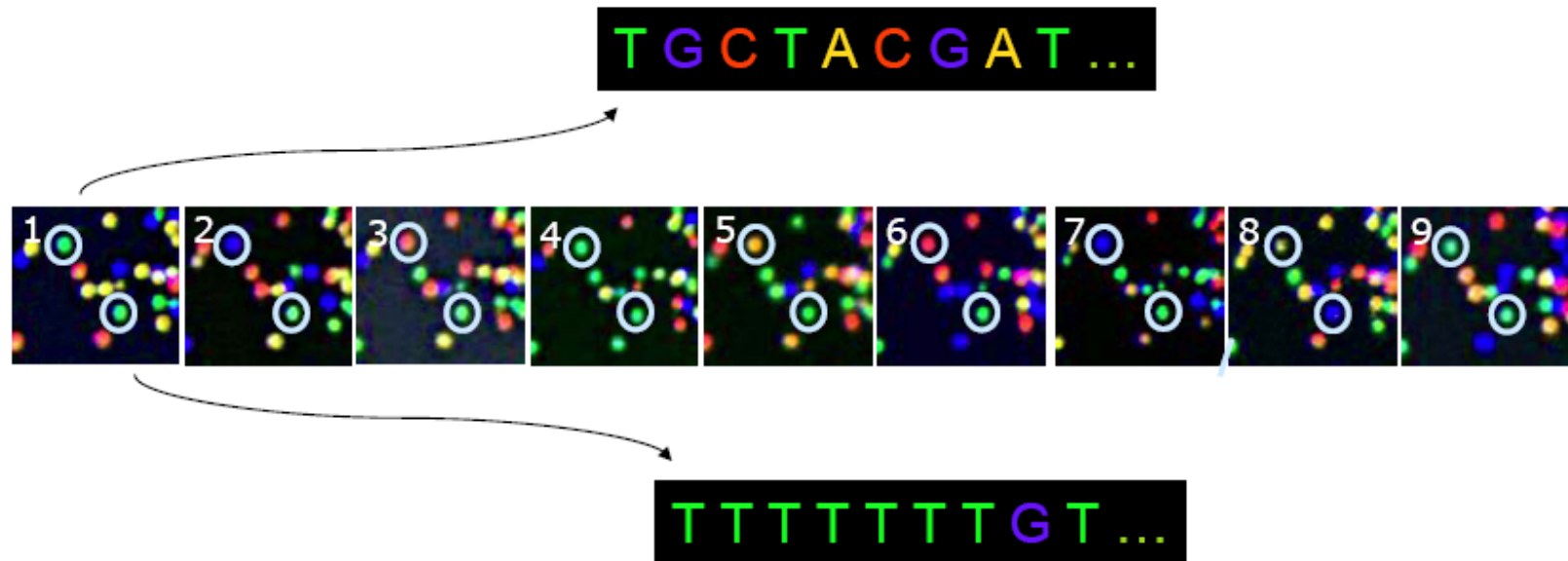
Reversible Terminator Chemistry



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



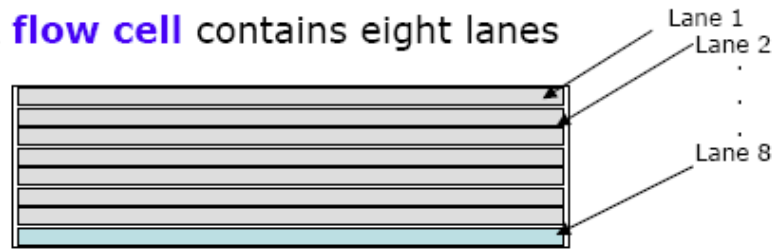
Base Calling From Images



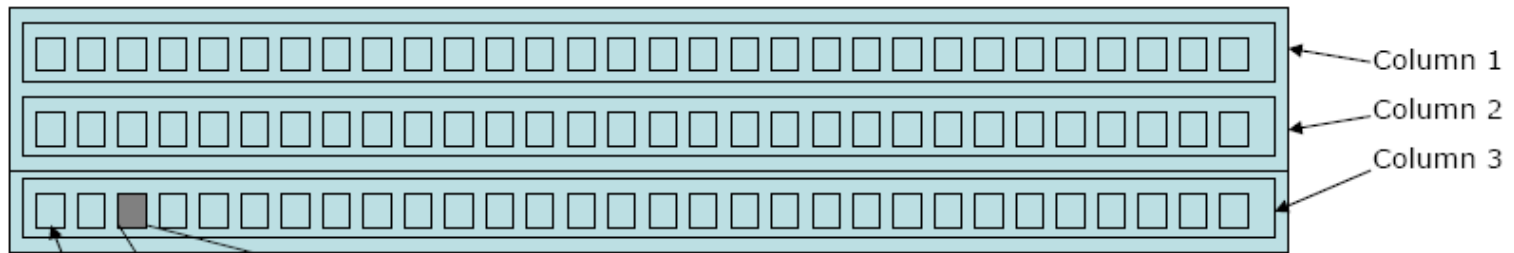
The identity of each base of a cluster is read off from sequential images



A **flow cell** contains eight lanes



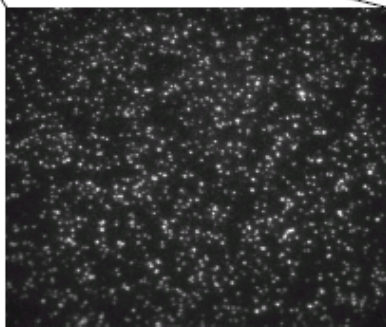
Each **lane/channel** contains **three columns** of tiles



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

Tile

20K-30K
Clusters

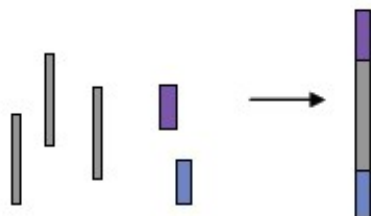


350 X 350 μm

https://www.youtube.com/watch?annotation_id=annotation_228575861&feature=iv&src_vid=womKfikWlxM&v=fCd6B5HRaZ8

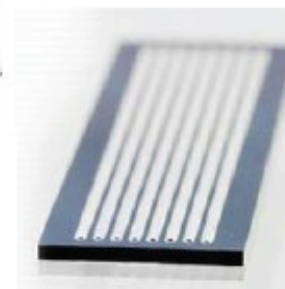
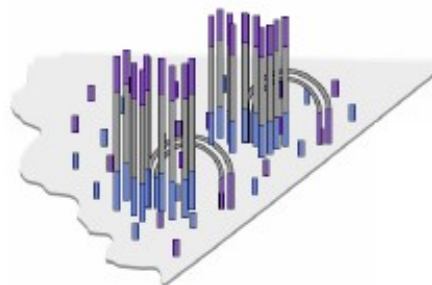
Illumina Sequencing pipeline

1. Sample Prep (1-5 days)



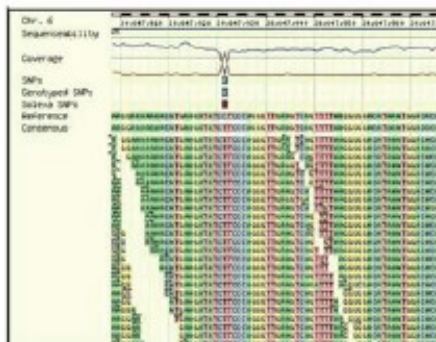
Ligate adapters

2. Cluster generation on flow cell (1.5 day)



Clonal Single molecular Array

4. Data Analysis (days-months)



3. Sequencing and imaging (2-3 days)



Illumina fastq

= one „read“



```
1           2           3           4           5           6 7           8
@HWI-ST226:253:D14WFACXX:2:1101:2743:29814 1:N:0:ATCACG
TGC GGAAGGATCATTGTGGAATTCTCGGGTGCCAAGGA ACTCCAGTCACATCACGATCTCGTATGCCGTCTTCTGCTT
GAAAAAAAAAAAAAAAAAATTA
+
B@CFFFFFFHFFHJIIGHIHIJJJIJIIJJGDCHIIJJJJJJGJGIHHEH@)=F@EIGHHEHFFFDCBBD:@CC@C
:<CDDDD50559<B#####
```

1. unique instrument ID and run ID
2. Flow cell ID and lane
3. tile number within the flow cell lane
4. 'x'-coordinate of the cluster within the tile
5. 'y'-coordinate of the cluster within the tile
6. the member of a pair, /1 or /2 (*paired-end or mate-pair reads only*)
7. N if the read passes filter, Y if read fails filter otherwise
8. Index sequence

All this generates a lot of Data!

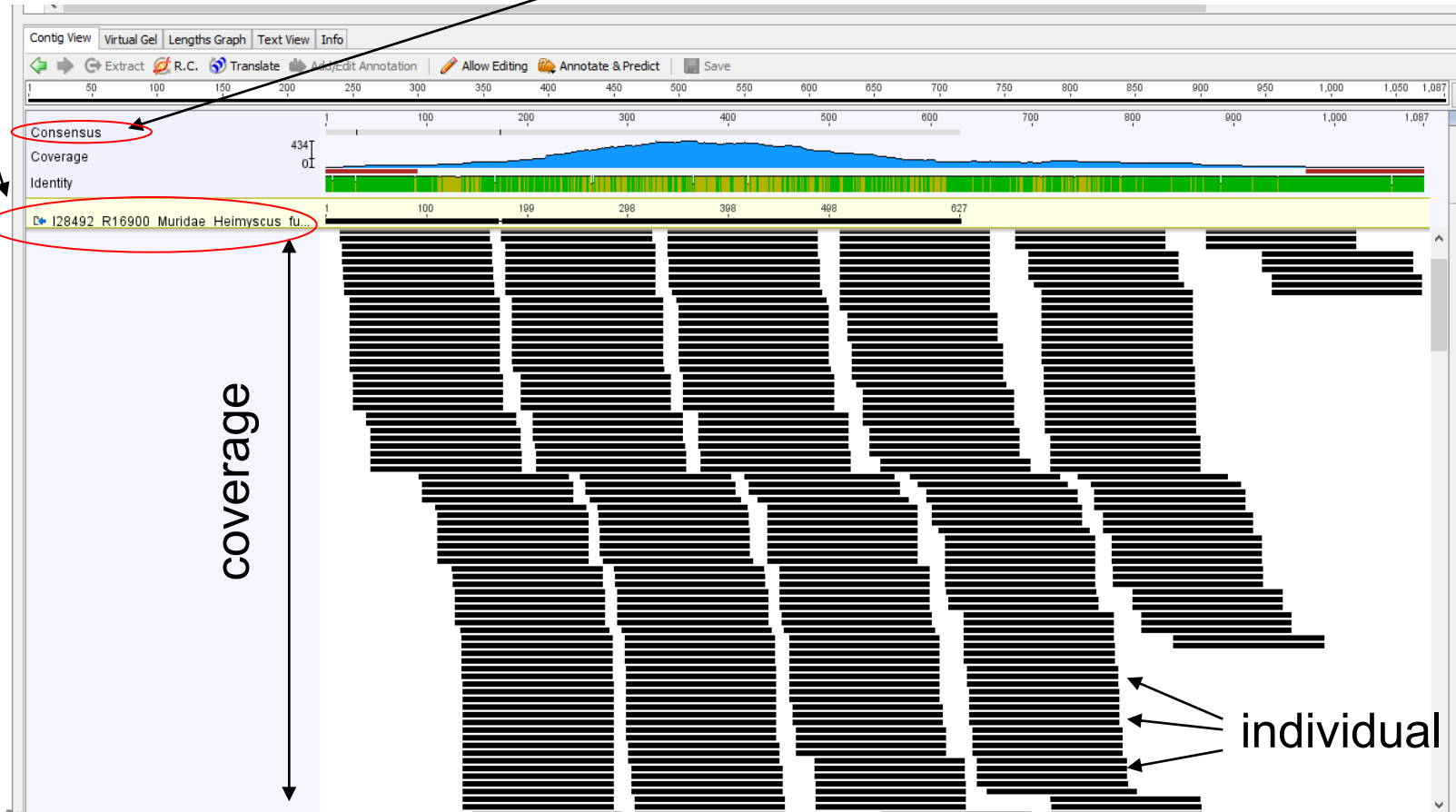
1.5 TB data/run

- 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

Data analysis in Geneious

consensus

reference (in resequencing)

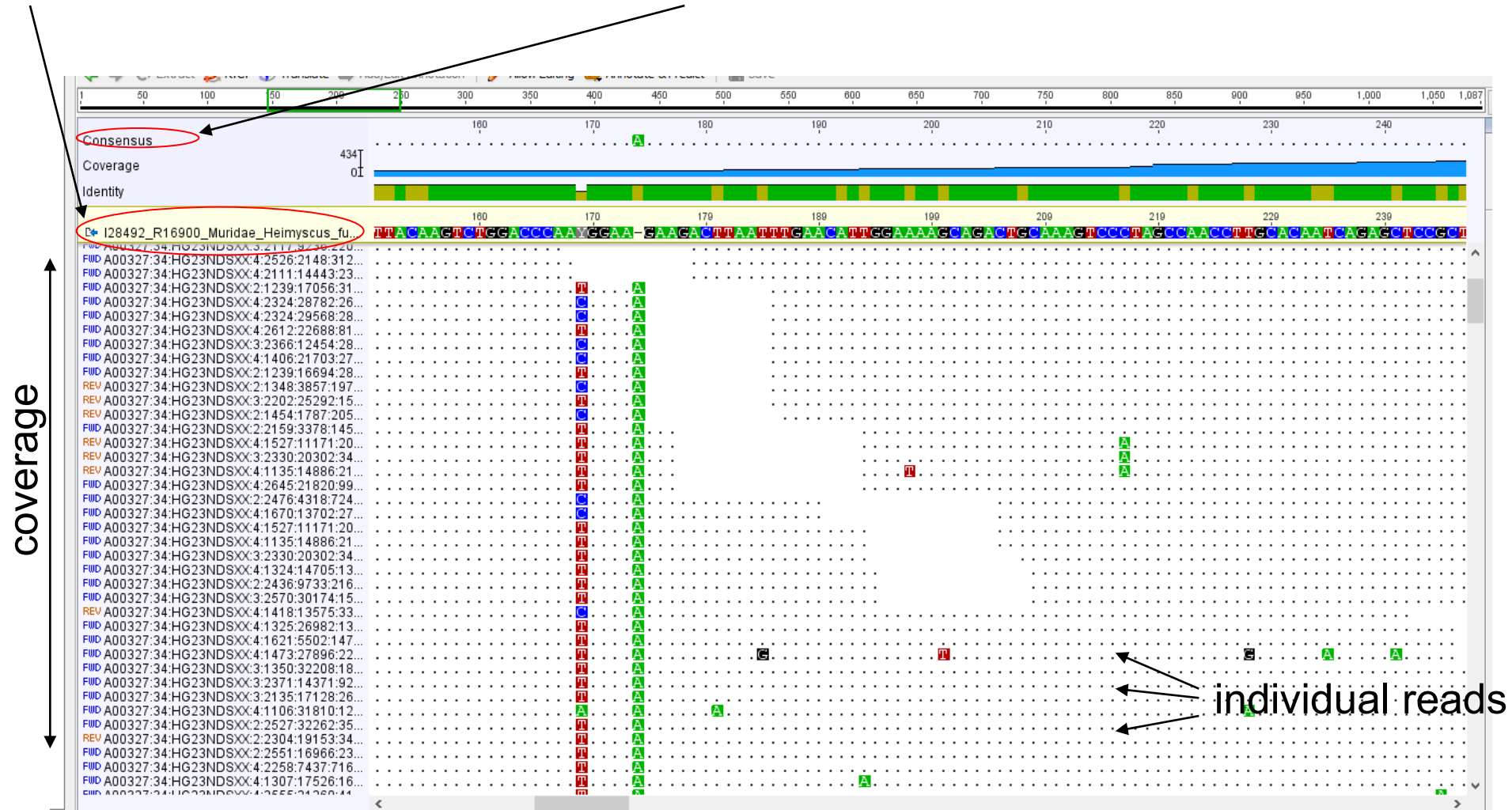


individual reads

Data analysis in Geneious

reference (in resequencing)

consensus



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



NovaSeq 6000 Sequencing System (2017)

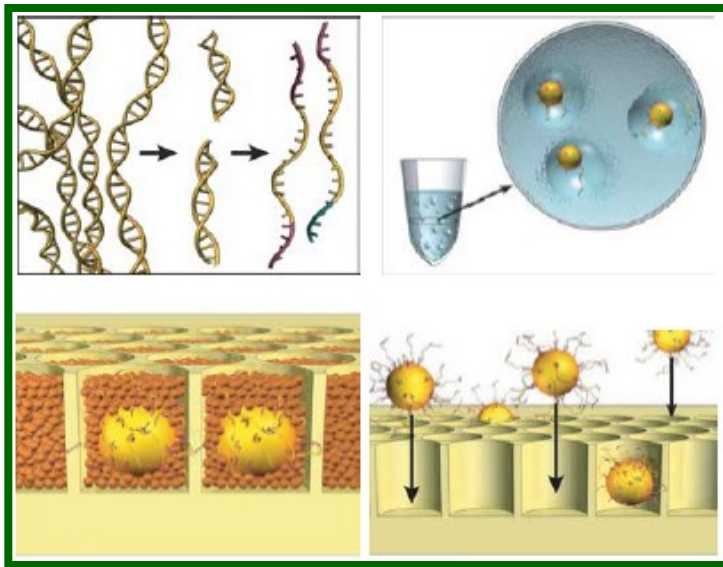
ca. 48 human genomes/run

Sequencing Output per Flow Cell

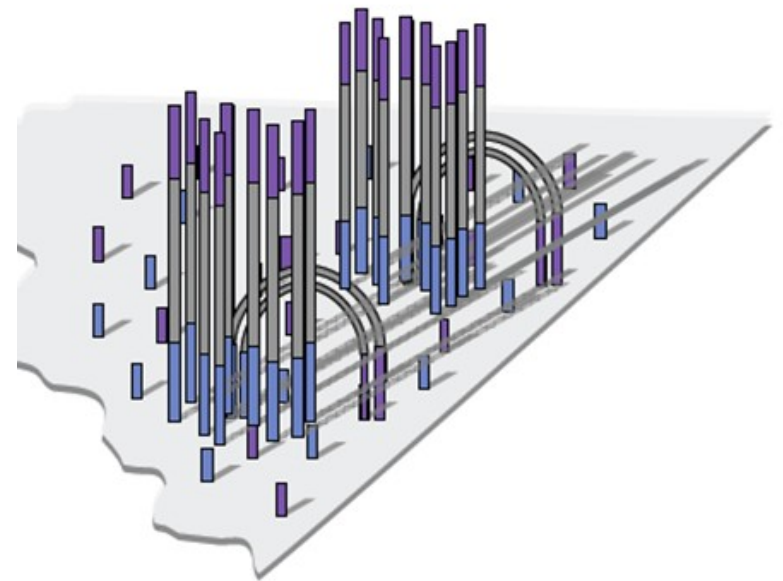
Flow Cell Type	NovaSeq 6000 System		
	S1	S2	S4
2 × 50 bp	134–167 Gb	333–417 Gb	N/A*
2 × 100 bp	266–333 Gb	667–833 Gb	N/A*
2 × 150 bp	400–500 Gb	1000–1250 Gb	2400–3000 Gb

Specifications based on Illumina PhiX control library at supported cluster densities.
* N/A: not applicable

Další NGS technologie



454 pyrosequencing
(Roche)



Illumina

Ion Torrent technology



Microbial sequencing



Targeted sequencing



Transcriptome sequencing



Exome sequencing



Ion PGM™ Sequencer

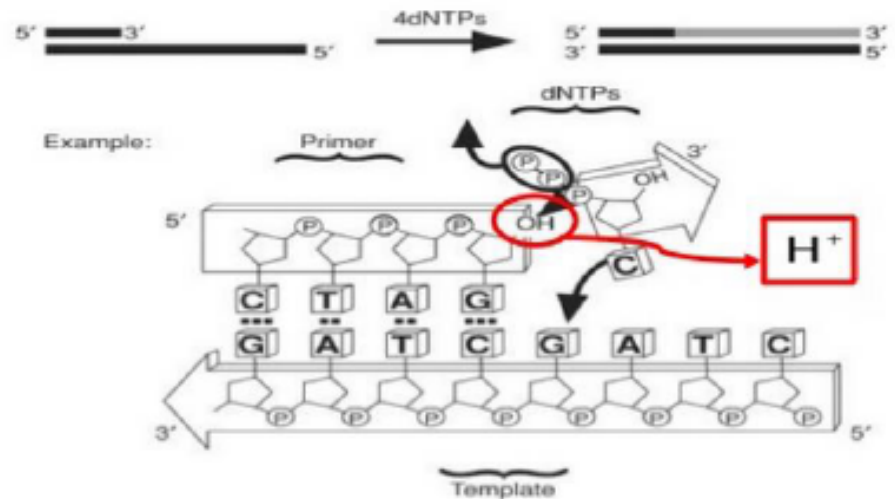


Ion Proton™ Sequencer

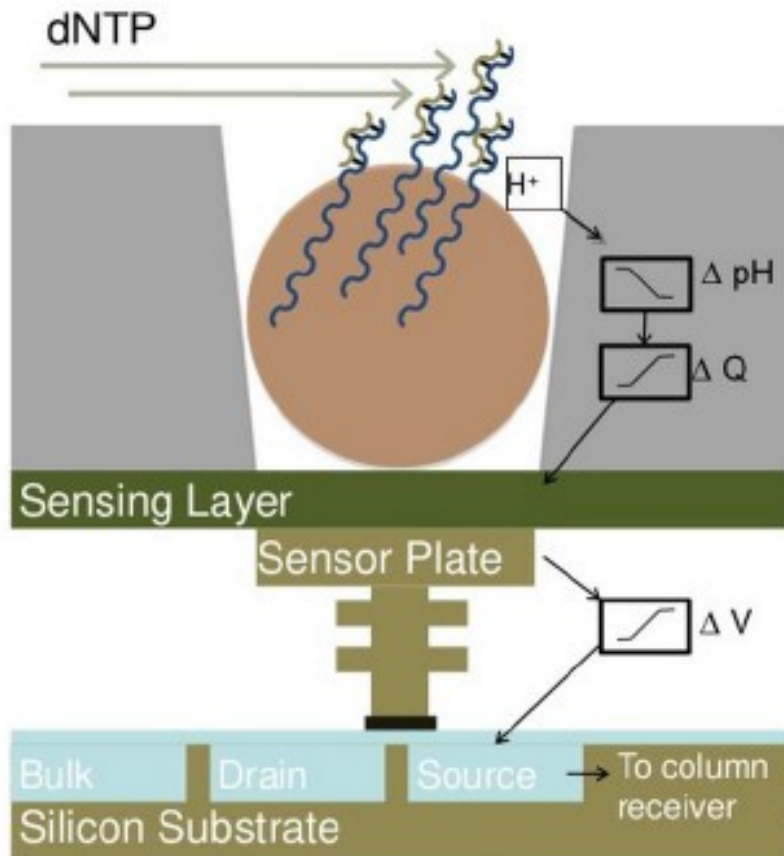
Ion sequencing: Life Technologies

Využívá změny pH při syntéze DNA

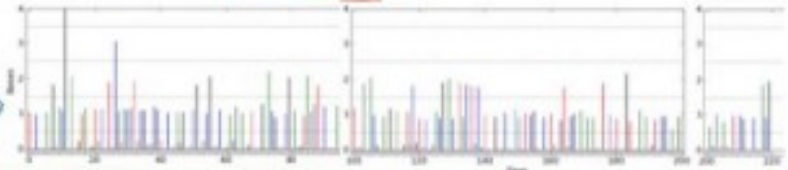
- Ion Semiconductor Sequencing
- Detection of hydrogen ions during the polymerization DNA
- Sequencing occurs in microwells with ion sensors
- No modified nucleotides
- No optics



Ion Torrent



- DNA \rightarrow Ions \rightarrow Sequence
 - Nucleotides flow sequentially over Ion semiconductor chip
 - One sensor per well per sequencing reaction
 - Direct detection of natural DNA extension
 - Millions of sequencing reactions per chip
 - Fast cycle time, real time detection



Ion Torrent: System Updates

314 Chip

- 100bp reads ~10 Mb/run (1.5 hrs)

316 Chip

- 100 bp reads ~100 Mbp / run (2 hrs)
- 200 bp reads ~200 Mbp/run (3 hrs)

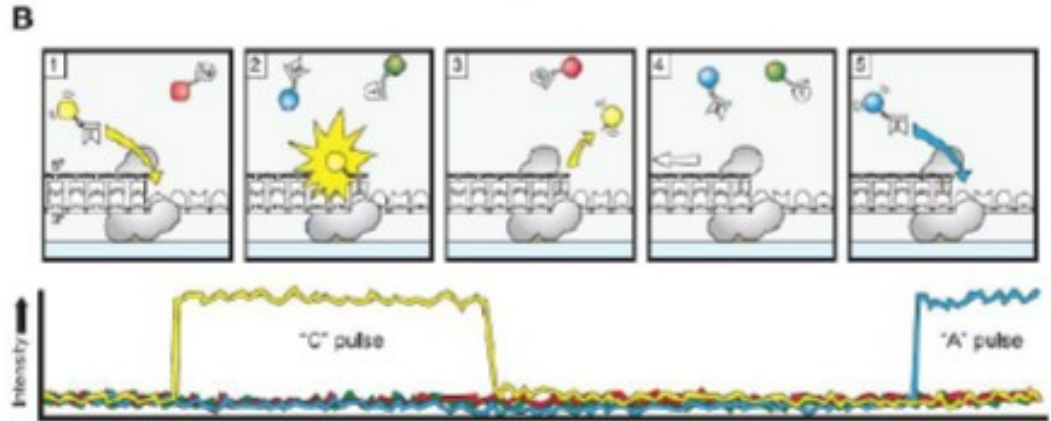
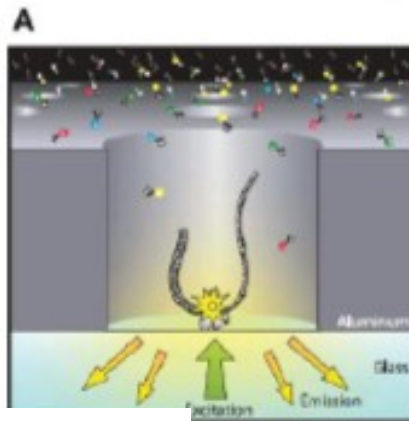
318 Chip

- 200 bp reads ~1 Gbp / run (4.5 hrs)

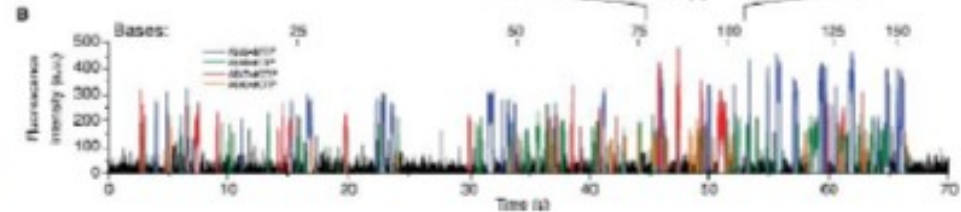
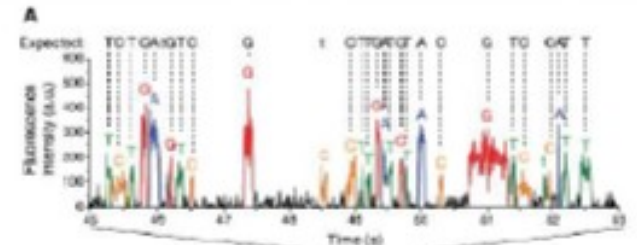
400 bp reads



SMRT („single molecule real-time sequencing”) – Pacific Biosciences

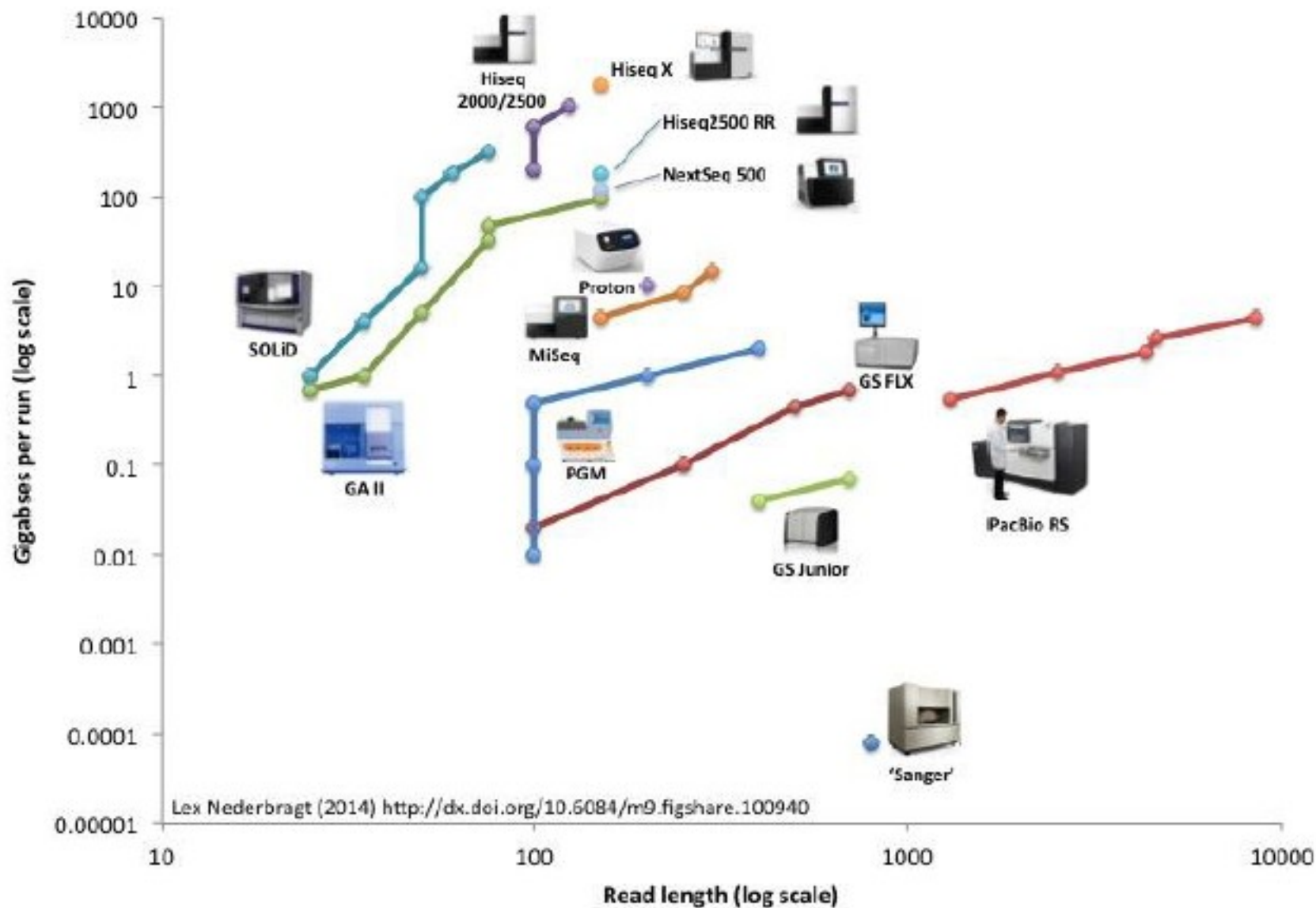


Pacbio RS – raw data



dlouhé čtení (15 kb), hodně chyb

Developments in High Throughput Sequencing



Lex Nederbragt (2014) <http://dx.doi.org/10.6084/m9.figshare.100940>

3rd generation: Oxford Nanopore



MinION
512 pores



GridION
5 000 pores

Future Sequencing Technologies

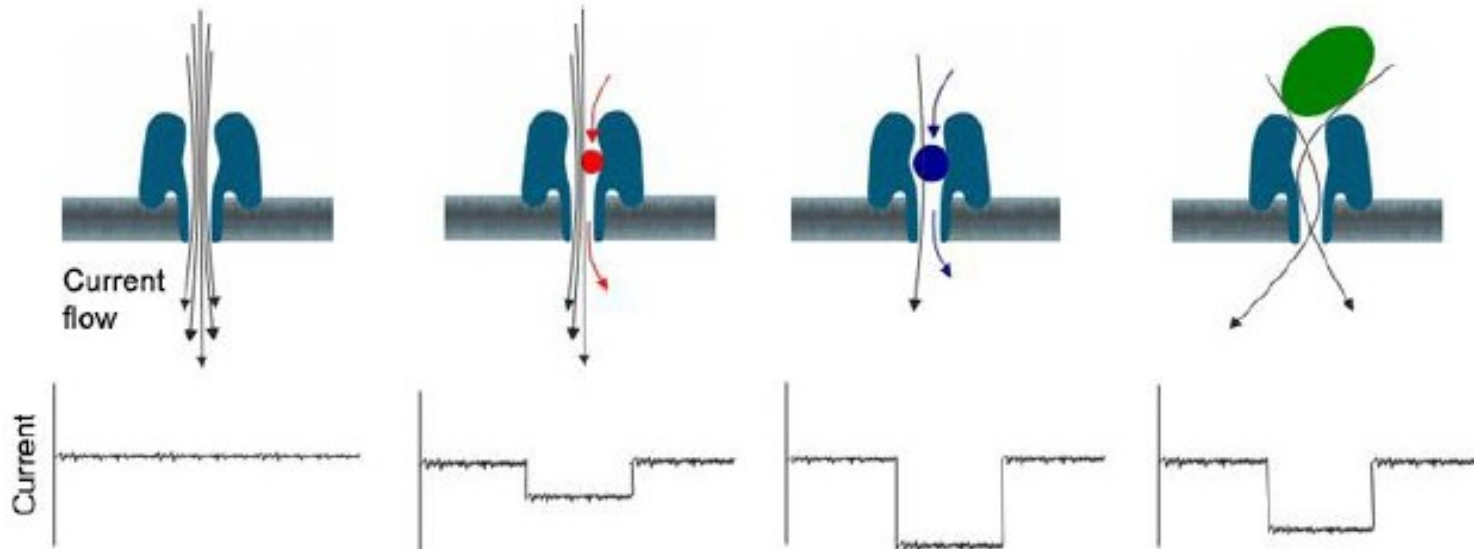
Oxford Nanopore

Nanopore sequencing
up to 50 kb

„Run until sequencing ...“



Princip technologie



<http://www.youtube.com/watch?v=3UHw22hBpAk>

Sekvenování přímo v terénu (?)



Ebola outbreak

Quick et al., Nature 2016



Přehled NGS metod (2012, regularly updated)

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

<https://www.molecularecologist.com/next-gen-fieldguide-2016/>

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

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

Traditional Sequencing vs. Next Generation Sequencing: Data Throughput

1 x Illumina GAI



200+ of 3730xl



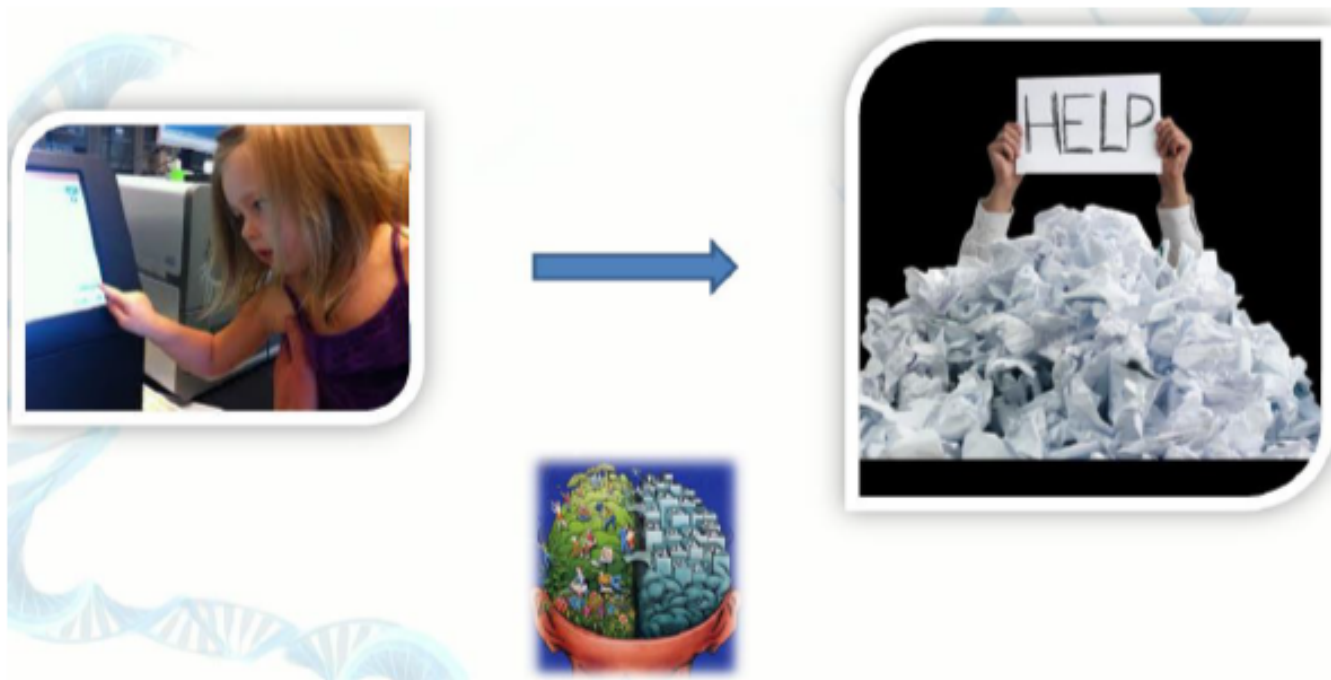
Vs.

Days vs. Years

The Sequencing Landscape is Changing

Bioinformatika - největší brzda dalšího rozvoje

Basically, analyzing genomes in interaction with their environment is now feasible and accessible to anyone



Sekvenační strategie

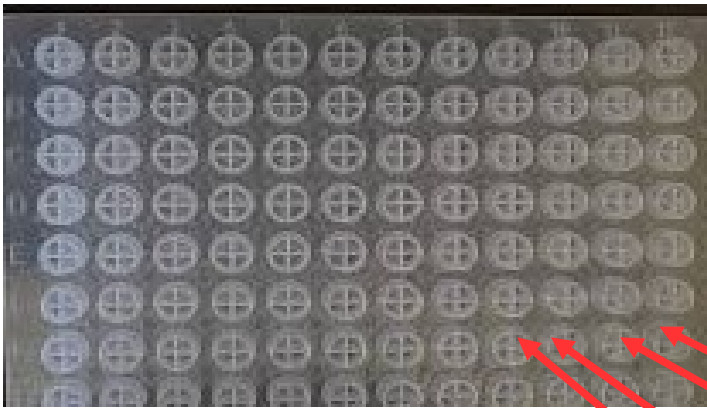
- nutno velmi dobře počítat než se začne sekvenovat
- celkový výtěžek sekvenování = **počet „reads“ * délka „reads“ * coverage**
- zásadně závisí na konkrétním cíli výzkumu a použité technologii

Sekvenační strategie

...JEDEN VZOREK NA RUN JE MÁLO

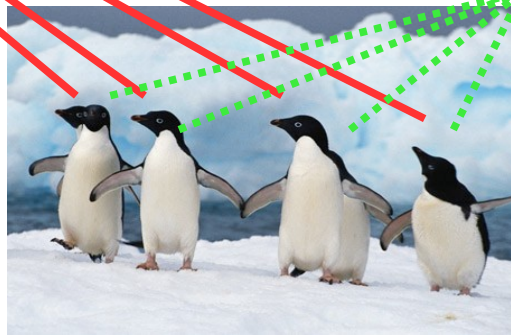
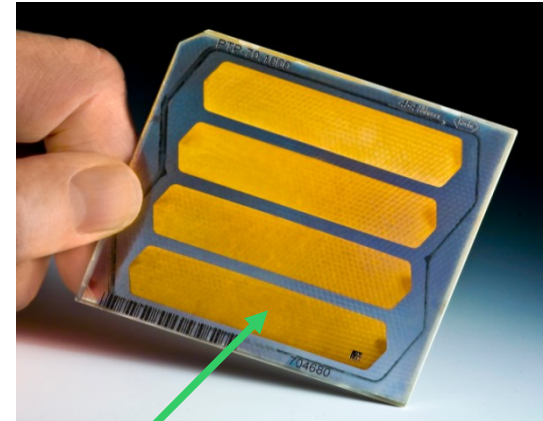
Kapilární sekvenátor

U kapilárních sekvenátorů není problém přiřadit sekvenci k jednotlivým vzorkům na základě pozice na platíčku



Sekvenátor druhé generace

U sekvenátorů druhé generace se najednou sekvenuje pool desítek až stovek vzorků



Sekvenační strategie

...JEDEN VZOREK NA RUN JE MÁLO

Jednotlivé vzorky pro sekvenátory druhé generace se značí tzv. barcodes (midy, tagy)

Krátká (obvykle 6-12bp) oligonukleotidová sekvence před primerem (pokud sekvenujeme PCR amplikon), která je specifická pro daný vzorek

Přiřazení identity jednotlivých sekvencí k vzorkům probíhá bioinformaticky

BARCODE

PRIMER

SEQUENCE

```
AGCGTAGGTCATTTCGATGCGGTCATGCCTGGATTAAAGCT.....  
TTCGTAGGTCATTTCGATGCGGTCATGCCTGGATTAAAGCT.....  
TGGGTAGGTCATTTCGATGCGGTCATGCCTGGATTAAAGCT.....  
TGCCTAGGTCATTTCGATGCGGTCATGCCTGGATTAAAGCT.....  
TGCGCAGGTCATTTCGATGCGGTCATGCCTGGATTAAAGCT.....  
TGCGTIGGTCATTTCGATGCGGTCATGCCTGGATTAAAGCT.....
```


Sekvenační strategie

AMPLIKONOVÉ SEKVENOVÁNÍ (amplikony kratší než délka readů)

SHOT GUN SEKVENOVÁNÍ

LONG-RANGE PCR + SHOT GUN (amplikony delší než délka readů)

COMPLETE GENOME (e.g. viral genome from enriched samples)

REDUCED GENOME

- **PCR** amplicons
- Enriched libraries by **hybridization** (development of microsatellite markers, exom, anchored phylogenomics, UCE = ultraconserved elements, etc.)
- Enriched libraries by **restriction enzymes** (RAD sequencing)
- RNAseq (**transcriptomics**)

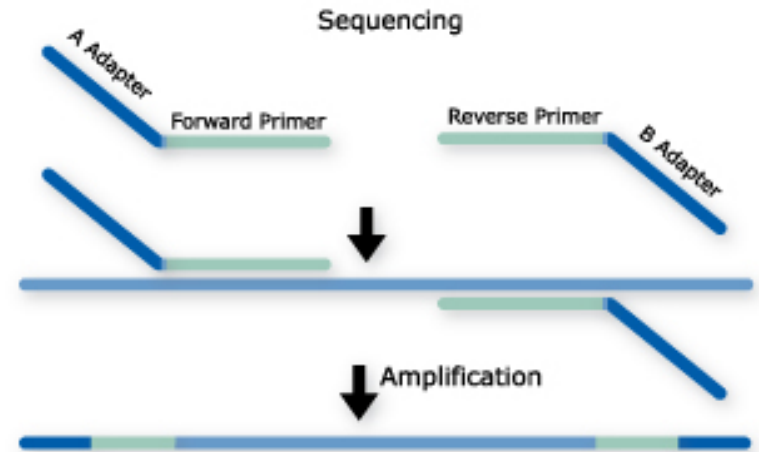
Sekvenační strategie

AMPLIKONOVÉ SEKVENOVÁNÍ

PCR Amplifikace konkrétního úseku daného genomu pomocí specifických primerů (se sekvenačními adaptory)

Následná sekvenace

Taxonomické složení daného vzorku („metabarcoding“), variabilita konkrétních genů apod.



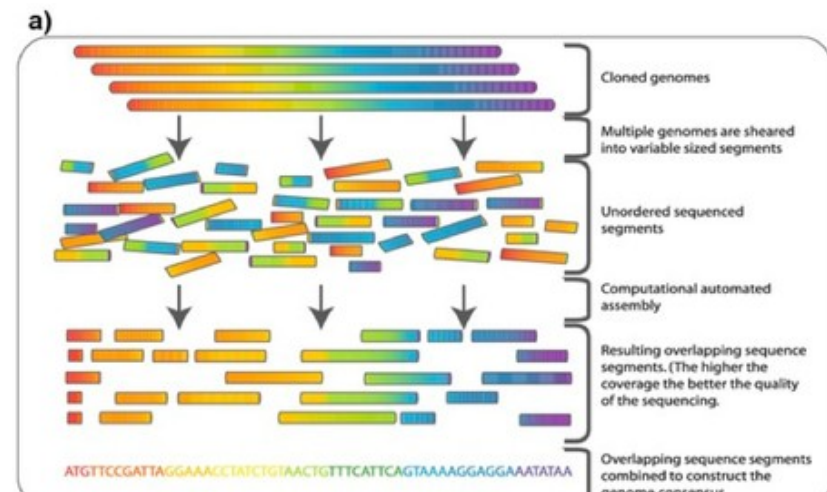
SHOT GUN SEKVENOVÁNÍ

Fragmetace celogenomové DNA

Ligace sekvenačních adaptorů

Následná sekvenace náhodných fragmentů

De novo assembly, resekvenování, transkriptomika, funkční složení daného společenstva



Sekvenační strategie

LONG RANGE PCR + SHOT GUN

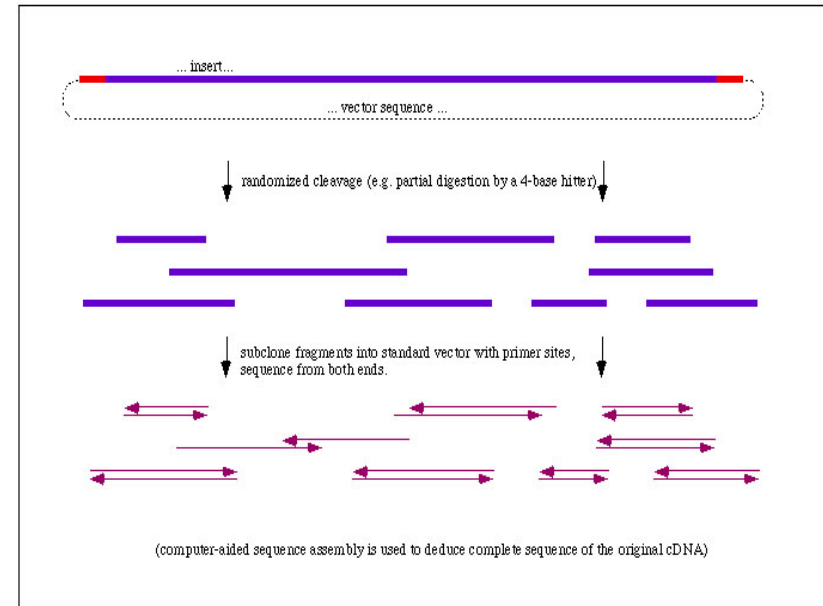
Dlouhé PCR produkty, které nejdou vcelku osekvenovat

Jejich fragmentace

Sekvenování fragmetů

Zpětná rekonstrukce původní sekvence („assembly“)

Použitelné pokud nás zajímá variabilita v jednolitém úseku DNA. Např. sekvenace kompletní mitochondriální DNA (3 různé PCR produkty).



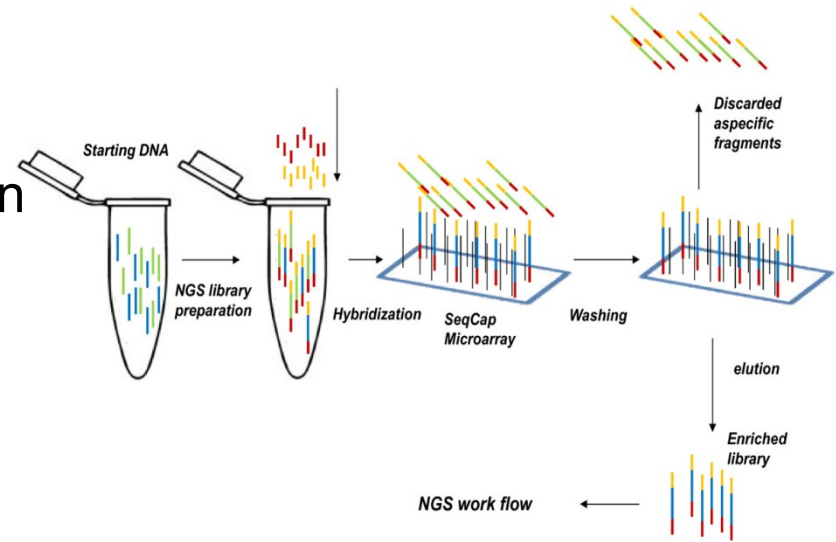
Sekvenační strategie

Enrichment by hybridization + shot gun

Separace úseků genomu které nás zajímají na základě jejich hybridizace

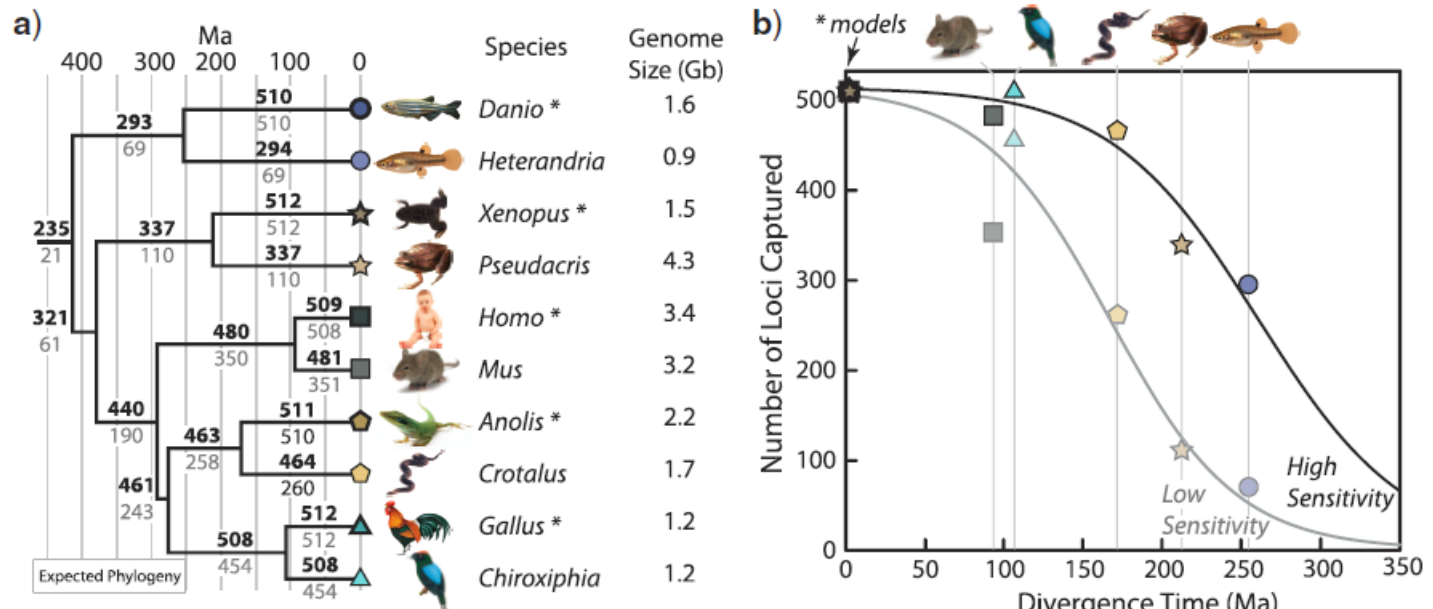
Následná sekvenace obohacených knihoven („enrichment“)

Nové markery (mikrosatelity apod.), kódující oblasti genomu („exom“), „anchored phylogenomics“ apod.



Anchored phylogenomics

- hundreds of conserved loci
- hybridization enrichment
- u velmi příbuzných taxonů bude málo variability





CENTER FOR ANCHORED PHYLOGENOMICS

ACCELERATING THE RESOLUTION OF LIFE™



A comprehensive phylogeny of birds (Aves) using targeted next-generation DNA sequencing

Richard O. Prum^{1,2*}, Jacob S. Berv^{3*}, Alex Dornburg^{1,2,4}, Daniel J. Field^{2,5}, Jeffrey P. Townsend^{1,6}, Emily Moriarty Lemmon⁷ & Alan R. Lemmon⁸



Nature Paper Resolves Bird Tree of Life

October 2015

Posted on [October 6, 2015](#) by [ameer](#)

198 species

259 nuclear loci (ca 1500 bp each)

> 390 000 bp

Sekvenační strategie

Sekvenování podél restričních míst (Enriched libraries by restriction enzymes)

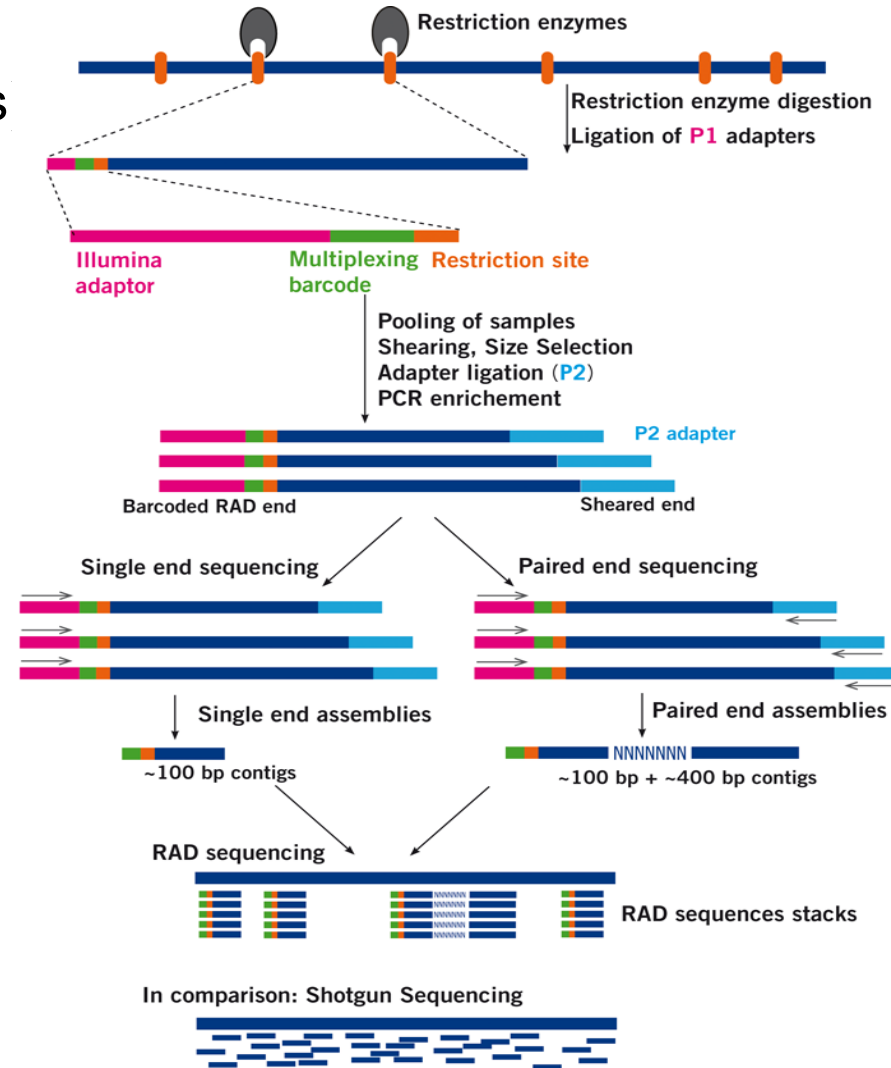
Fragmetace gelogenomové DNA po mocí restričních enzymů

Ligace sekvenačních adaptorů na výsledné fragmenty

Následná sekvenace podél restričních míst

Celogenomové scany genetické variability

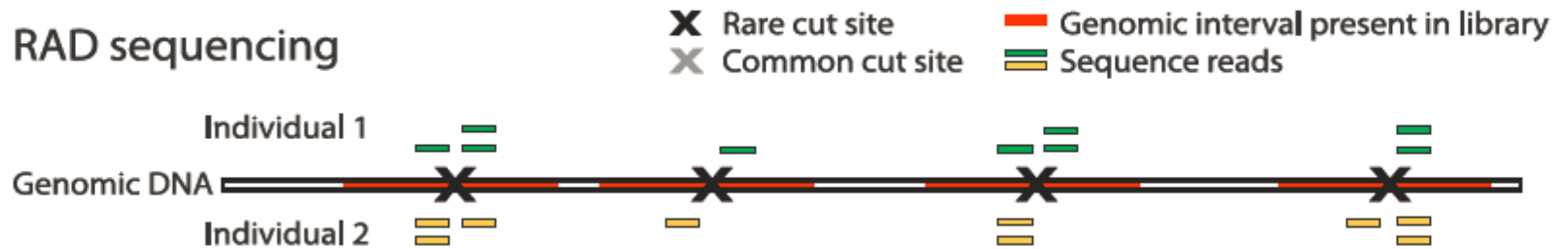
Hledání SNPs, populační genomika (např. RAD-SEQ) apod.



RAD vs. ddRAD

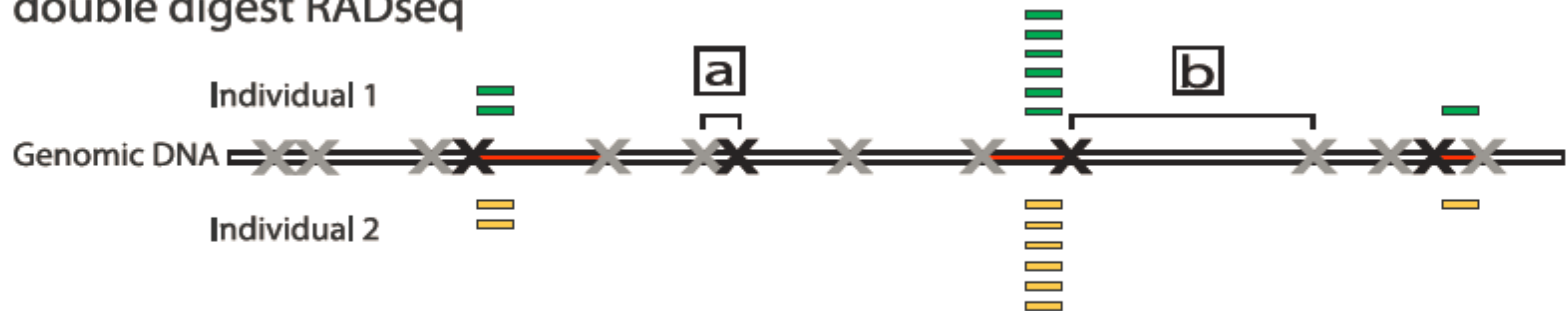
A

RAD sequencing

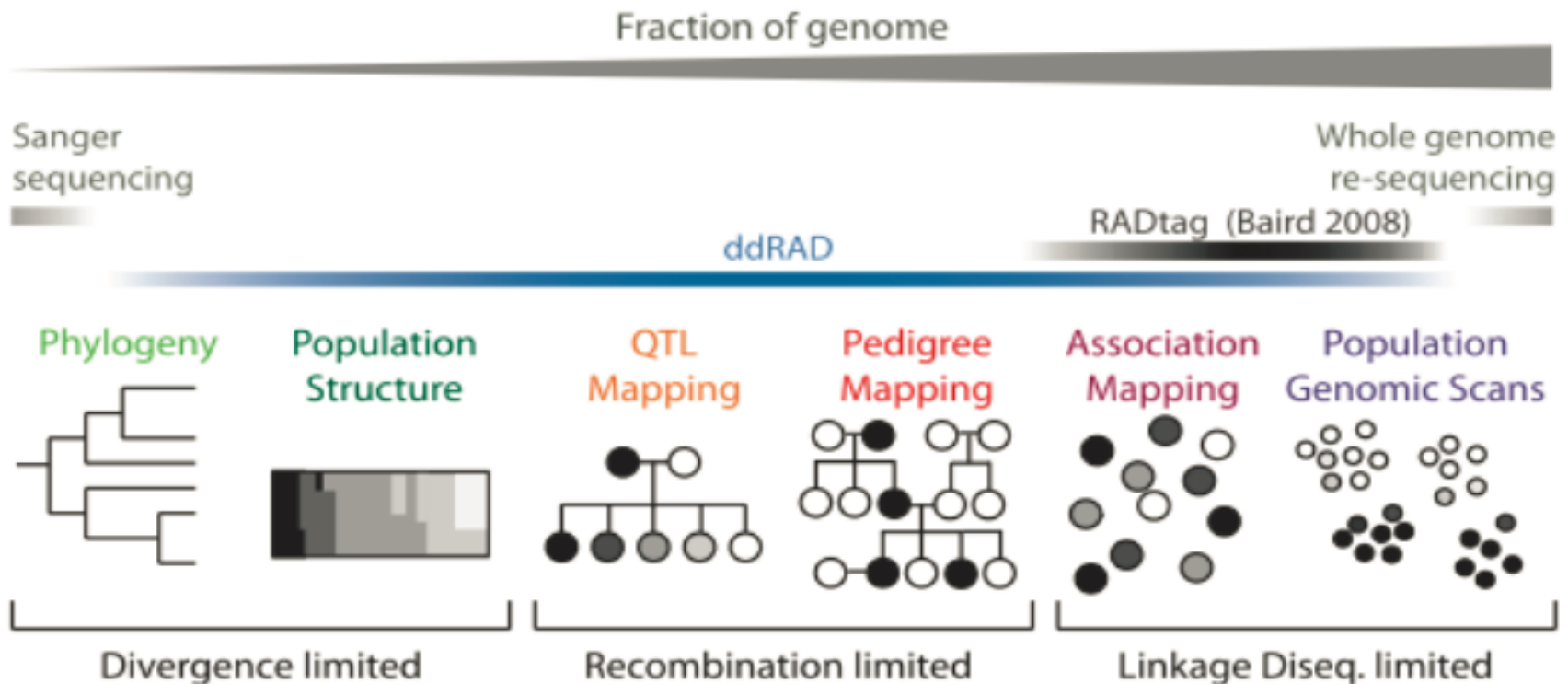


B

double digest RADseq



Sekvenování podél restričních míst



ddRAD library

o tuto sekvenci nám jde!

DATA ANALYSIS

Complete adapter+insert(EcoRI and MspI) = SEQUENCING LIBRARY :

5' -AATGATACGGCGACCACCAGATCTACACACCGACAACACTCTTTCCCTACACGACGCTCTTCCGATC-CATCCAAAT-
 3' -TTACTATGCCGCTGGTGGCTCTAGATGTGTGGCTGTTGTGAGAAAGGGATGTGCTGCGAGAAGGCTAG-GTAGGTTTA-CGAGATCGGAAGAGCACACGTCGTAACCCAGTCACAGGTCAGTATCTCGTATGCCGCTTCTTGCTTG-3'

Illumina adapter

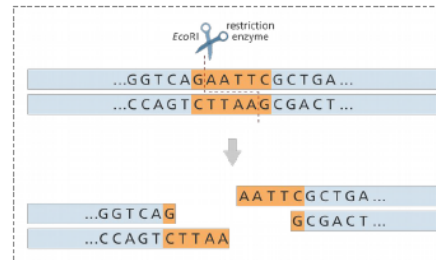
sekvenační primery

Illumina adapter

ACCGACAA P5 Index example
 TCCAGTGA P7 Index example
 CATCCA Inline barcode

(can be preceded by 1-2 bp to increase complexity)

AATT RE overhang
 CG RE overhang
 -----> R1 sequence
 <----- R2 sequence
 -----> I1 sequence
 <----- I2 sequence
 XXXXXX insert - the RE fragment



identifikace vzorku (jedince)

Data analysis in ddRADseq

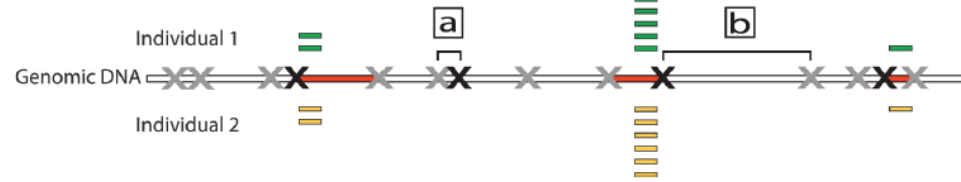
DATA ANALYSIS

B) DEFINE LOCI AND FIND VARIABILITY

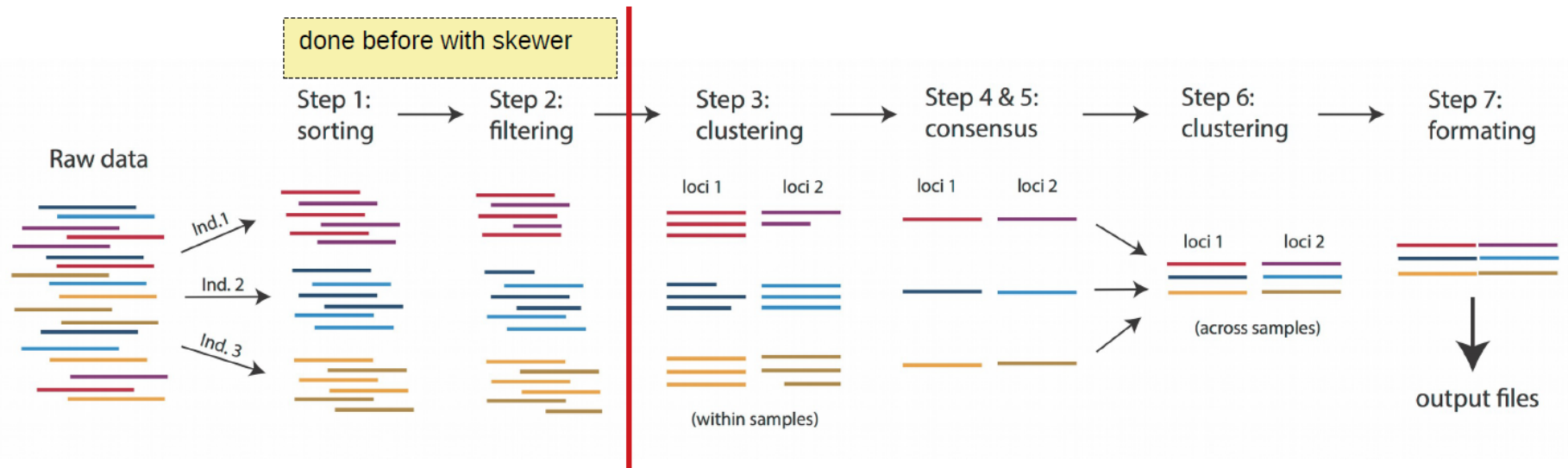
SOFTWARE AVAILABLE:

Stacks, dDocent, **iPyrad**....

double digest RADseq



iPyrad denovo assembly workflow (no reference genome)



program Skewer

program iPyrad

Aplikace

1. Celogenomové sekvenování de novo
2. Celogenomové resekvenování
3. Sekvenování amplikonů (PCR produktů)
4. Další aplikace - např. hledání klasických DNA markerů (mikrosatelity, SNPs)

1. Celogenomové sekvenování de novo

Problém: **KRÁTKÝ READ LENGTH**

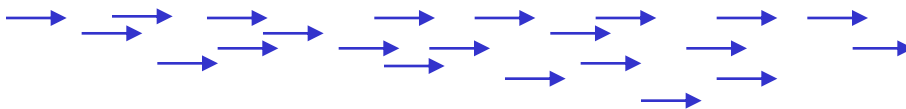
- **400bp** 454 FLX Roche (dnes i Illumina), **35-75bp** Solid vs **800-1000bp** Sanger
- nové technologie (PacBio, Nannopore) už s tím takový problém nemají



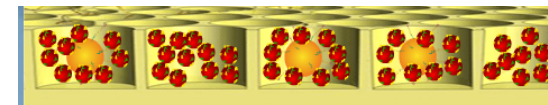
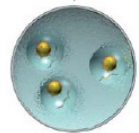
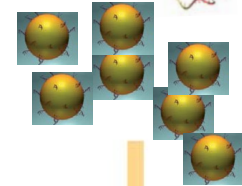
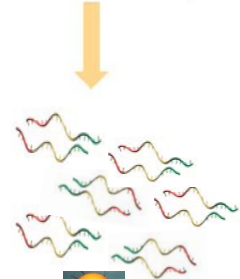
→ Uspořádání (assembly) ještě stále může být problém z hlediska výpočetní kapacity

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

GTAAAAAAAAAAAAAAAAAAAAAAC



Zvláště komplexní eukaryotické genomy - úseky souvislých oblastí přerušovaných 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 Sangerů)
- viry, prokaryota, malá eukaryota, mitochondrie/plastidy/plasmidy

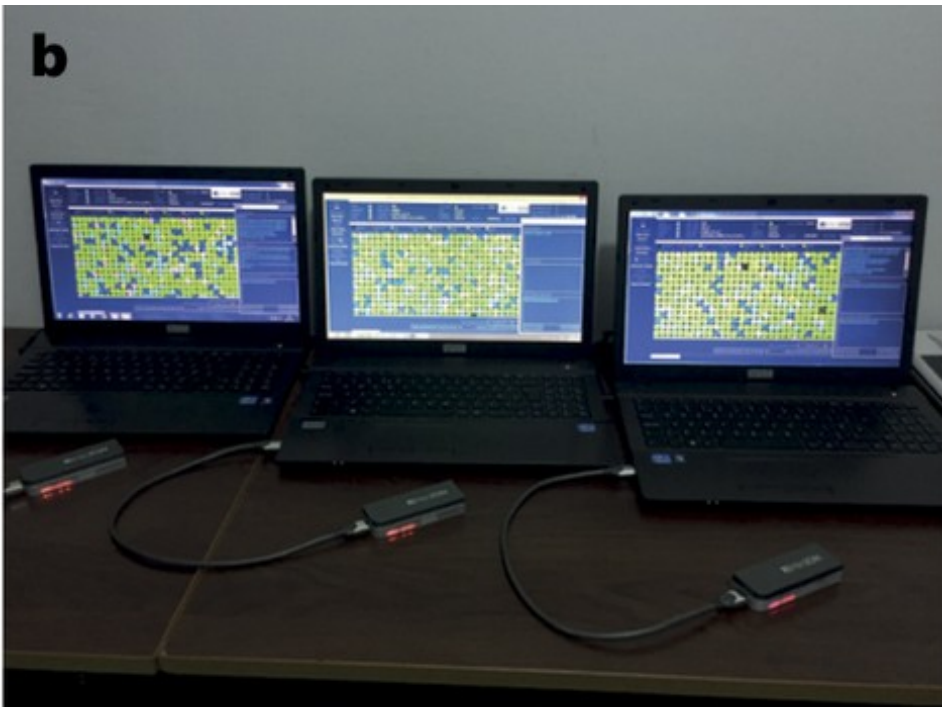
Genetic Detection of a New Hemorrhagic Fever Virus in Southern Africa

Thomas Briese^{1,3*}, Jan Gustavo Palacios¹, Maureen T. Smith¹, Stuart T. Nichol³, W. Ian Lipman⁴, and Robert S. Baruch^{1,2}

Abstract

Lujo virus (LUJV), a new Old World discovered in nosocomial transmission, was first identified in serum and tissue extracts from serum and tissue extracts within 72 hours of sampling. LUJV is a novel, genetically distinct, highly pathogenic arenavirus.

b



The image shows three laptops on a desk, each displaying a different view of genomic data analysis software. The screens show various plots, including what appears to be a sequence alignment or assembly graph. The laptops are connected to external devices, possibly sequencing instruments or storage units.

2009

2015

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

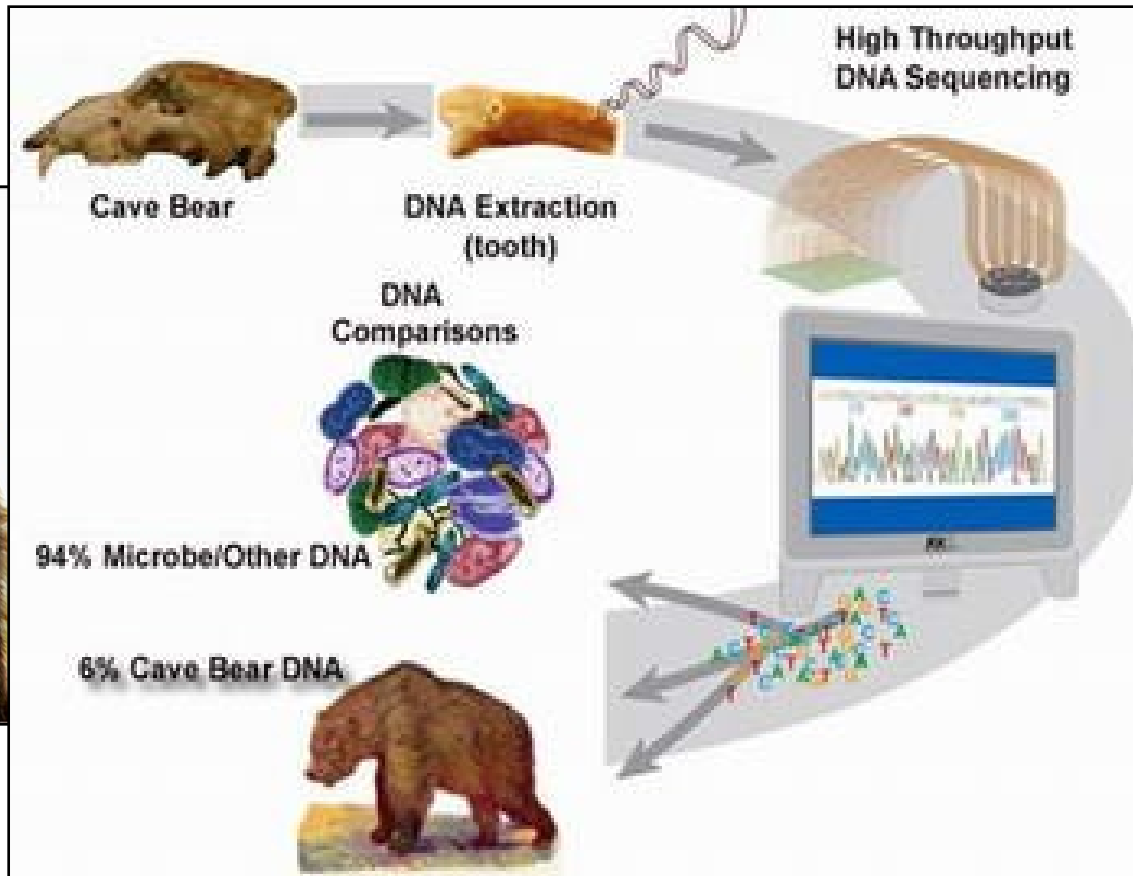
Cell

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 Märten Wikström,⁹ Liisa Laakkonen,¹⁰ Janet Kelso,¹ Montgomery Slatkin,² and Svante Pääbo¹

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

3. Sekvenování amplikonů (PCR produktů)

SMĚSNÉ VZORKY - paralelní sekvenování nahrazuje klonování

Metagenomika (= hlavně prokaryota)

- Celé společenstvo půdních, vodních mikroorganismů, střevní mikroflóra - **mikrobiom**
- PCR genu 16S rRNA
- lze i kvantifikovat

Metabarcoding (= hlavně eukaryota, ale dnes používáno jako obecný termín)

- COI gen, příp. jiný barcodingový marker
- složení potravy, monitoring společenstev

Metabarcoding: Taxonomické složení společenstva v environmentální DNA na základě taxonomicky informativního úseku DNA (cyt b, COI, ITS, rRNA...)

Princip

- Směsný vzorek environmentální DNA
- Amplifikace pomocí primerů specifických pro cílovou skupinu, pokrývající taxonomicky informativní úsek (COI, 16s/18s RNA...)
- Paralelní sekvenování
- Filtrování nekvalitních sekvencí
- Klastrování na základě sekvenční podobnosti do OTUs („operational taxonomic units“)
- Jejich taxonomické zařazení na základě referenčních databází

Využití: Analýza druhového vzorků kde lze makroskopicky jednotlivé druhy obtížně odlišit

- Potravní analýza z trusu
- Vzorky půdy
- Mikrobiální společenstva
- Permafrost
- Exotická/špatně probádaná společenstva
- Druhově bohatá společenstva („insect traps“ v tropech)
- Rutinní analýza velkého množství vzorků

Metabarcoding

Taxonomické složení společenstva na základě taxonomicky informativního úseku DNA

Alternativy:

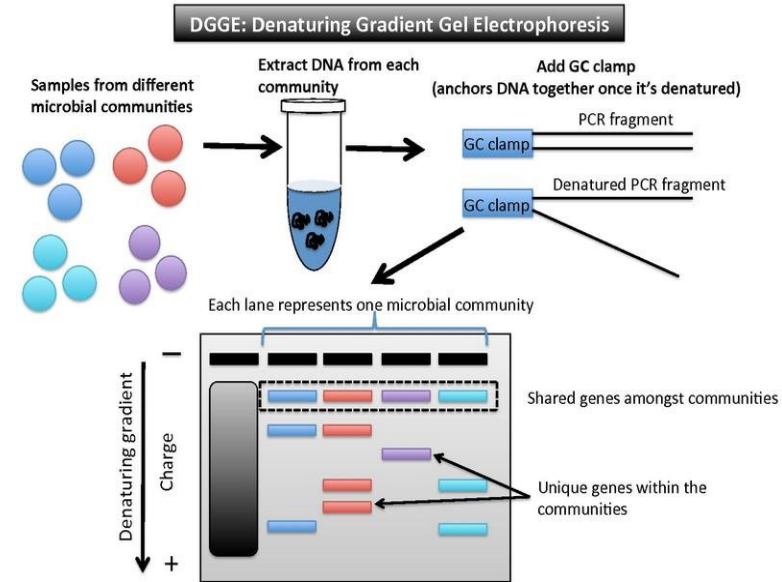
Klonování amplikonů a sekvenování klonů
Specifické elektroforézy - např. DGGE

Výhody paralelního sekvenování

- Cenově i časově míň nákladné
- Lépe se zachytí vzácné taxony (zlomky promile)

Ale:

- Riziko umělého navýšení diversity díky chybám při procesování dat
- Do jaké míry jsou referenční databáze dostatečné ke klasifikaci vzorků?
- Lze použít tato data kvantitativně a nebo vypovídají jen o přítomnosti/nepřítomnosti?



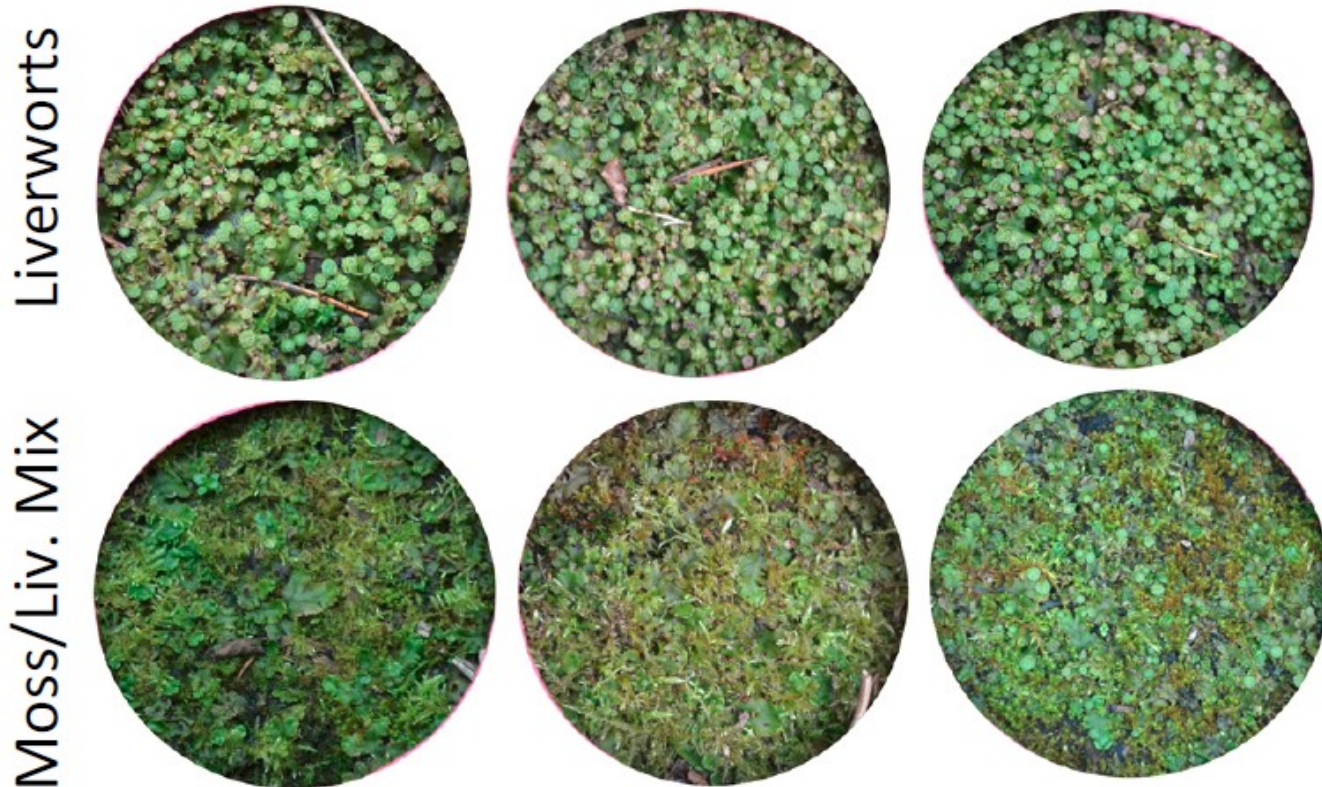
Metabarcoding - příklady využití

- Liverwort only vs. Mixed moss/liverwort (50:50)
- Collected at fixed distance from each other
- 3 replicates each



Společenstvo eukaryot ve vrchní vrstvě půdy

Metabarcoding - příklady využití



Společenstvo eukaryot ve vrchní vrstvě půdy

Metabarcoding - příklady využití

**low diversity
PCR products**

RTA 1.17.28



**high quality
data**

Eukaryotic nSSU barcoding

6 samples

3 replicates each of two ecosystems

1200 clusters/mm²

2% phiX174 spike-in

17 million raw pass filter pairs

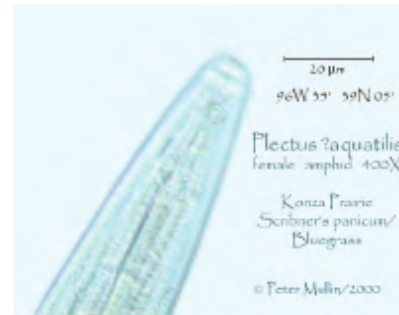
Metabarcoding - příklady využití

Phylum	98% MOTU	proportion of total reads
Nematoda	2862	.3275761886787317
Dikarya	6965	.1894664458485315
Cercozoa	4254	.085598403024025
Annelida	682	.0688691096605889
null	4867	.0579833558234776
Streptophyta	614	.0579039901203119
Oomycetes	487	.0569565860018453
Bacillariophyta	666	.0250973907279004
Arthropoda	286	.0218196255280743
Fungi incertae sedis	417	.0195828162900598
Tardigrada	158	.0169930788889338
Chytridiomycota	473	.0138886146448126
Ciliophora	544	.009428990604366
Chlorophyta	473	.0080418161403385
Synurophyceae	34	.005969106037372
Centramoebida	288	.0053245951821951
Platyhelminthes	94	.0051997954895359
Chrysophyceae	198	.005026302829234
Nucleariidae	61	.0048583696022456
Tubulinea	194	.0025431531840504
Blastocladiomycota	76	.00210858862609
Apicomplexa	74	.0016743479503615
Flabellinea	53	.0013524759319671
Dinophyceae	139	.000952196733392
Bicosoecia	46	.0007160166698649
Uncultured_banisveld_eukaryote	17	.0005992685702805
Micronuclearia_podoventralis	20	.0005377313946375
Codonosigidae	30	.0005166438889655
Ichthyophonida	28	.0004928725189351
Px_clade	60	.0004213667042472
Fungal_endophyte_sp_sx01	4	.0003439180470516
Heterophryidae	27	.0002599514335574
Hypochytridiomycetes	9	.0002386722232883
Salpingoecidae	13	.000235604949736
Fungal_sp_gmg_c6	37	.0002262114244821
Eustigmatophyceae	14	.0001882539142724
Capsaspora	10	.0001878705050784
Stramenopile_sp_mast-12_kkts_d3	15	.000173684364899
Raphidophyceae	31	.0001799408169568
Schizopyrenida	16	.0001793457031658
Environirenal_samples	8	.00016573196745086
Trinastix_pyriformis_atcc50562	5	.0001548375140474
Labyrinthella	16	.0001521436503891
Gastrotricha	1	.0001415996975531
Telonema	26	.0001291107737918
Pollicaria	26	.0001268072826276
Ascomoradidae	3	.000125997814932
SoL_amoeba_and16	11	.00012478493141
Acanthocystidae	4	.00012297142125379
Voronomas	4	.00012291390987468
Leukarctonion_sp_atcc_pra-24	1	.0001206455234986
Rodifera	10	.000120231962562993
Ancyromonadidae	3	.0001090101140599
Peronos	3	.00010446009103284
Nyctozoa	3	.0001044492057314
Ecorticaceae	1	.00010038940919404
Glomeromycota	2	.0001003047273553
Eukaryote_marine_clone_mel-24	1	.00010023004551642
Fungal_sp_fca90	1	.00010021087505672
Cryptomonadales	1	.00010011502275821
Phaeobryozoa	2	.00010011502275821
Phaeocharnophyceae	1	.00010009585229851
Chordata	1	.0001000380409194
Unclassified_alveolata	1	.00010000191704597

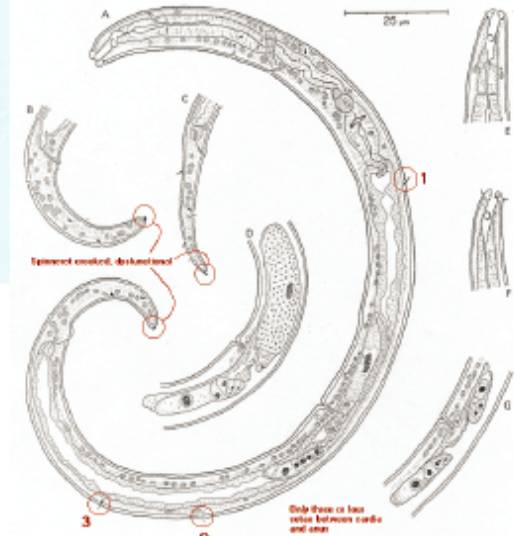
Eight animal phyla represented

Most frequent are **Nematoda**

Most frequent “98% MOTU” is *Plectus* (cf *aquatilis*)



Plectus minimus - a small yet easily identified species



Metabarcoding - příklady využití

Monitoring vzácných, nedávno popsáných druhů savců na základě sekvenování krve pijavic

Výrazně větší úspěšnost prokázání přítomnosti než za použití klasických technik – fotopasti, terénní pozorování apod.

Correspondences

Screening mammal biodiversity using DNA from leeches

Ida Bærholm Schnell^{1,2,†},
Philip Francis Thomsen^{2,†},
Nicholas Wilkinson³,
Morten Rasmussen²,
Lars R.D. Jensen¹, Eske Willerslev²
Mads F. Bertelsen¹,
and M. Thomas P. Gilbert^{2,*}

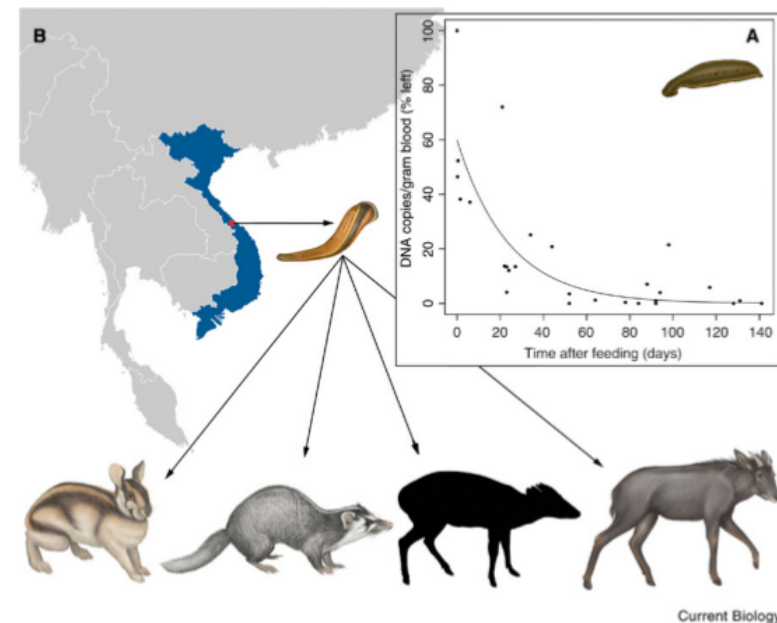
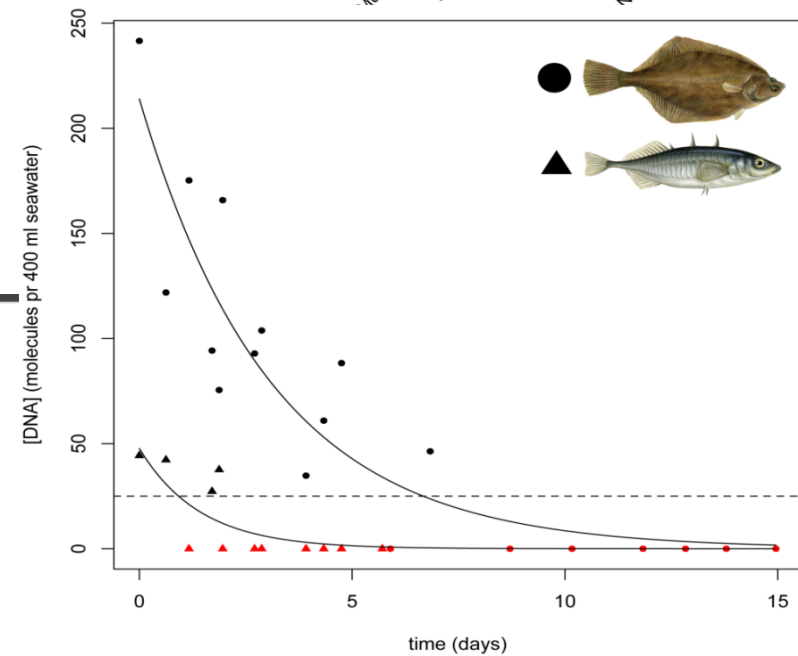
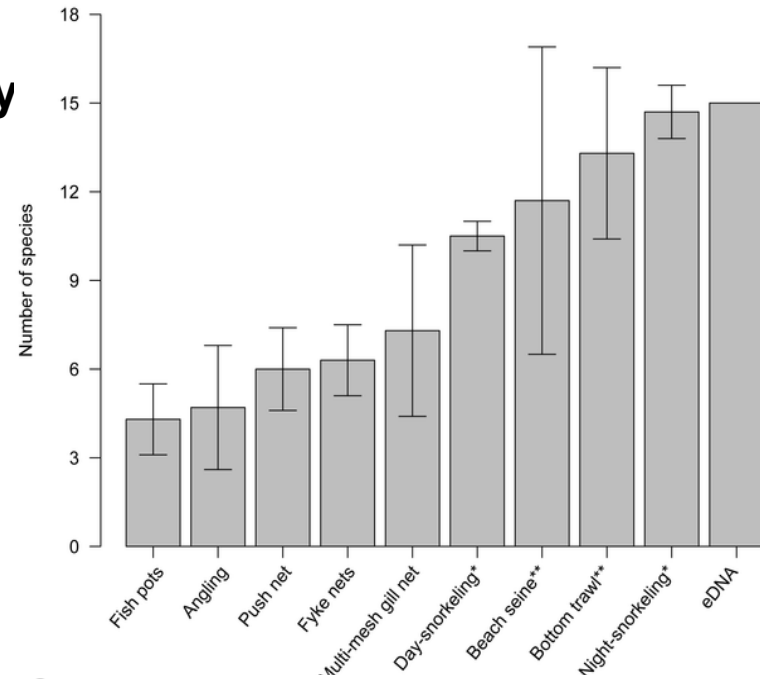
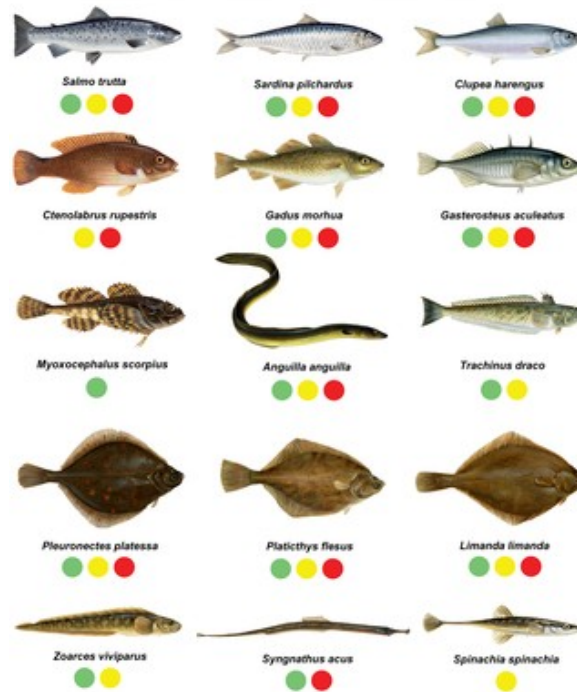


Figure 1. Monitoring mammals with leeches. (A) Survival of mtDNA in goat blood ingested by *Hirudo medicinalis* over time, relative to freshly drawn sample (100%, ca. $2.4E+09$ mtDNA copies/gram blood). Mitochondrial DNA remained detectable in all fed leeches, with a minimum observed level at $1.6E+04$ mtDNA/gram blood ingested. The line shows a simple exponential decay model, $p < 0.001$, $R^2 = 0.43$ (Supplemental information). (B) Vietnamese field site location and examples of mammals identified in *Hae madipsa* spp. leeches. From left to right: Annamite striped rabbit, small-toothed ferret-badger Truong Son muntjac (coat coloration and markings remain unknown), serow. Pictures do not reflect true size proportions. See also Supplemental information.

Metabarcoding - příklady využití

Detekce ryb pomocí izolace eDNA z mořské vody
-taky jedna z nejefektivnějších metod



OPEN ACCESS Freely available online

PLOS ONE

Detection of a Diverse Marine Fish Fauna Using Environmental DNA from Seawater Samples

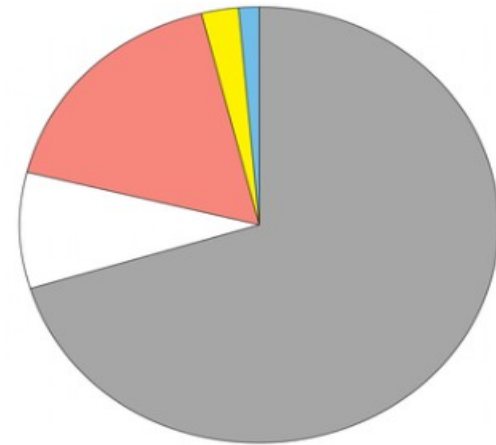
Philip Francis Thomsen^{1*}, Jos Kielgast^{1,3}, Lars Lønsmann Iversen², Peter Rask Møller³, Morten Rasmussen¹, Eske Willerslev^{1*}

¹Centre for GeoGenetics, Natural History Museum of Denmark, University of Copenhagen, Øster Voldgade, Copenhagen, Denmark, ²Freshwater Biology Section, Department of Biology, University of Copenhagen, Helsingørgade, Hillerød, Denmark, ³Vertebrate Department, Natural History Museum of Denmark, University of Copenhagen, Universitetsparken, Copenhagen, Denmark

Metabarcoding - příklady využití

Analýza potravy

Podíl hospodářských zvířat v potravě irbise je minimální



OPEN ACCESS Freely available online

PLoS one

Prey Preference of Snow Leopard (*Panthera uncia*) in South Gobi, Mongolia

Wasim Shehzad¹, Thomas Michael McCarthy², Francois Pompanon¹, Lkhagvajav Purevjav³, Eric Coissac¹, Tiayyba Riaz¹, Pierre Taberlet^{1*}

¹Laboratoire d'Ecologie Alpine, Centre National de la Recherche Scientifique, Unité Mixte de Recherche 5553, Université Joseph Fourier, Grenoble, France, ²Snow Leopard Program, Panthera, New York, New York, United States of America, ³Snow Leopard Conservation Fund, Ulaanbaatar, Mongolia

Siberian ibex
(*Capra sibirica*)

Domestic sheep
(*Ovis aries*)

Argali sheep
(*Ovis ammon*)

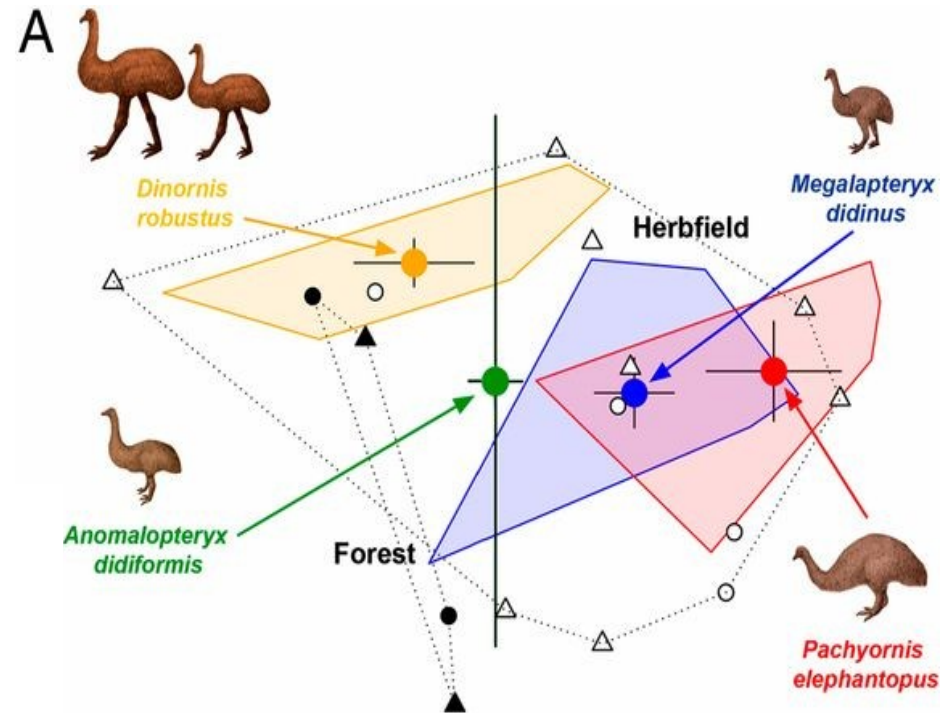
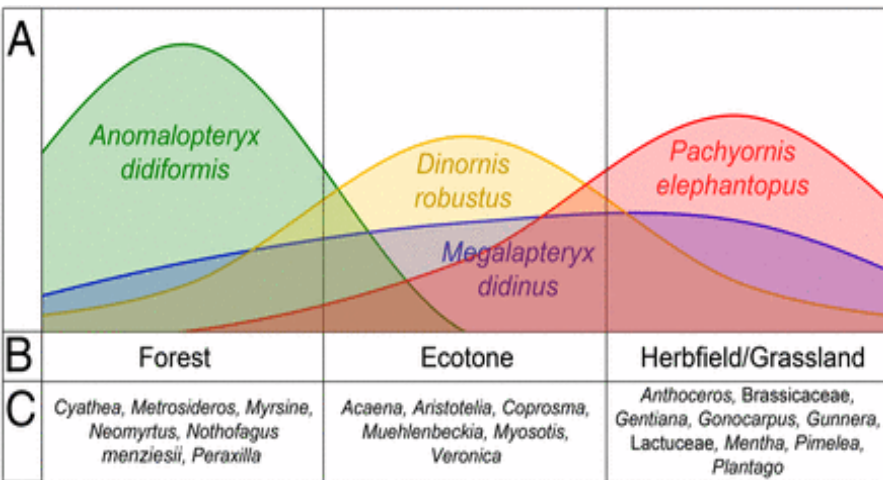
Chukar partridge
(*Alectoris chukar*)

Domestic goat
(*Capra hircus*)

Metabarcoding - příklady využití

Analýza složení společenstva na základě ancient DNA z koprolitů moa (Nový Zéland)

Umožňuje odhadnout typ prostředí které jednotlivé druhy obývaly a separaci ekologických nik



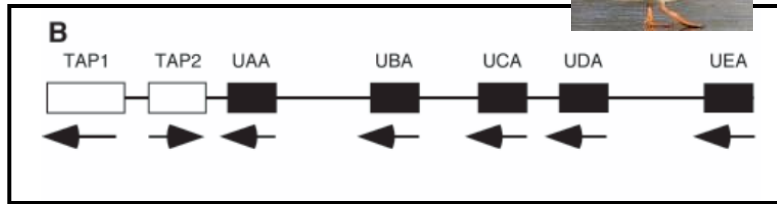
Resolving lost herbivore community structure using coprolites of four sympatric moa species (Aves: Dinornithiformes)

Jamie R. Wood^{a,1}, Janet M. Wilmshurst^a, Sarah J. Richardson^a, Nicolas J. Rawlence^{b,2}, Steven J. Wagstaff^a, Trevor H. Worthy^{a,3}, and Alan Cooper^b

^aLandcare Research, Lincoln, Canterbury 7640, New Zealand; ^bAustralian Centre for Ancient DNA, University of Adelaide, Adelaide, SA 5005, Australia;

3. Sekvenování amplikonů (PCR produktů)

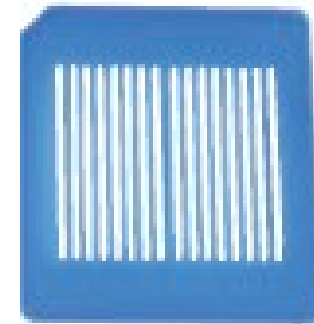
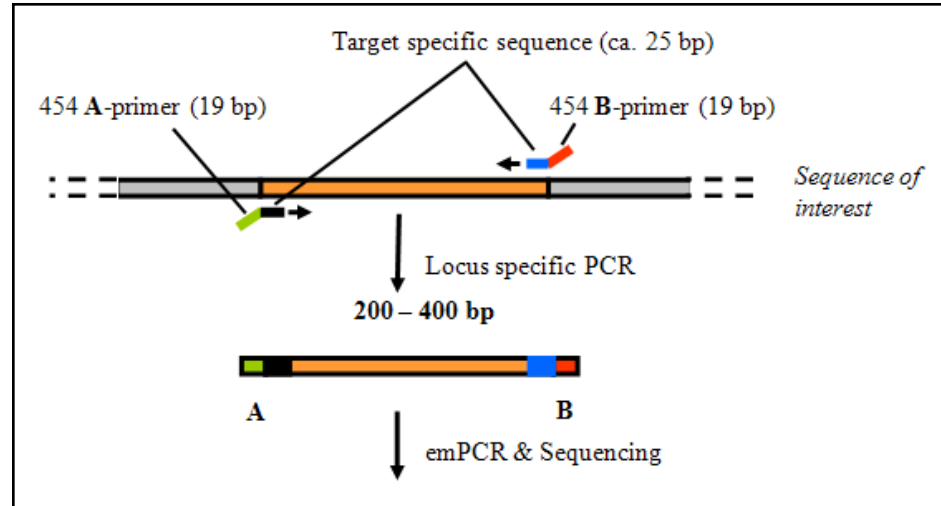
Genové duplikace



Označí jedince

Amplifikuje všechny kopie MHC genů

Potřeba k emPCR, sekvenování..

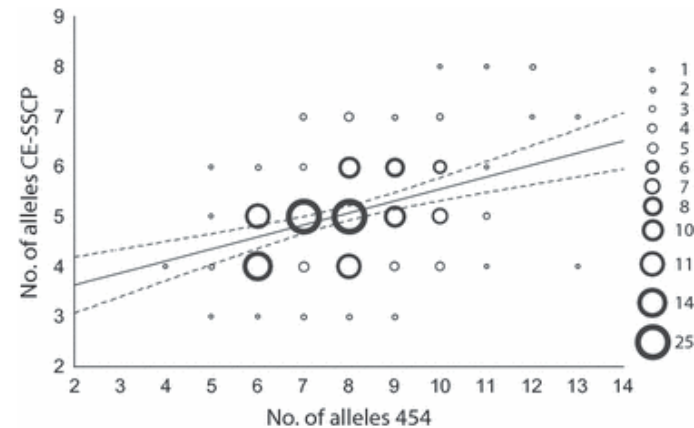
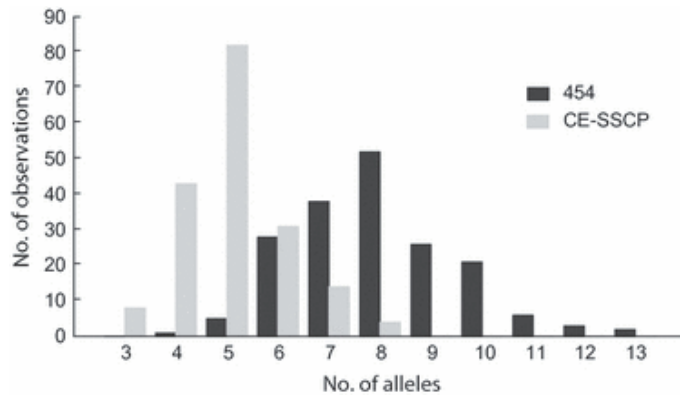


192 jedinců u 454 pyrosekvenování

Amplikonové sekvenování

MHC u hýla rudého

- NGS má větší rozlišovací schopnost než SSCP + klonování



MOLECULAR ECOLOGY RESOURCES

Molecular Ecology Resources (2012) 12, 285–292

doi: 10.1111/j.1755-0998.2011.03082.x

Evaluation of two approaches to genotyping major histocompatibility complex class I in a passerine—CE-SSCP and 454 pyrosequencing

MARTA PROMEROVÁ,* WIESŁAW BABIK,† JOSEF BRYJA,* TOMÁŠ ALBRECHT,*‡ MICHAŁ STUGLIK† and JACEK RADWAŃŚ

4. Další aplikace - hledání nových genetických markerů

Mikrosatelity

- sekvenování obohacených knihoven

SNPs

- kompletní genomické sekvence pro hledání diagnostických SNPs
- např. RAD-sequencing

Hledání nových genetických markerů - mikrosatelity

Obvyklý postup:

- Obohacení genomické knihovny o mikrosatelitové motivy – sequence capture
- Sekvenování obohacených knihoven
- Detekce mikrosatelitů a návržení vhodných primerů

MOLECULAR ECOLOGY RESOURCES

Molecular Ecology Resources (2011) 11, 638–644

doi: 10.1111/j.1755-0998.2011.0295

High-throughput microsatellite isolation through 454 GS-FLX Titanium pyrosequencing of enriched DNA libraries

THIBAUT MALAUSA,* ANDRÉ GILLES,† EMESE MEGLÉCZ,† HÉLÈNE BLANQUART,‡ STÉPHANIE DUTHOY,‡ CAROLINE COSTEDOAT,† VINCENT DUBUT,† NICOLAS PECH,† PHILIPPE CASTAGNONE-SERENO,* CHRISTOPHE DÉLYE,§ NICOLAS FEAU,¶ PASCAL FREY,** PHILIPPE GAUTHIER,†† THOMAS GUILLEMAUD,* LAURENT HAZARD,*‡ VALÉRIE LE CORRE,§ BRIGITTE LUNG-ESCAARMANT,¶ PIERRE-JEAN G. MALÉ,§§ STÉPHANIE FERREIRA‡ and JEAN-FRANÇOIS MARTIN††

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Experts in Microsatellite Development

Microsatellites (also known as short tandem repeats) are repetitive DNA elements usually found in non-coding regions of the genome. They have high mutation rates, and therefore are frequently highly polymorphic. Variations in the number of repetitions generate different alleles. This makes them appropriate molecular markers for population genetics and molecular ecology projects.

We develop microsatellite markers for your study species

At AllGenetics, we use next-generation sequencing to obtain primer pairs which amplify polymorphic microsatellite loci in your study species. Genomic DNA is used to generate genomic libraries. We usually enrich these libraries with 4 to 6 different microsatellite motifs. However, we can customise the number of motifs to your needs. We obtain thousands of microsatellite-containing reads by using high-throughput sequencing. Our bioinformaticians then filter these reads for primer design. The primers obtained are multiplexed and tested for polymorphism in a number of individuals from different populations.

How we work

High quality DNA at a concentration of 100 ng/μL in a minimum volume of 50 μL from a number of individuals is required. Alternatively, we can isolate DNA from your samples. These samples should be adequately preserved to ensure DNA integrity. We will deliver tested primer pairs which amplify polymorphic loci for your study species. A detailed methodological report and all sequencing reads generated will also be provided.

Our microsatellite development projects are divided into four steps. For your convenience, we can carry out the entire project or only the parts you need.

OPEN ACCESS Freely available online

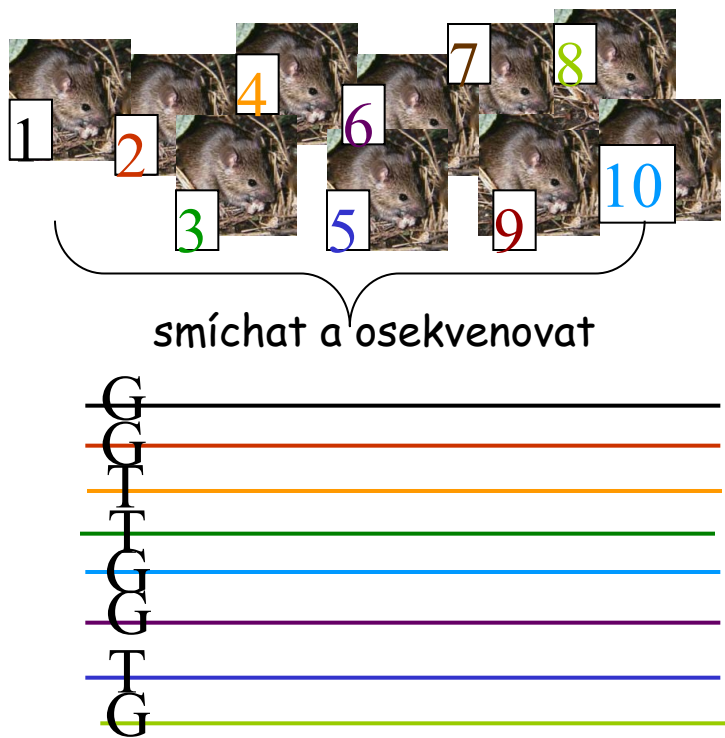
PLOS ONE

32 species validation of a new Illumina paired-end approach for the development of microsatellites

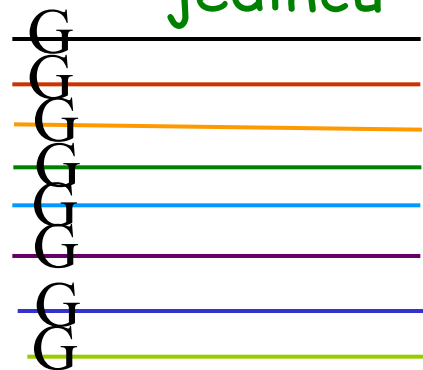
Stacey L. Lance^{1*}, Cara N. Love¹, Schyler O. Nunziata¹, Jason R. O'Bryhim¹, David E. Scott¹, R. Wesley Flynn¹, Kenneth L. Jones²

¹ Savannah River Ecology Laboratory, University of Georgia, Aiken, South Carolina, United States of America, ² Department of Biochemistry and Molecular Genetics, University of Colorado, Fort Collins, Aurora, Colorado, United States of America

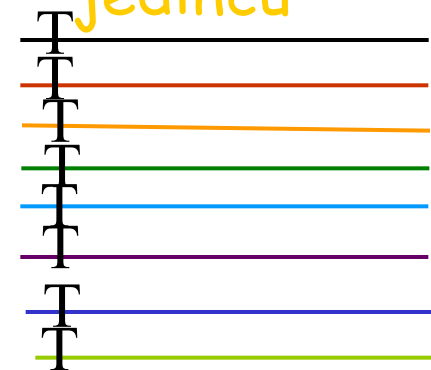
Hledání diagnostických SNP (např. pro studium hybridizace)



10 jedinců



10 jedinců



Hledání nových SNPs - RAD-sequencing

Sekvenování podél restričních míst

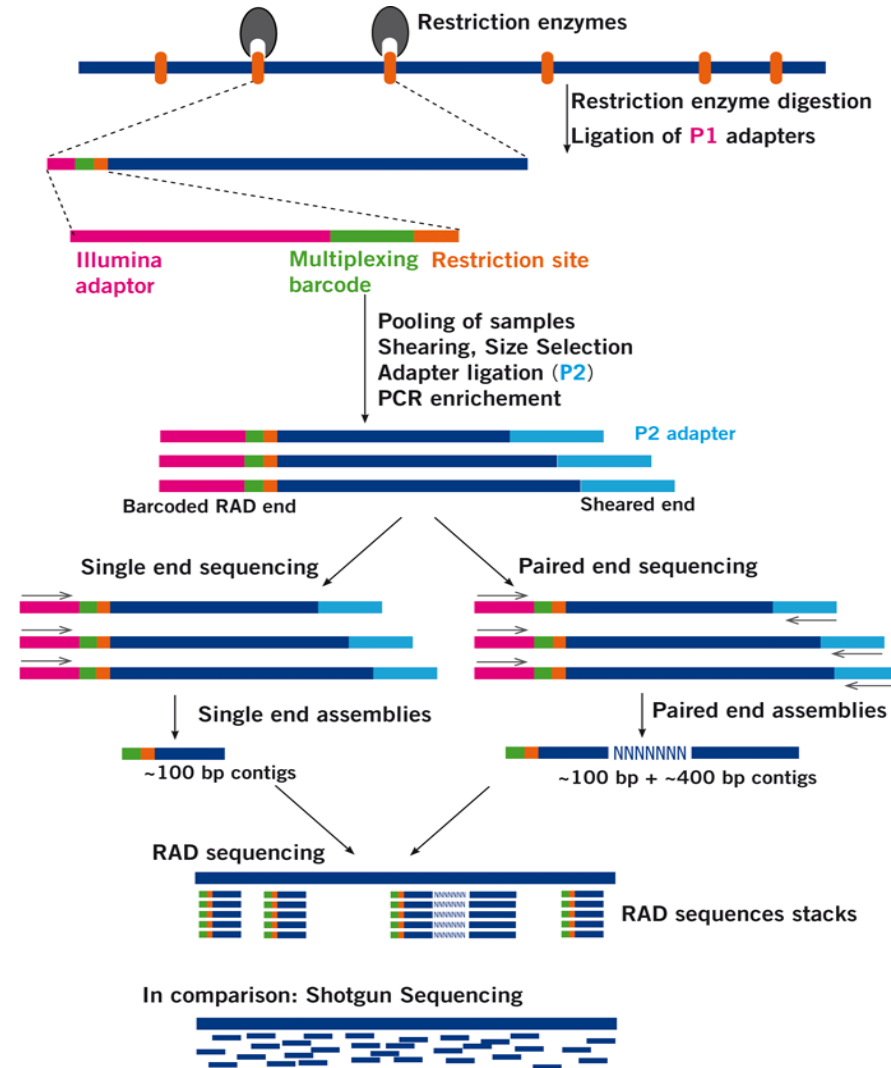
Fragmetace gelogenomové DNA po mocí restričních enzymů

Ligace sekvenačních adaptorů na výsledné fragmenty

Následná sekvenace podél restričních míst

Celogenomové scany genetické variability

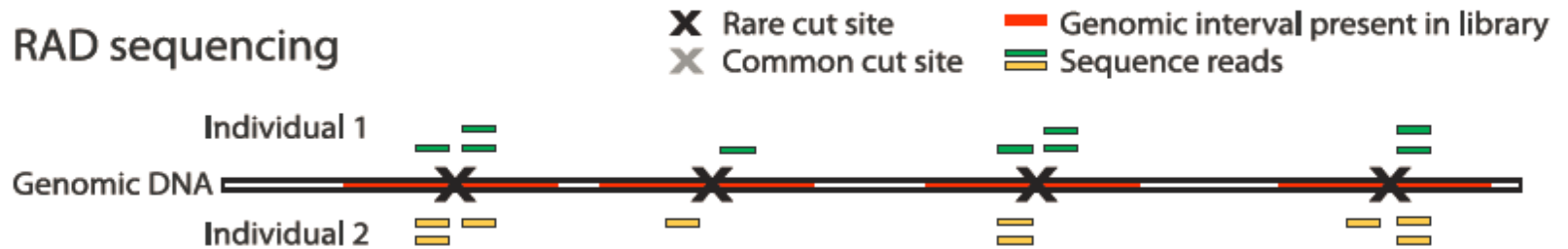
Hledání SNPs, populační genomika (např. RAD-SEQ) apod.



RAD vs. ddRAD

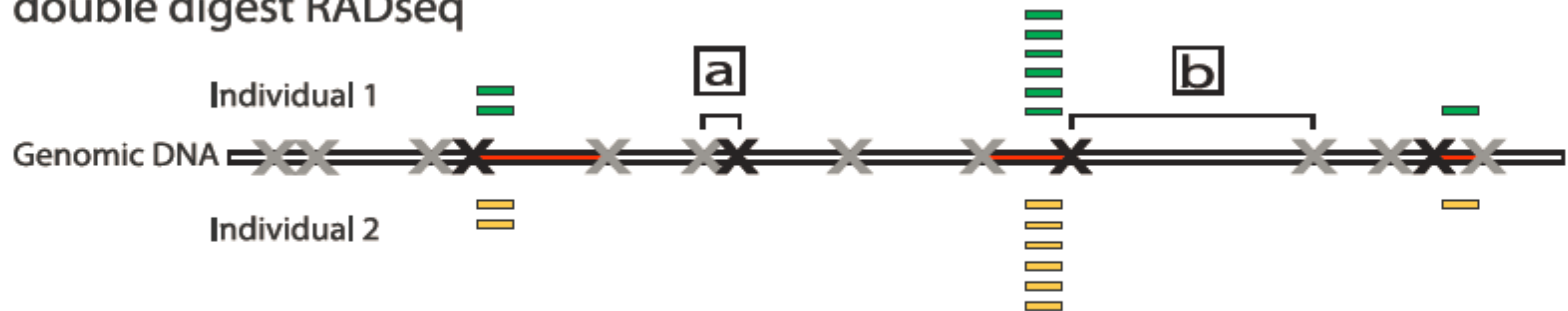
A

RAD sequencing

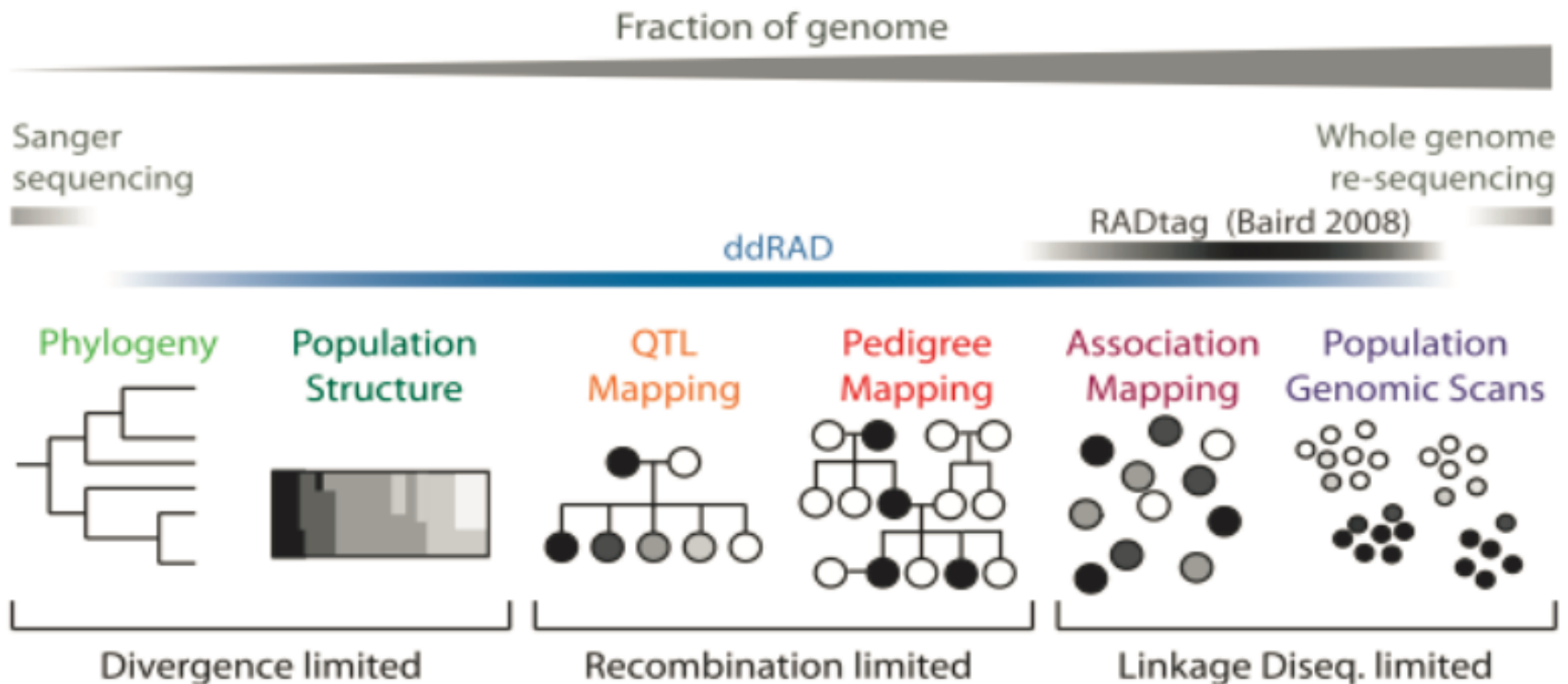


B

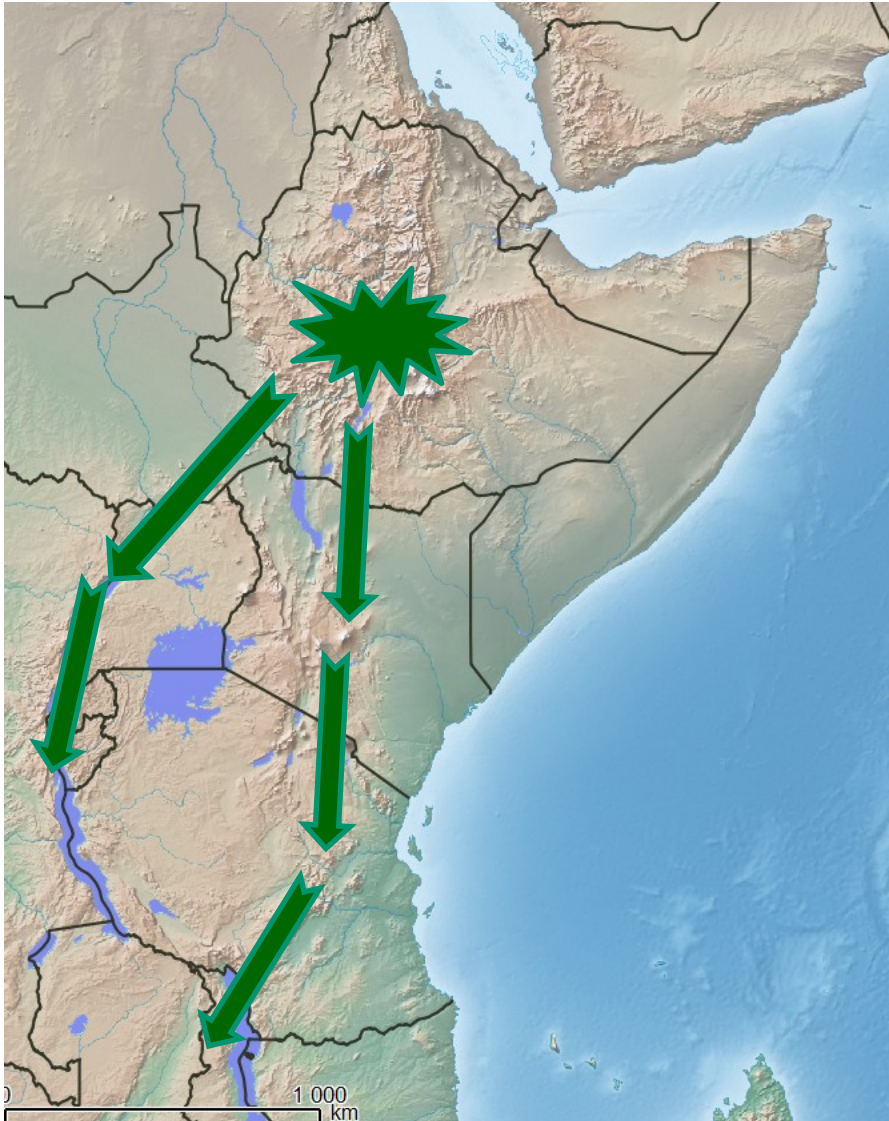
double digest RADseq



Sekvenování podél restričních míst



Phylogenomics of *Lophuromys*



- ancestral lineage „trapped“ in Ethiopian highlands, where diversified and sourced the colonization of other mountains (mostly in Pleistocene)
- *Lophuromys flavopunctatus* complex (9 Ethiopian species)



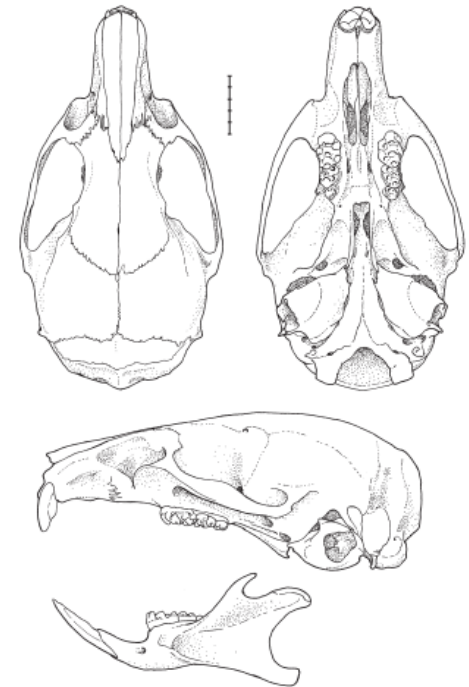
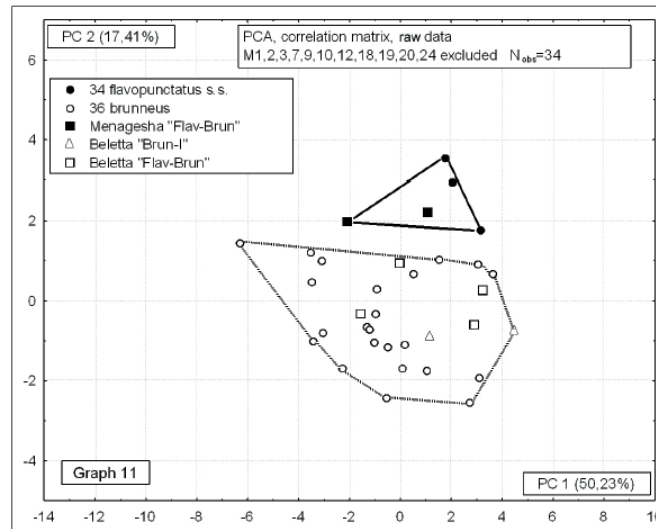
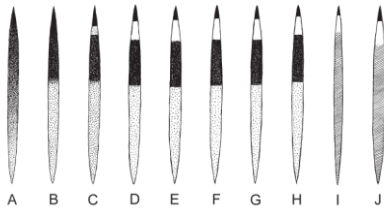
9 endemic species in Ethiopia

BULLETIN DE L'INSTITUT ROYAL DES SCIENCES NATURELLES DE BELGIQUE
BULLETIN VAN HET KONINKLIJK BELGISCH INSTITUUT VOOR NATUURWETENSCHAPPEN

BIOLOGIE, 77: 77-117, 2007
BIOLOGIE, 77: 77-117, 2007

Morphometric and genetic study of Ethiopian *Lophuromys flavopunctatus* THOMAS, 1888 species complex with description of three new 70-chromosomal species (Muridae, Rodentia)

by Leonid A. LAVRENTCHENKO, Walter N. VERHEYEN, Erik VERHEYEN, Jan HULSELMANS & Herwig LEIRS



3.2. Views of skull and mandible of *Lophuromys menageshae* n.sp. (ZMMU S-165969, holotype). Scale bar = 5 mm.

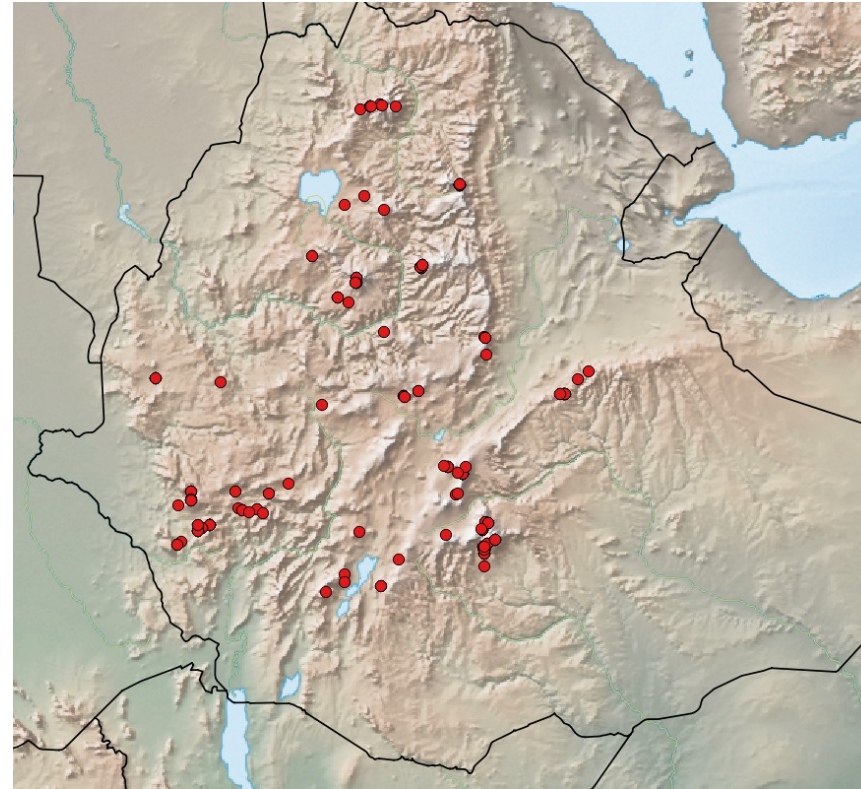
Lophuromys - questions

- Are there really 9 well delimited species?
- Are they easily (genetically) recognizable? (e.g. mtDNA-barcoding)
- What is their distribution and ecological requirements? -> IUCN assessment, etc.



Material and Methods

- cca 500 specimens from all major mountain ranges
- mtDNA marker (CYTB)
- 4 nuclear markers (2 introny + 2 exony)
- **genomic approach - ddRAD sequencing**



Retaining well-covered & informative loci

All loci

No. of individuals:	213
No. of loci:	80570
No. of informative loci:	69724
No. of SNPs / PISs per informative locus:	
Min:	1 / 1
25%:	5 / 4
50%:	10 / 9
75%:	20 / 17
Max:	60 / 57
Loci per individual:	
Min:	5178
25%:	9719
50%:	12000
75%:	14607
Max:	23205
Individuals per locus:	
Min:	4
25%:	6
50%:	13
75%:	37
Max:	208
Proportion of missing data:	0.85

HQ loci

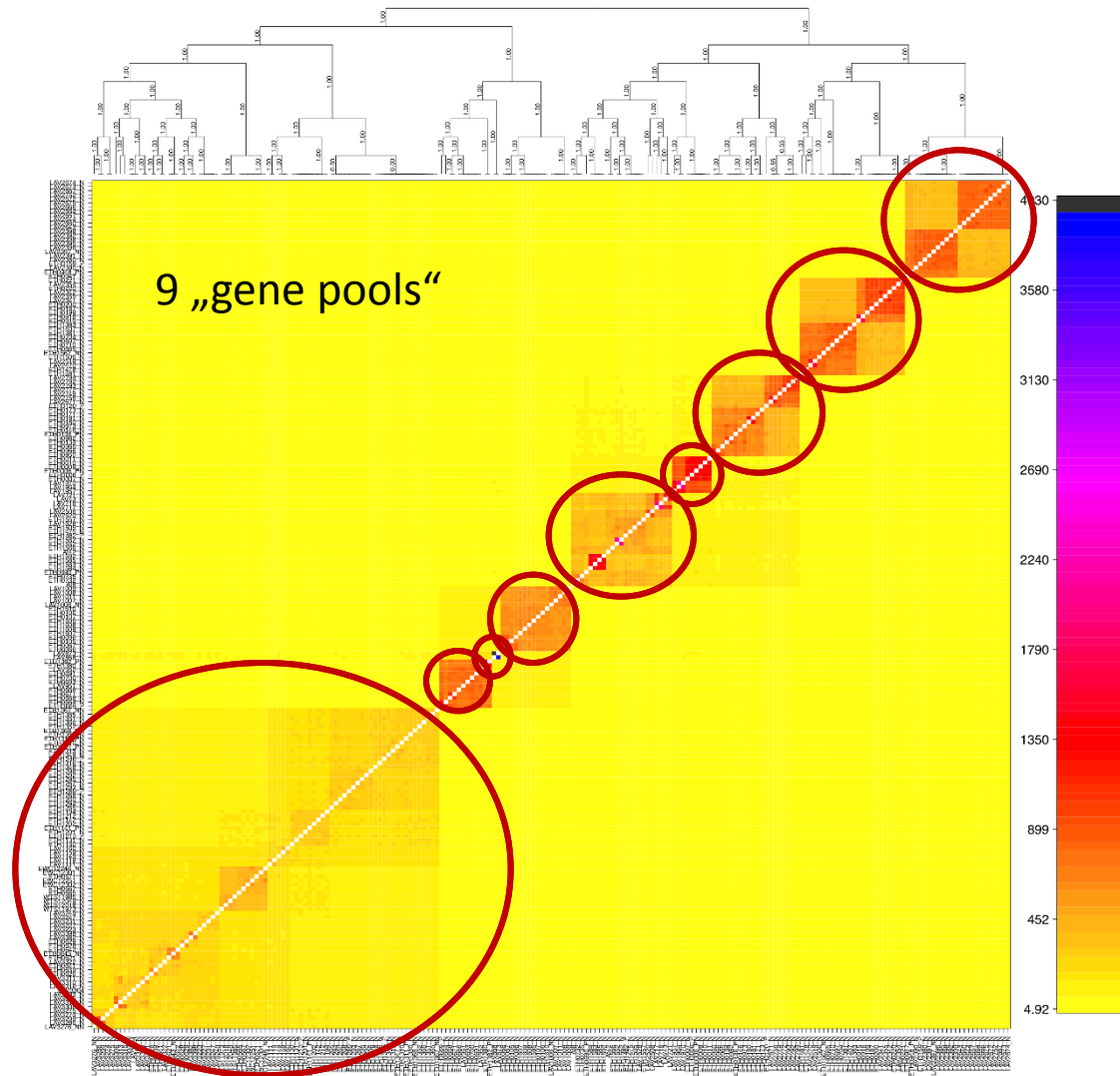
No. of individuals:	213
No. of loci:	15164
No. of informative loci:	15164
No. of SNPs / PISs per informative locus:	
Min:	1 / 1
25%:	17 / 14
50%:	25 / 21
75%:	32 / 28
Max:	57 / 54
Loci per individual:	
Min:	3393
25%:	6912
50%:	8074
75%:	9297
Max:	11912
Individuals per locus:	
Min:	54
25%:	74
50%:	103 ✓
75%:	149
Max:	208
Proportion of missing data:	0.47 ✓

80 570 loci → filtering → 15 164 loci

ddRADseq: co-ancestry matrix

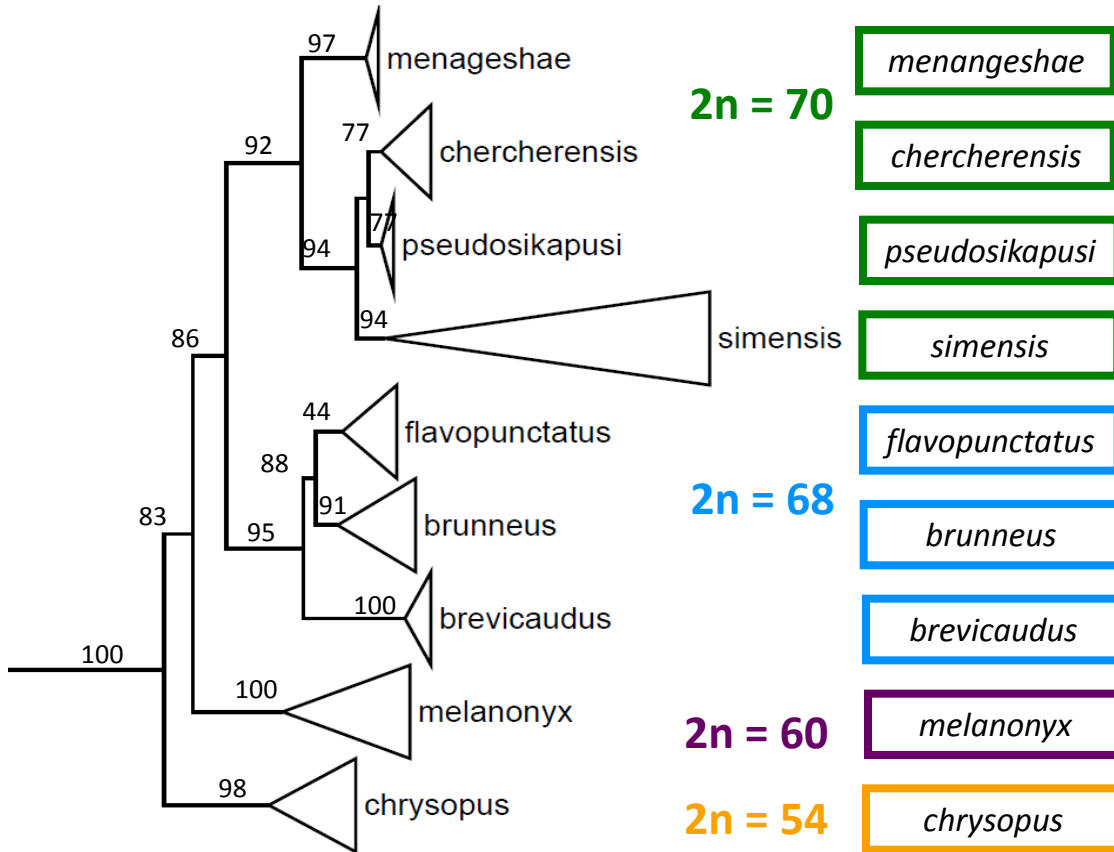
209
individuals

15 623
informative
loci



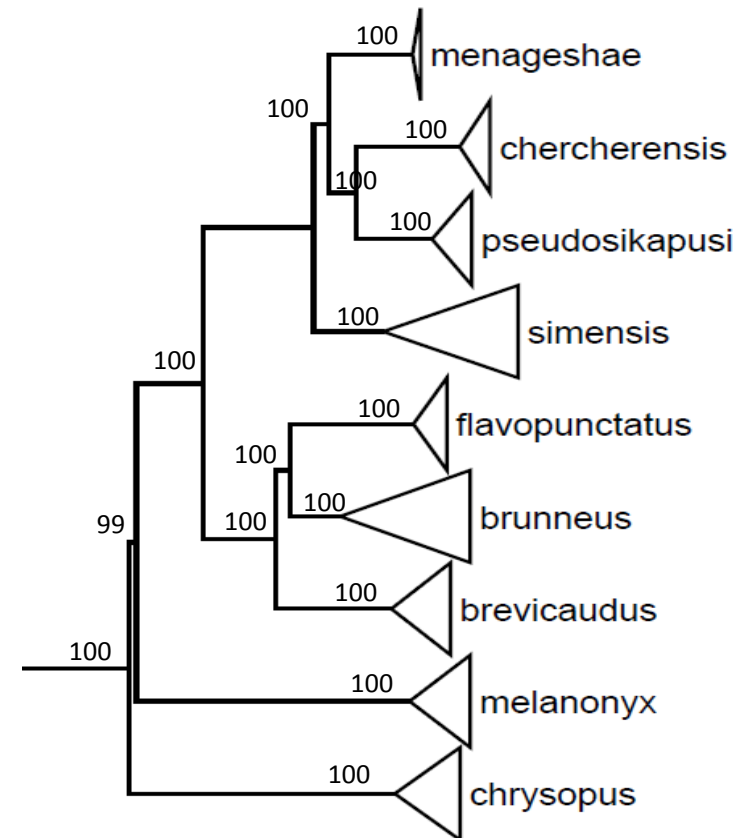
Maximum likelihood analysis of concatenated nuclear dataset

Sanger sequencing



4 nuclear markers (V. Komarova et al.)
(2 604 bp concatenated dataset)

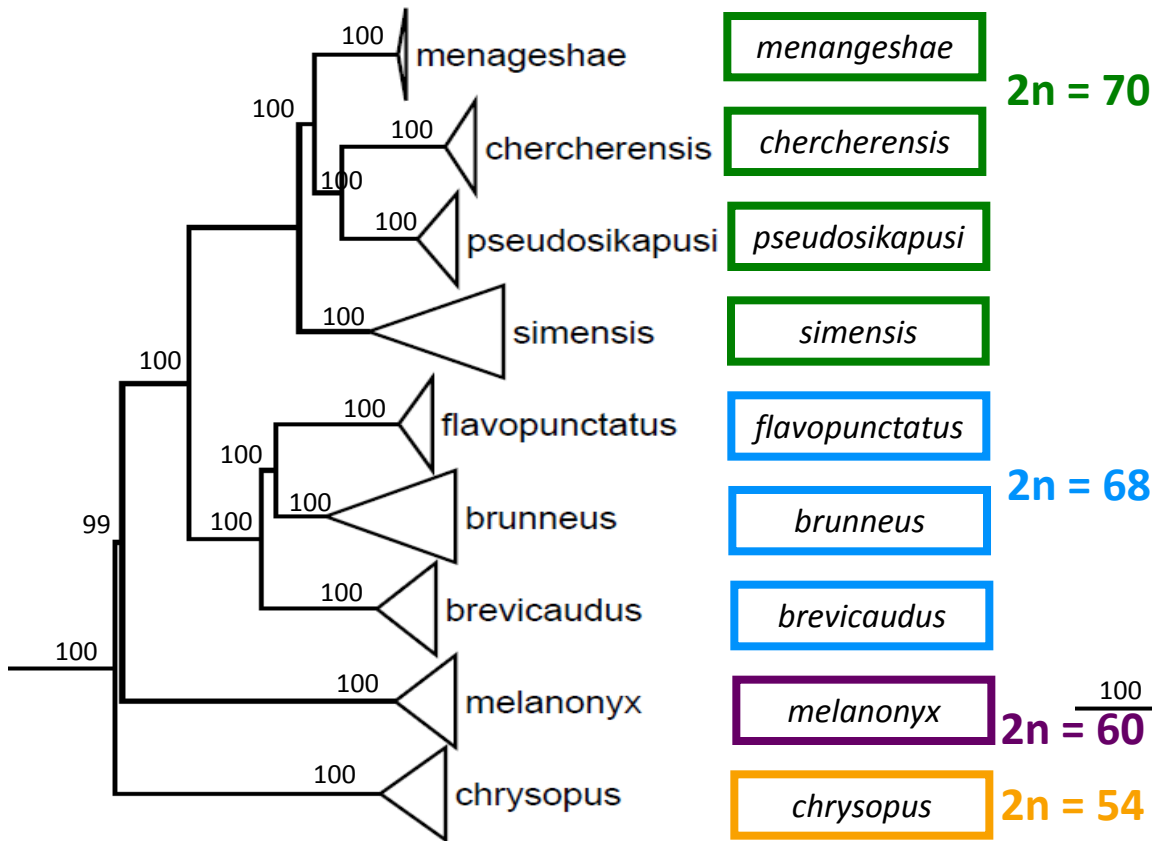
ddRADseq



15 623 informative loci

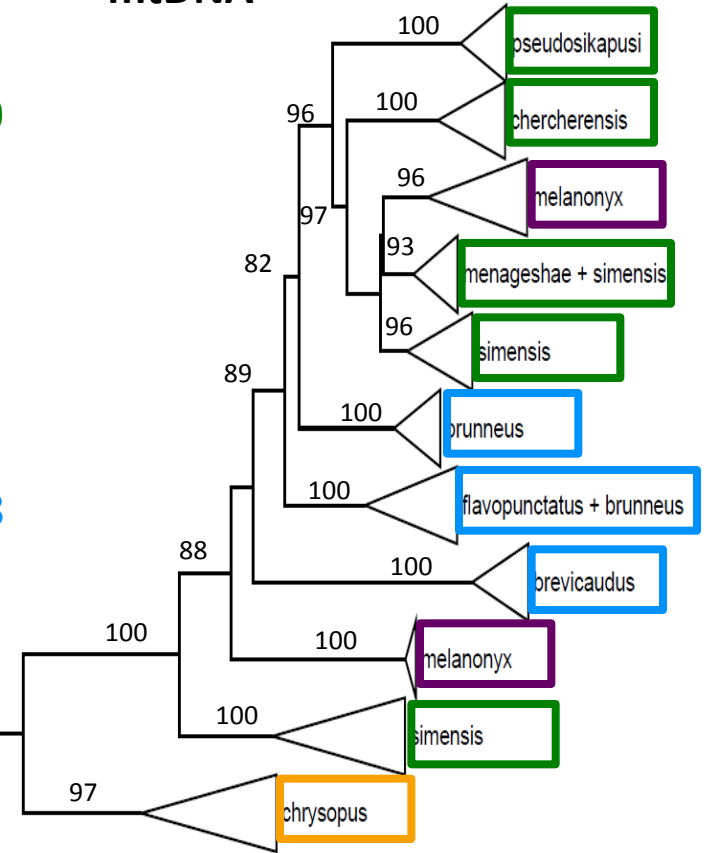
And what about mtDNA?

ddRADseq



15 623 informative loci

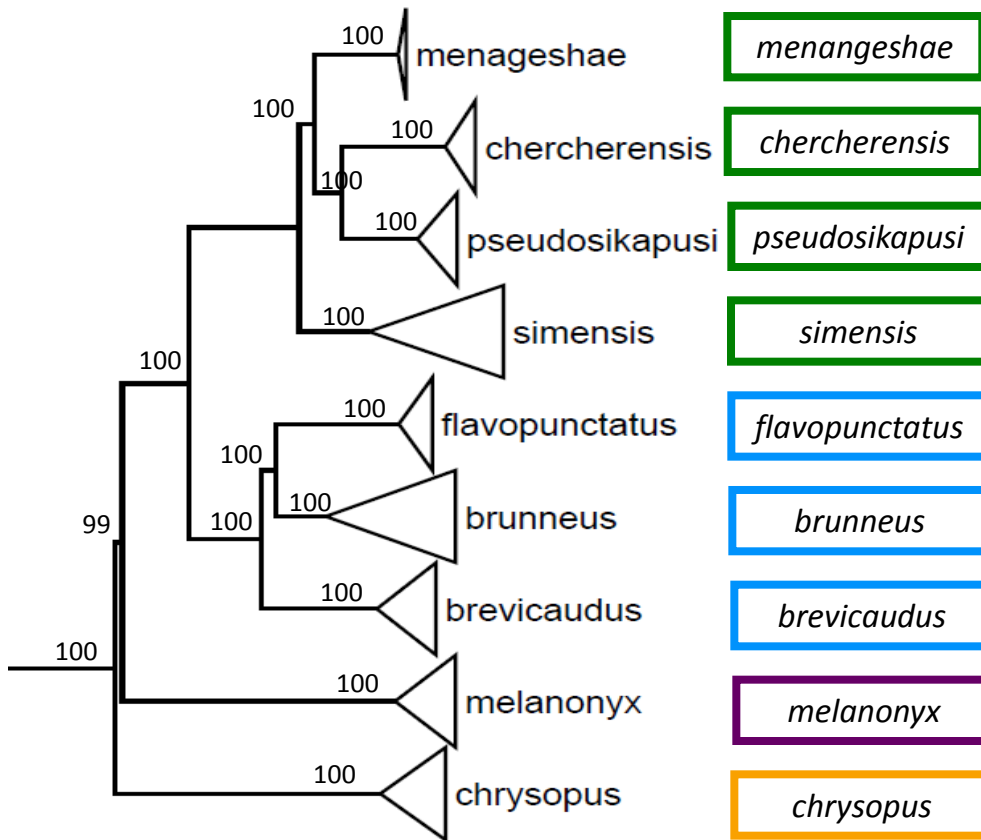
mtDNA



cytochrome *b* (1140 bp)

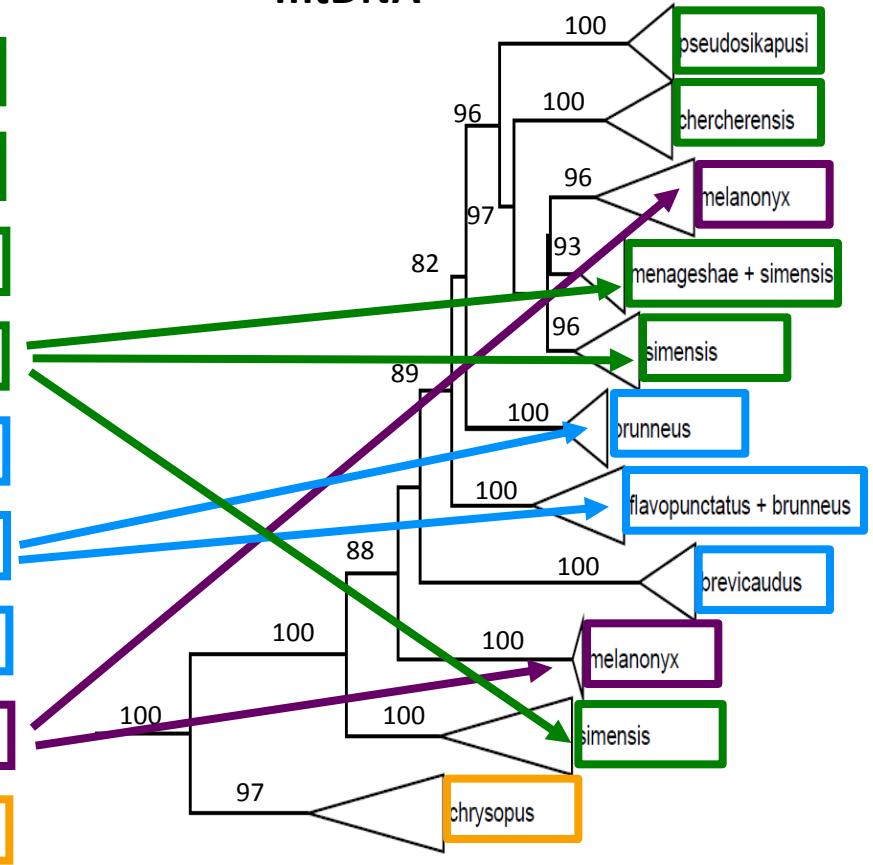
And what about mtDNA?

ddRADseq



15 623 informative loci

mtDNA



cytochrome *b* (1140 bp)

„reticulate evolution“