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**RÜÇHAN
SERTÖZ**



VİRÜS GENOTİPLERİ VE İLAÇ DİRENCİNİN YENİ NESİL DİZİLEME ANALİZİNDEN ÖRNEKLER

RÜÇHAN YAZAN SERTÖZ
EGE ÜNİVERSİTESİ TIP FAKÜLTESİ

3. Ulusal
Klinik Mikrobiyoloji
Kongresi-2015

18-22 Kasım 2015
Titanic Kongre Merkezi
Belek, Antalya



Deep sequencing: Becoming a critical tool in clinical virology

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454



GS Jr. **GS FLX+**

Amplification Method	Emulsion PCR on beads	
Chemistry	Synthesis (pyrosequencing)	
Read length (bp)	400	700
Yield/run (Gb)	0.05	0.9
Primary Error	Indel	
Error rate	~1%	
Run time (hours)	10	20
Virus-related Publications	187	
Advantage(s)	Long reads, maturity	
Disadvantage(s)	Homopolymer misreads, high cost/Mb	

Illumina



MiSeq **HiSeq**

Amplification Method	Bridge PCR in situ	
Chemistry	Synthesis (reversible termination)	
Read length (bp)	250	125
Yield/run (Gb)	8	1,000
Primary Error	Substitution	
Error rate	~0.1%	
Run Time (hours)	39	276
Virus-related Publications	129	
Advantage(s)	Easy work flow, maturity	
Disadvantage(s)	Shortest reads, long run	

**Ion
Torrent**



PGM **Proton**

Amplification Method	Emulsion PCR on beads	
Chemistry	Synthesis (H ⁺ detection)	
Read length (bp)	400	200
Yield/run (Gb)	2	10
Primary Error	Indel	
Error rate	~1%	
Run time (hours)	7	4
Virus-related Publications	13	
Advantage(s)	Low cost, fast run	
Disadvantage(s)	Homopolymer misreads	

PacBio



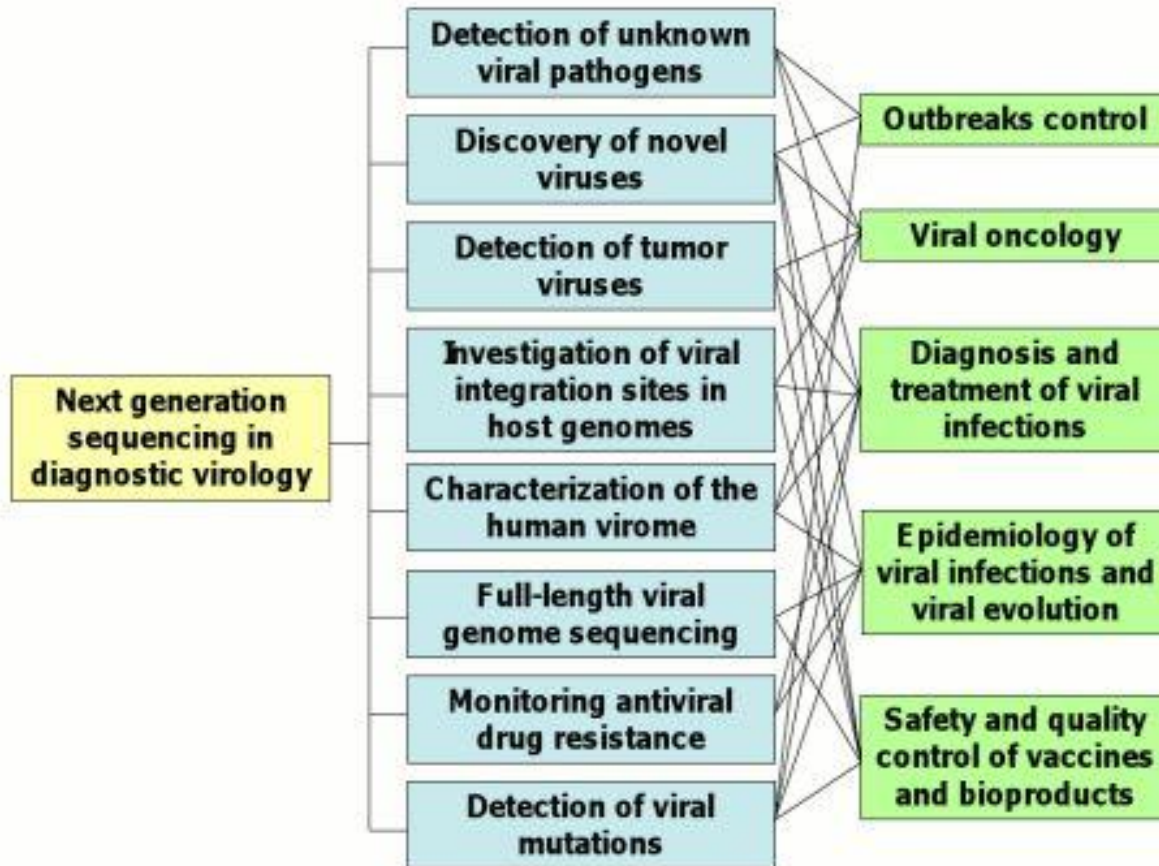
RS II

Amplification Method	No PCR
Chemistry	Single-molecule real-time sequencing
Read length (bp)	8,500
Yield/run (Gb)	0.15
Primary Error	Indel
Error rate	~13%
Run time (hours)	2
Virus-related Publications	6
Advantage(s)	Longest reads
Disadvantage(s)	High error rate, expensive



Applications of Next-Generation Sequencing Technologies to Diagnostic Virology

Luisa Barzon ^{1,*}, Enrico Lavezzo ¹, Valentina Militello ¹, Stefano Toppo ² and Giorgio Palù ¹



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REVIEW

Next-generation sequencing in clinical virology: Discovery of new viruses

Sibnarayan Datta, Raghvendra Budhaliya, Bidisha Das, Soumya Chatterjee, Vanlalhmua, Vijay Veer

- ***YND temelli metagenomik yaklaşımlar***
 - **Nükleik asit dizilerinden bağımsız**
 - **Nonspesifik amplifikasyon yöntemleri**
 - **Sequence-independent single-primer amplification (SISPA),**
 - **Virus discovery based on cDNA-AFLP (VIDISCA),**
 - **Rolling circle amplification (RCA)**
 - **Virüs yapısı, genomu hakkında ön bilgiye gerek yok**
 - **Çoğaltma, zenginleştirme gerekli**
 - **Fiziksel çoğaltma**
 - **Virüs kapsid pürifikasyonu**
 - **Filtrasyon**
 - **Ultrasontrfuj**



Virus Identification in Unknown Tropical Febrile Illness Cases Using Deep Sequencing

Nathan L. Yozwiak^{1,9}, Peter Skewes-Cox^{2,3,4,9}, Mark D. Stenglein^{3,4,9}, Angel Balmaseda⁵, Eva Harris¹, Joseph L. DeRisi^{3,4,6*}

¹ Division of Infectious Diseases and Vaccinology, School of Public Health, University of California, Berkeley, California, United States of America, ² Biological and Medical Informatics Program, University of California San Francisco, San Francisco, California, United States of America, ³ Howard Hughes Medical Institute, University of California San Francisco, San Francisco, California, United States of America, ⁴ Department of Biochemistry and Biophysics, University of California San Francisco, San Francisco, California, United States of America, ⁵ Departamento de Virología, Centro Nacional de Diagnóstico y Referencia, Ministerio de Salud, Managua, Nicaragua, ⁶ Department of Medicine, University of California San Francisco, San Francisco, California, United States of America

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- **Ateş veya bir haftadan kısa süre önce ateş**
- **Baş ağrısı,**
- **Artralji,**
- **Myalji,**
- **Retroorbital ağrı,**
- **Pozitif turnike testi,**
- **Peteşi,**
- **Kanama bulgularından biri**

- ***Dang benzeri hastalıklar***



Virus Identification in Unknown Tropical Febrile Illness Cases Using Deep Sequencing

Nathan L. Yozwiak^{1,9}, Peter Skewes-Cox^{2,3,4,9}, Mark D. Stenglein^{3,4,9}, Angel Balmaseda⁵, Eva Harris¹, Joseph L. DeRisi^{3,4,6*}

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- **Çalışma dışında**
 - **Pnömoni tanılılar**
 - **DENV izole edilenler**
 - **DENV RT-PCR pozitifler**
 - **Seroloji pozitifler**

- **123 hasta (6ay-14yaş)**



Virus Identification in Unknown Tropical Febrile Illness Cases Using Deep Sequencing

Nathan L. Yozwiak^{1,9}, Peter Skewes-Cox^{2,3,4,9}, Mark D. Stenglein^{3,4,9}, Angel Balmaseda⁵, Eva Harris¹, Joseph L. DeRisi^{3,4,6*}

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- **Virochip panviral Mikroarray ve YND (Illumina) ile metagenomik çalışmalar sonucu**
 - **45/123 pozitif - %37**
 - **13 HHV-6**
 - **Bilinen ve/veya yeni virüslerden gelişmiş olduğu düşünülen**
 - **Herpesviridae,**
 - **Flaviviridae,**
 - **Circoviridae,**
 - **Anelloviridae,**
 - **Asfarviridae,**
 - **Parvoviridae**

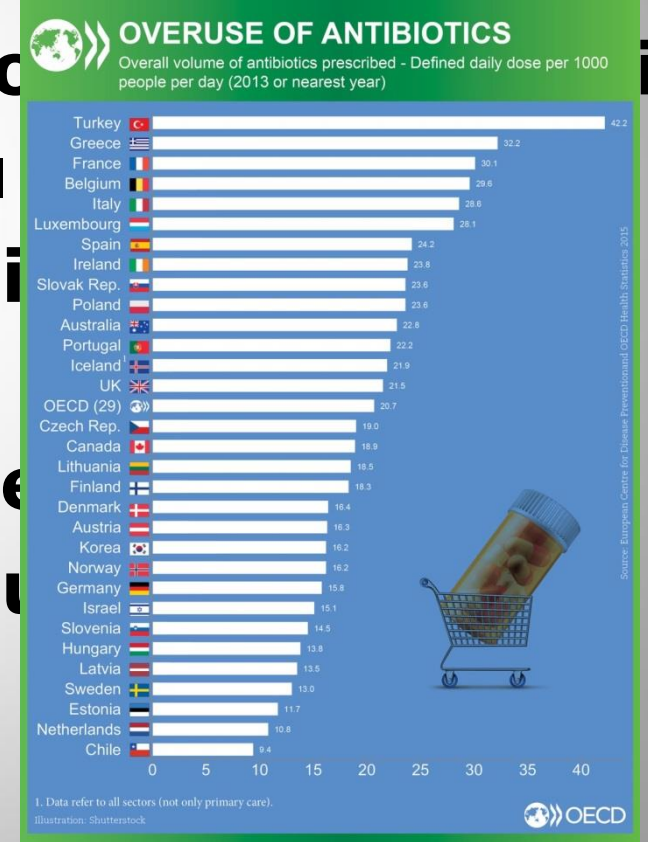


The human gut virome: Inter-individual variation and dynamic response to diet

Samuel Minot,¹ Rohini Sinha,¹ Jun Chen,² Hongzhe Li,² Sue A. Keilbaugh,³ Gary D. Wu,³ James D. Lewis,² and Frederic D. Bushman^{1,4}

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- İnsan barsak viromu
- Diyet ile insan barsak viromu
- Aynı diyetle bireylerarası
- Bakteri florası ile ilişkileri
- Fajlar arası rekabet
- Fajlar bakteriler birlikte
- AB direnci-dar spektrumlu tedavileri????





Dynamic of Mixed HCV Infection in Plasma and PBMC of HIV/HCV Patients Under Treatment With Peg-IFN/Ribavirin

Sabrina Bagaglio, PhD, Caterina Uberti-Foppa, MD, Clelia Di Serio, PhD, Filippo Trentini, PhD, Andrea Andolina, MD, Hamid Hasson, MD, Emanuela Messina, MD, Marco Merli, MD, Lucy Porrino, MD, Adriano Lazzarin, MD, and Giulia Morsica, MD

- **Koinfekte bireylerde risk faktörleri ve çoklu karşılaşma nedeniyle mikst infeksiyonlar sık**
- **HIV/HCV koinfekte bireylerde farklı kompartmanlarda HCV mikst genotip dinamiği ve interferon, ribavirin yanıtı ile uyumu**
- **GS FLX (454 Life Sciences, Roche)**
- **19 koinfekte hasta**
 - **10'u yanıtızsız veya relaps**
 - **9'u kalıcı viral yanıt**



Dynamic of Mixed HCV Infection in Plasma and PBMC of HIV/HCV Patients Under Treatment With Peg-IFN/Ribavirin

Sabrina Bagaglio, PhD, Caterina Uberti-Foppa, MD, Clelia Di Serio, PhD, Filippo Trentini, PhD, Andrea Andolina, MD, Hamid Hasson, MD, Emanuela Messina, MD, Marco Merli, MD, Lucy Porrino, MD, Adriano Lazzarin, MD, and Giulia Morsica, MD

- **Plazmada**
 - **11/19 (%58) mikst genotip**
- **Periferik kan mononükleer hücrelerinde**
 - **HCV pozitif 15 hastanın 6'sı (%40) mikst genotip**
- **Tedavi sırasında 3 yanıtızsız hastada iki kompartmanda da baskın genotipler farklılaştı!**
- **Plazma örneklerinde mikst genotipler !!**
 - **Tedavi yanıtını etkileyen en önemli faktör**
- **Farklı tedavi yaklaşımları, genotip test takibi**



Dynamic of Mixed HCV Infection in Plasma and PBMC of HIV/HCV Patients Under Treatment With Peg-IFN/Ribavirin

Sabrina Bagaglio, PhD, Caterina Uberti-Foppa, MD, Clelia Di Serio, PhD, Filippo Trentini, PhD, Andrea Andolina, MD, Hamid Hasson, MD, Emanuela Messina, MD, Marco Merli, MD, Lucy Porrino, MD, Adriano Lazzarin, MD, and Giulia Morsica, MD

TABLE 3. Viral Population Analysis by Next-Generation Sequencing During Treatment With P-R and Posttreatment Follow-Up (HCVG-W24PT) in HIV/HCV Coinfected Individuals

	HCVG-BL	HCVG-W12	HCVG-W24	HCVG-W24PT
Plasma	1b-1a-1c-3a	3a	3a	1b-1a-1c-3a
PT1				
PBMC	1b	1b	1b-1a	neg
Plasma	1a-1c	1a-1c	-	-
PT2				
PBMC	3a-1b	1a	-	-
Plasma	4c/d-1b-1a-3a-2a	4c/d-2a-1a	4c/d-3a	-
PT3				
PBMC	4c/d-1b-3a-2a	neg	neg	-
Plasma	1a	1a-4c/d	3a	1a-4c/d-1b-3a
PT4				
PBMC	1c	1a	1c	1a
Plasma	1b-1a-3a-2a	1b-2a	-	-
PT5				
PBMC	1b	-	-	-
Plasma	4c/d-4a-2a	4a-4c/d-3a	4c/d-3a	-
PT6				
PBMC	4c/d-4a-1b	4a-4c/d	3a-2a	-
Plasma	1a-1b-2a	1a-1b	-	-
PT7				
PBMC	1a	-	-	-
Plasma	1b-3a	neg	neg	1b-3a
PT8*				
PBMC	1b	neg	neg	1b
Plasma	1b-1a-1c	neg	neg	1c-1a-1b
PT9*				
PBMC	4c/d-4a-3a	neg	neg	-
Plasma	4c/d	4c/d	4c/d	-
PT10				
PBMC	4c/d	neg	3a-4c/d	-

Dominant genotype is indicated in bold. G = genotype, PT = patients. - = specimen not available.

* RE patients.



- **Luminex- MGP primer set**
- **YND-HPV genel primer set PGMY (DSÖ HPV manuel)**
 - **Duyarlılık 100 kopya/mL**
 - **HPV 13/15 10 kopya/mL**
- **36/60 servikal örnekte YND-Luminex uyumlu**



Next generation sequencing for human papillomavirus genotyping

L. Sara Arroyo^a, Vitaly Smelov^{a,b}, Davit Bzhalava^a, Carina Eklund^a,
Emilie Hultin^a, Joakim Dillner^{a,*}^a Department of Laboratory Medicine, Karolinska Institutet and Karolinska University Hospital, 141 86 Stockholm, Sweden^b Department of Urology and Andrology, Northwestern State Medical University n.a. I.I. Mechnikov, 191015 St. Petersburg, Russia**Table 3b**

Cervical samples that showed discrepancies between NGS and Luminex.

Cervical Sample	Genotypes detected by GS Junior	Luminex	Comments ^a
6038	16, 59	16	59 (2)
6047	18, 52, 68b	18	52 (1), 68b (4)
6129	18, 45, 59	18, 18v	45 (2), 59 (1)
6191	11, 33, 39	11, 39	33 (21)
6346	54, 61	61	54 (50)
6959	51, 53	51	53 (3)
6508	42, 58	58	42 (1)
6302	52, 68b, 70	52, 68b	70 (2577)
6251	16, 67	16	67 (2)
6434	53	Neg	53 (2001)
6387	32	Neg	32 NP ^b (2424)
6595	33	Neg	33 (20)
6464	45, 52, 54, 59, 62, 89	45, 52, 70, 89	54 (224), 59 (1), 62 NP ^b (58)
6468	114	83, 86	114 NP ^b (749)
6187	18, 89	18, 90	89 (279), 90 PGMym ^c
7020	67, 70	59, 70	67 (2)
6060	Neg	91	PGMym ^c
6196	Neg	90	PGMym ^c
6205	Neg	91	PGMym ^c
6217	Neg	91	PGMym ^c
6304	Neg	87	PGMym ^c
6423	18	18, 68a	68a PGMym ^c
6466	Neg	16	
6616	Neg	16	

^a Genotypes detected by NGS but not detected by Luminex are shown with their number of reads in brackets.^b Genotype detected by NGS that were not tested for by any one of the probes included in the Luminex. NP (no probe).^c Genotype detected by Luminex but not by NGS, possibly due to a failure in amplification because of mismatch with PGMym primers. PGMym (PGMY mismatch).



Cross-clade simultaneous HIV drug resistance genotyping for reverse transcriptase, protease, and integrase inhibitor mutations by Illumina MiSeq

Retrovirology 2014

Dawn M Dudley¹, Adam L Bailey¹, Shruti H Mehta², Austin L Hughes³, Gregory D Kirk⁴, Ryan P Westergaard⁵ and David H O'Connor^{1*}

Antiviral Direnç İzlemi

HIV örneği

- **Mevcut ticari testler**
- **Nonsubtype B de zayıf**
- **RT, proteaz**
- **İntegraz inhibitörleri**
- **Kombine preparatlar ile başlangıç tedavisi!**

YND

- **Multipleks kullanım**
- **Fiyat düşüklüğü**
- **Klonal özellik nedeniyle duyarlılık**
- **MiSeq en az hata eğilimli (%0.1)**



Cross-clade simultaneous HIV drug resistance genotyping for reverse transcriptase, protease, and integrase inhibitor mutations by Illumina MiSeq

Retrovirology 2014

Dawn M Dudley¹, Adam L Bailey¹, Shruti H Mehta², Austin L Hughes³, Gregory D Kirk⁴, Ryan P Westergaard⁵ and David H O'Connor^{1*}

- **Los Alamos referans dizileri ile universal primer çiftleri**
- **Nested PCR**
- **A,B,C,D, CRF 02AG, CRF02AE**
- **799 kopya/mL duyarlılıkta**
- **ALIVE 62 örnek**

Table 1 HIV-1 subtypes tested with the universal primer set

Virus	Subtype	TCID/mL*	P24 ng/mL*	RT-PCR
92UG_029	A	1.26x10 ⁵	150	+
93RW_024	A	NA	NA	+
00KE-KER2008	A	10 ^{2.60}	57	+
84US_MNp	B	1.02x10 ⁴	634	+
85US_BA-L	B	5.62x10 ⁶	39.3	+
91US_1	B	10 ^{5.0}	294	+
94US_33931N	B	10 ^{3.10}	235	+
00TZ_A246	C	1.45x10 ⁴	NA	+
02ET_14	C	10 ^{4.10}	12.2	+
94IN_20635-4	C	NA	NA	+
90SE_364	C	10 ^{6.0}	157	+
98US_MSC5016	C	10 ^{3.85}	11.5	+
93UG_065	D	NA	NA	+
98UG_57128	D	10 ^{2.39}	13	+
99UG_A03349M1	D	2.05x10 ⁴	290	+
90TH_CM244	CRF01_AE	4.1x10 ⁴	88	+
97TH_NP1525	CRF01_AE	7.11x10 ³	90	+
91DJ_263	CRF02_AG	2.3x10 ⁴	NA	+
98US_MSC5007	CRF02_AG	4x10 ⁴	127	+

* Provided by the NIH AIDS Research and Reference Reagent Program.



Cross-clade simultaneous HIV drug resistance genotyping for reverse transcriptase, protease, and integrase inhibitor mutations by Illumina MiSeq

Retrovirology 2014

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Table 2 Average sequencing read coverage for all drug resistance mutations identified in the ALIVE cohort

Gene product	Drug resistance mutation*	Ave. sequencing read coverage	
PR	L10IFVC	297	
	V11I	294	
	G16E	1022	
	K20RMITV	1917	
	L24I	1039	
	D30N	2169	
	L33FIV	3140	
	M36LIV	3639	
	M46I/L	2609	
	I50L/V	3895	
	F53LY	1213	
	I54VTALM	2122	
	D60E	3065	
	I62V	3198	
	L63P	3346	
	I64LMV	2635	
	A71VITL	3800	
	G73CSTA	3045	
	V82ATFSL	3300	
	L89MM	4199	
	L90M	4982	
	I93LM	5850	
	RT	M41L	5014
		A62V	4941
K70R		4324	
V75I		10460	
V77I		4787	
V90I		4177	
K103N		6048	
V106A/M/I		6492	
V108I		7424	
E138KAGQR		7401	
M184V/I		5906	
Y188LHC		5283	
G190ASE	4708		
P225H	5764		
M230LI	8668		
IN	S147G	3123	

*Boldface mutations are major drug resistance mutations, non-boldface mutations are accessory mutations.

➤ % 54'ünde çeşitli mutasyonlar

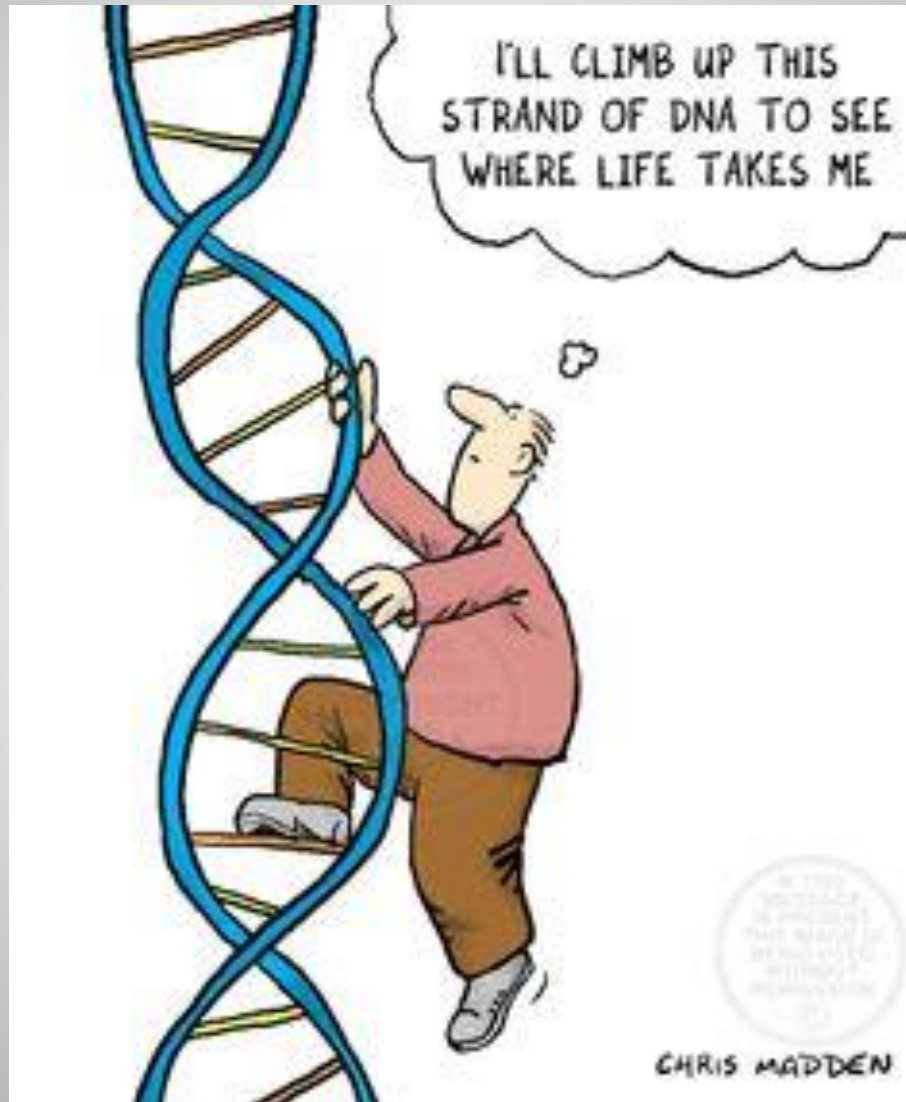
➤ % 59'u %2-20 sıklıkta

➤ Sanger ile kaçırılabilir !



Yeni Nesil Dizileme

- Hücre kültürü, moleküler testler ve dizi analizinin tamamlayıcısı rolünde
- **İlerlemeler**
- Metagenomik yaklaşımlarla virüs tanımı
- Konak içi ve konaklararası virüs değişkenliği
 - ilaç direnç testleri,
 - genotip,
 - moleküler epidemiyoloji,
 - antiviral ilaç ve aşı geliştirilmesinde
- Konak-virüs ilişkileri
 - RNA sekansı ile transkriptom analizi,
 - epigenomik analiz,
 - protein-nükleik asit ilişkileri
- Konak genomu ve infeksiyon hastalıklarına duyarlılık



I'LL CLIMB UP THIS
STRAND OF DNA TO SEE
WHERE LIFE TAKES ME

CHRIS MADDEN