

Gülhane Mikrobiyoloji Günleri

20 - 22 Nisan 2010

Antimikrobik Kemoterapi
Laboratuvar Uygulamaları ve Yenilikler





Kan Akımı Enfeksiyonlarında MRSA Moleküler Tanısı

Dr. Abdullah KILIÇ
GATA Tıbbi Mikrobiyoloji AD

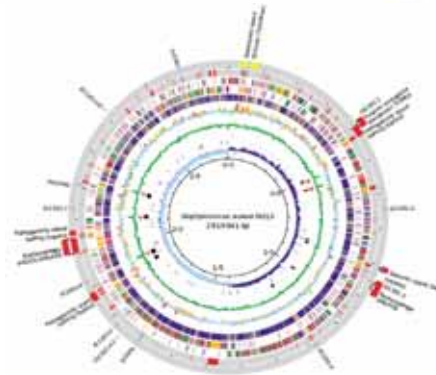
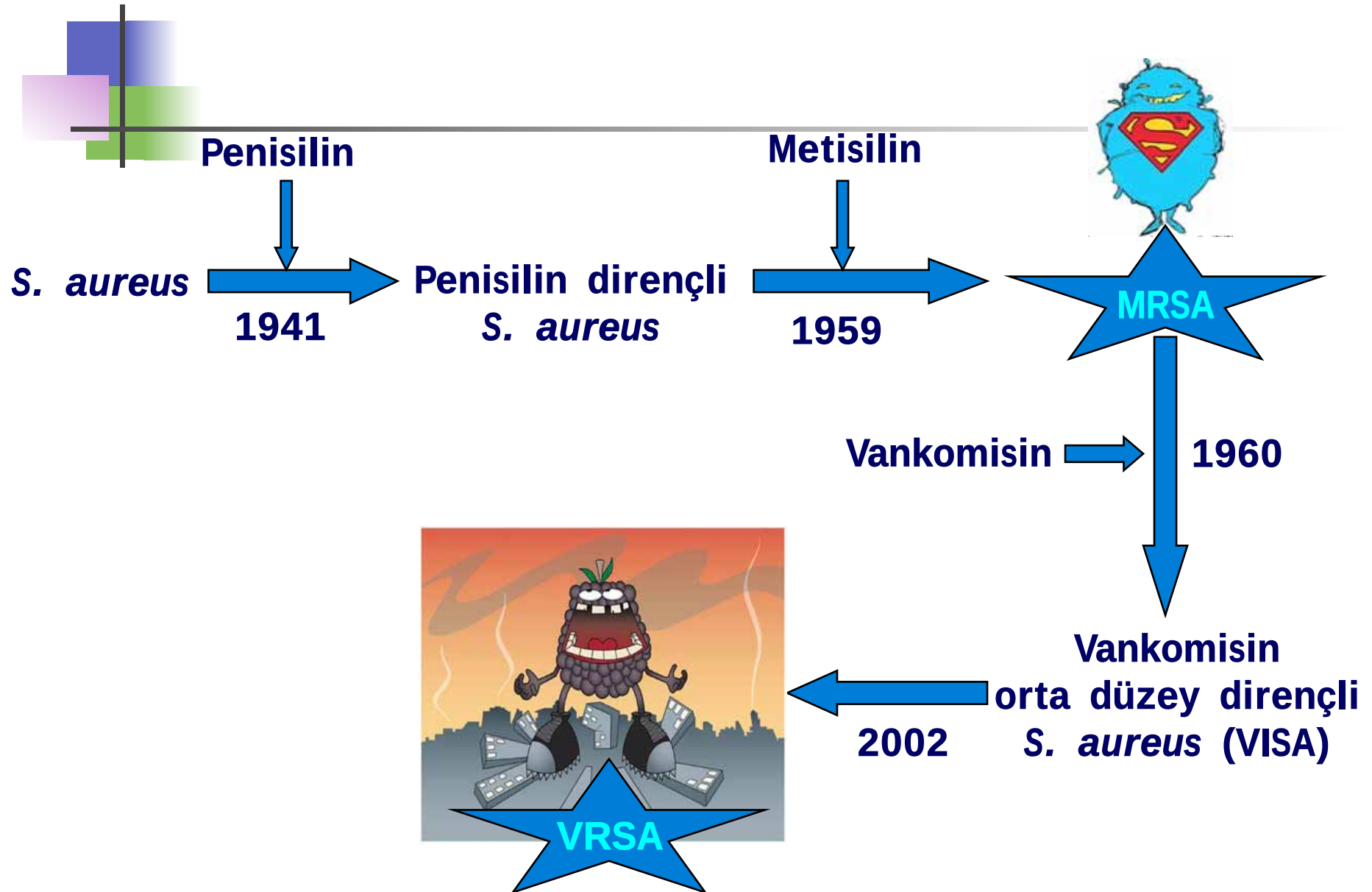


Figure 2. Circular representation of a genome chromosome (200,000) and plasmids (10,000) of Staphylococcus aureus.

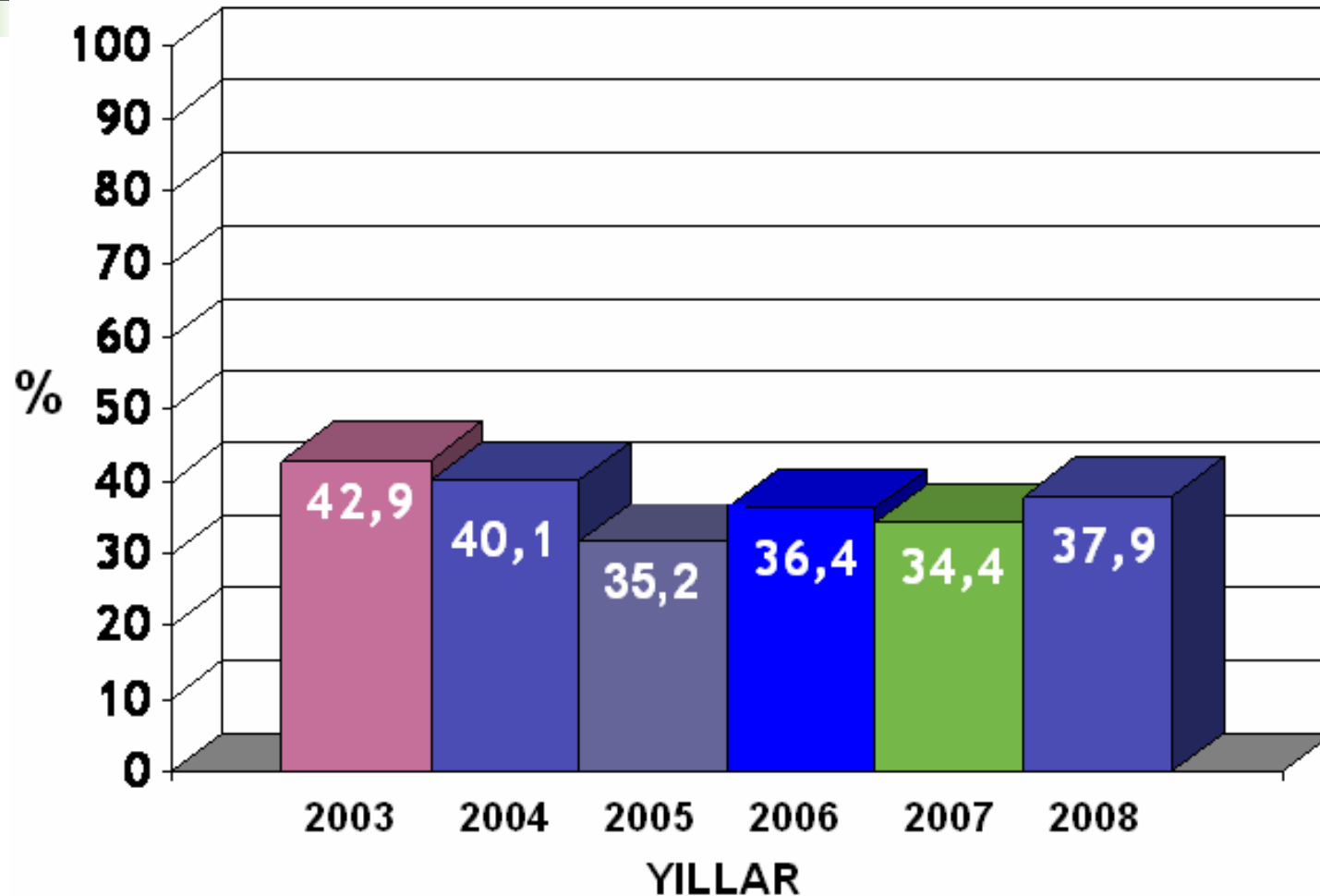
Staphylococcus aureus

- Hastane ve toplum kaynaklı enfeksiyonlara neden olmakta
- Enfeksiyonlar
 - Alt solunum sistemi
 - Cerrahi yara
 - Kan akımı
 - Kardiyovasküler sistem (endokardit)
 - Deri ve yumuşak doku enfeksiyonları
 - Osteomyelit, septik artrit
- ABD’de yıllık 300.000 vaka, 12.000 ölüm, 2,7 milyon gün yatış süresi, 9.5 milyar \$ ilave maliyet

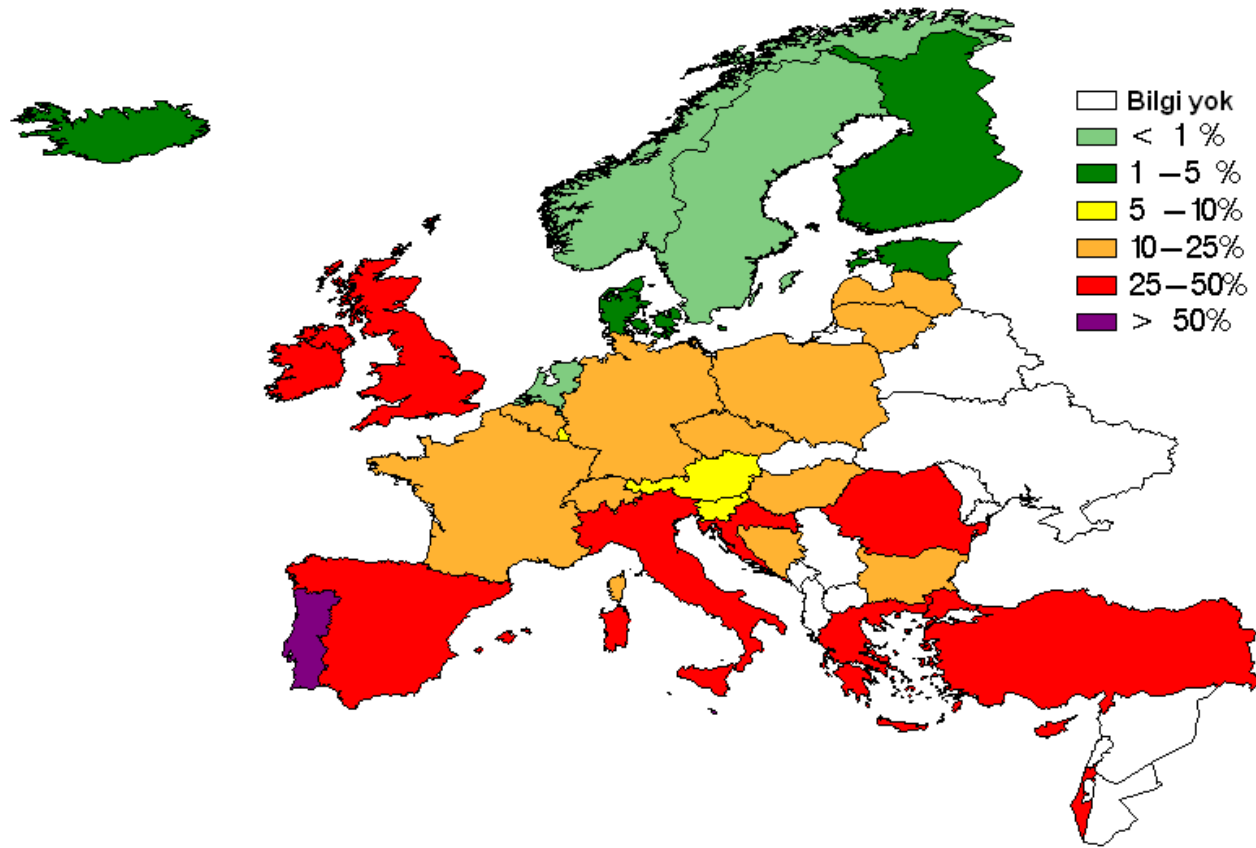
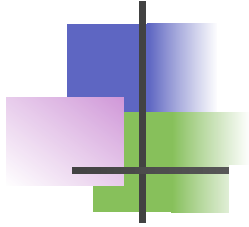




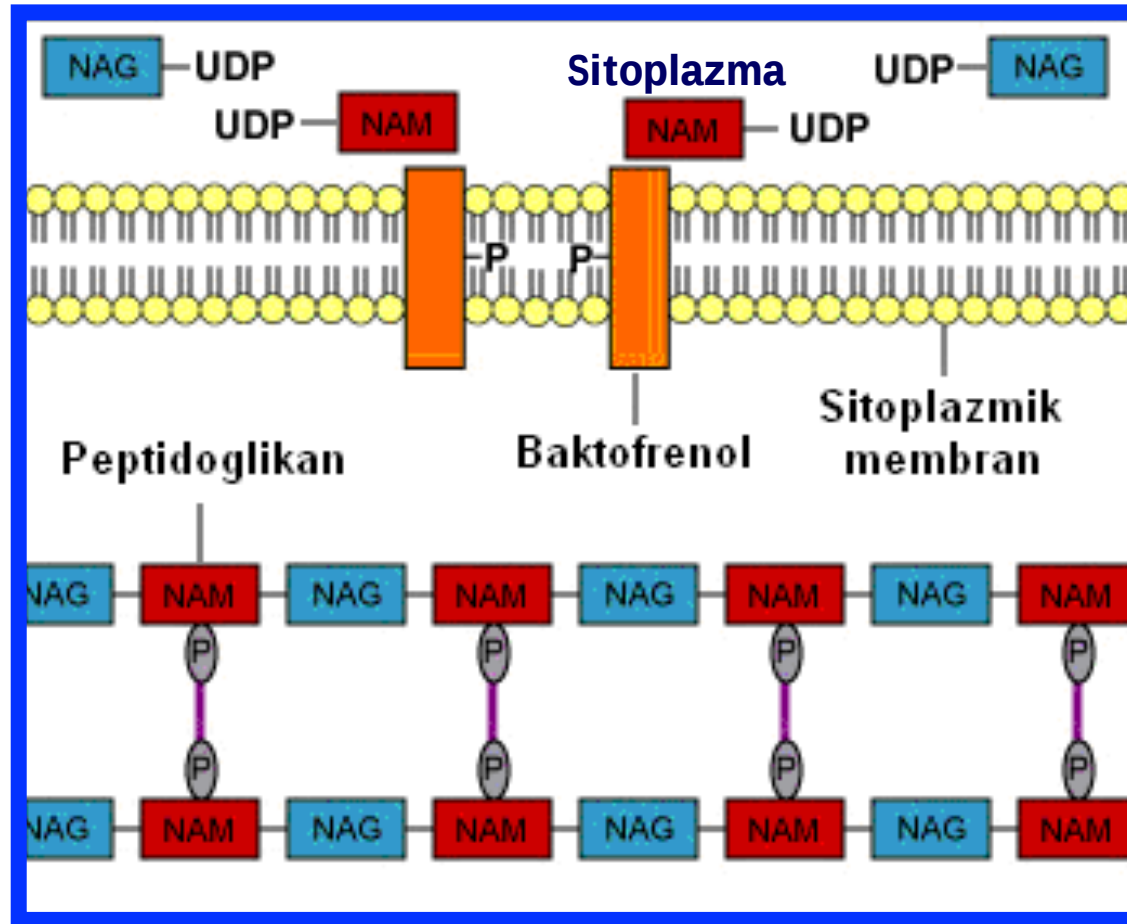
European Antimicrobial Resistance Surveillance System Türkiye MRSA Oranları



European Antimicrobial Resistance Surveillance System Avrupa MRSA Oranları

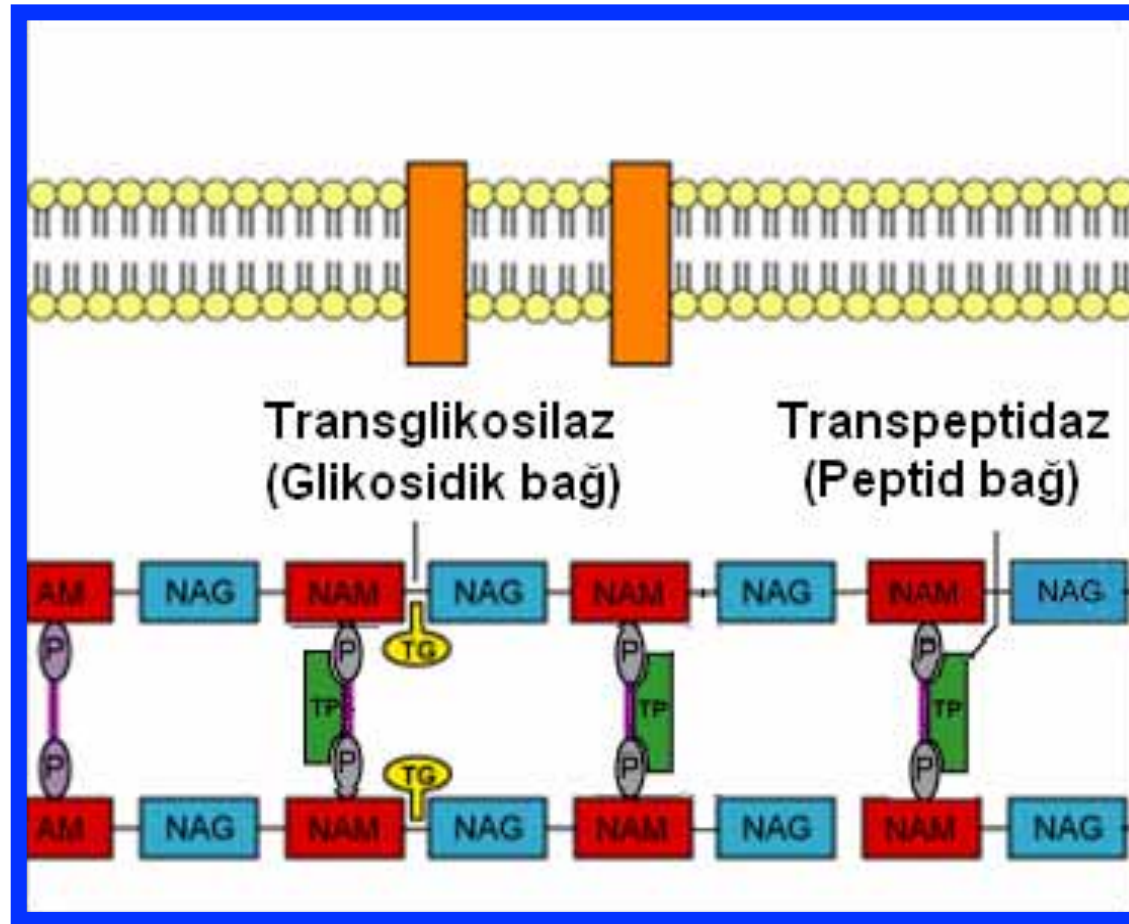


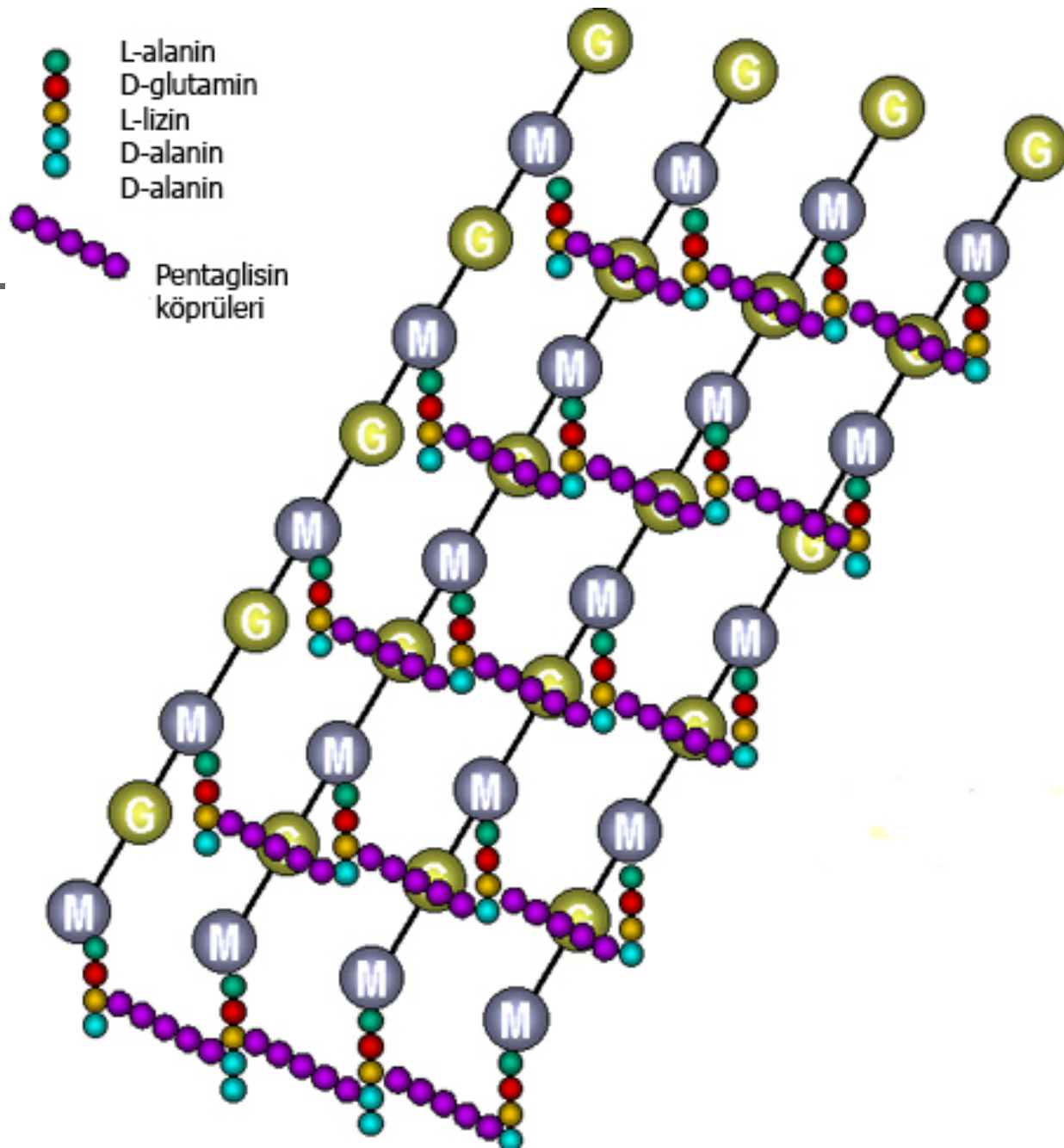
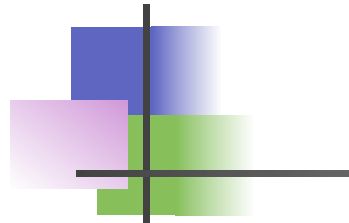
Hücre Duvar Sentezi



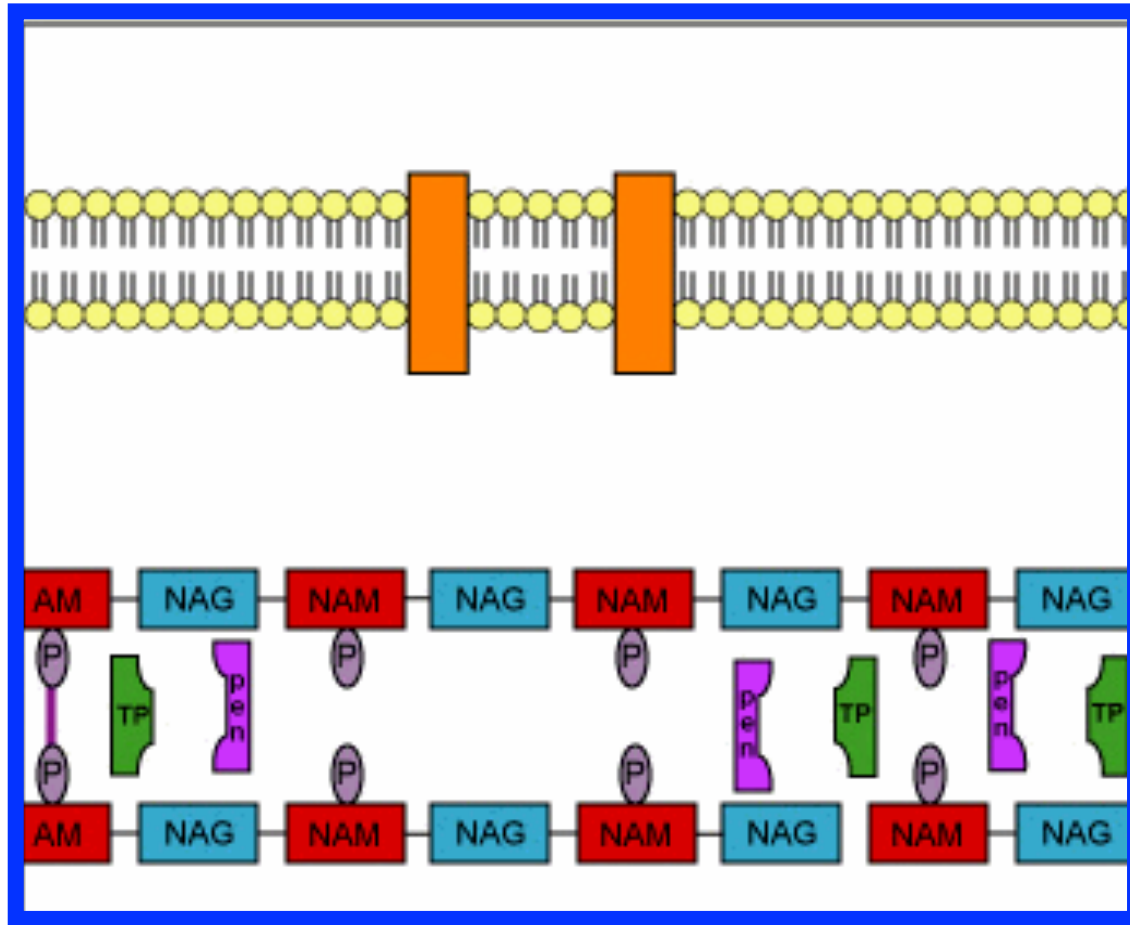
NAG: N-Asetil Glukoz Amin
NAM: N-Asetil Muramik Asit

Hücre Duvar Sentezi

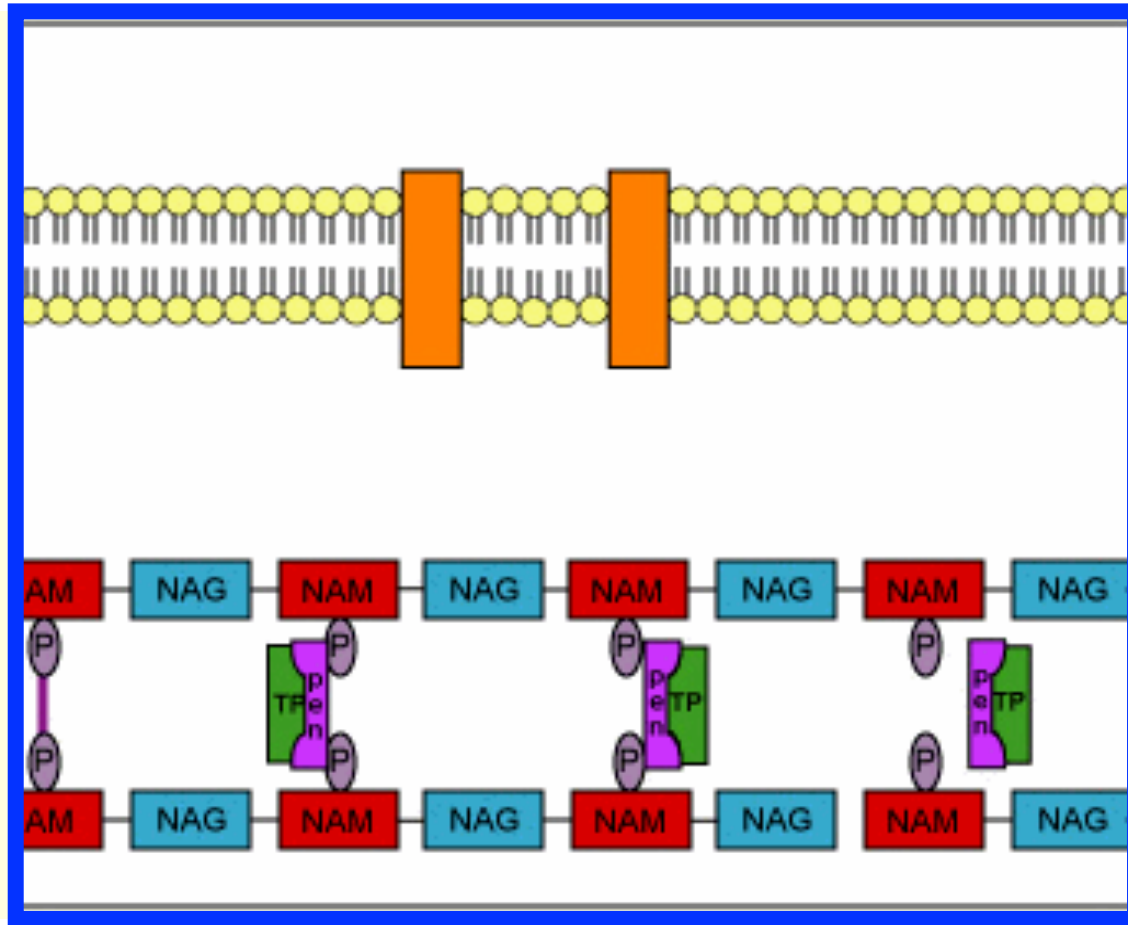


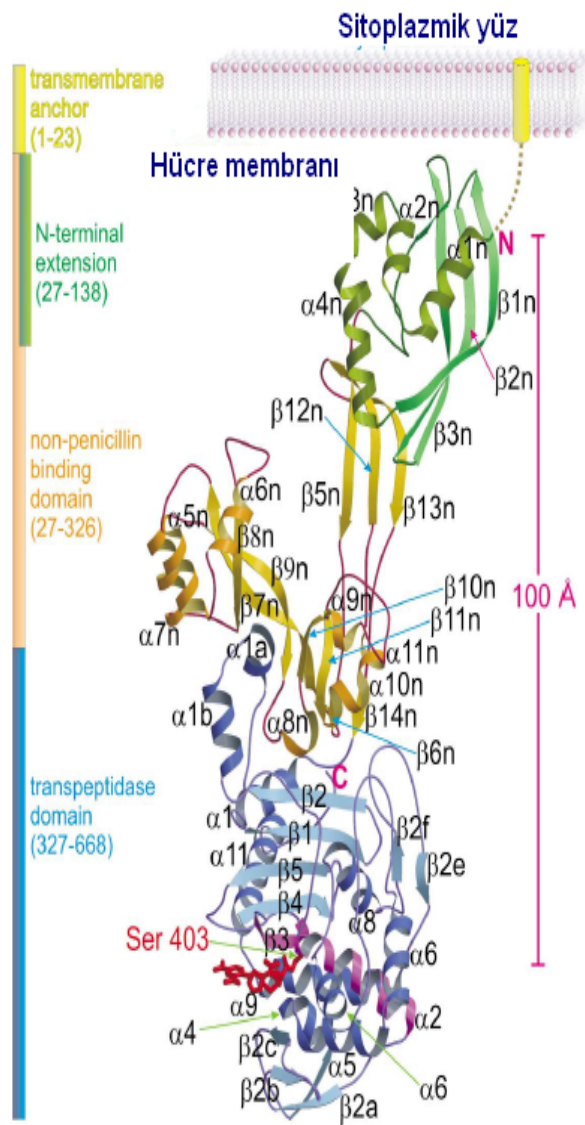


Beta-laktam AB Etkisi

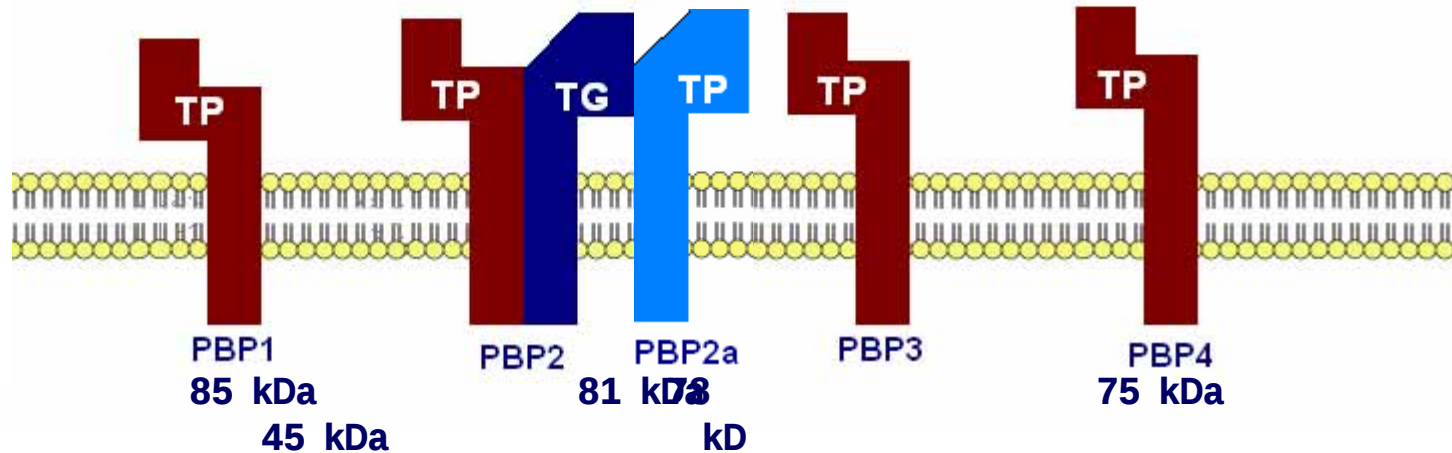
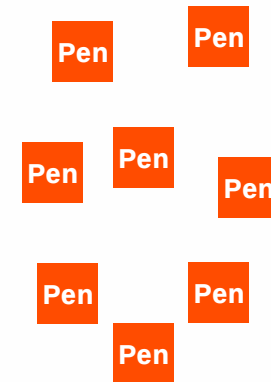
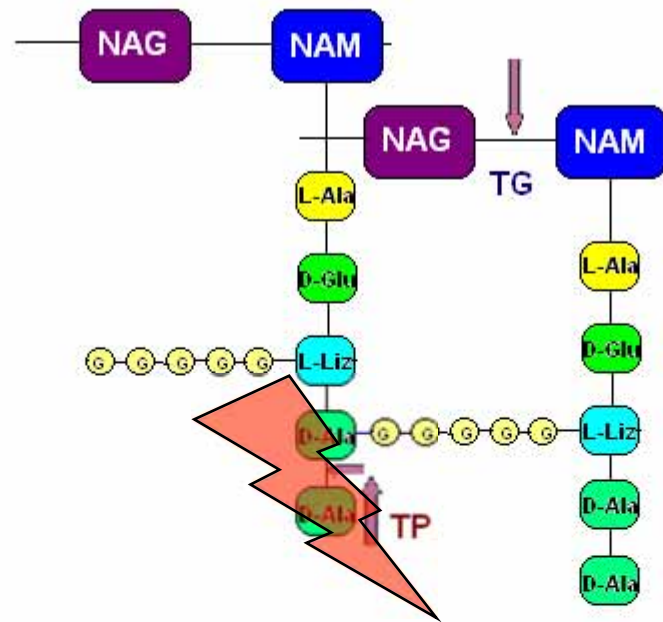


Beta-laktam AB Etkisi





PBP yapısı



YMA

YMA

B

B

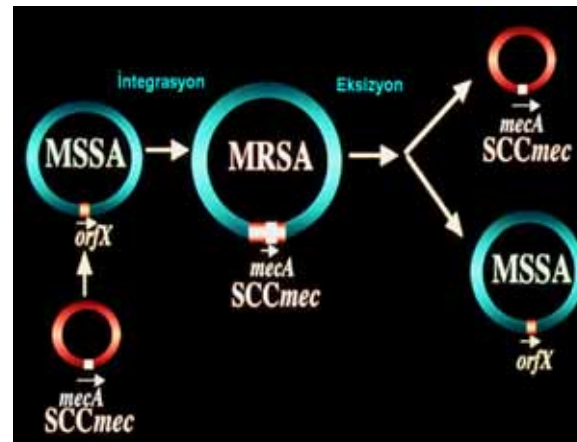
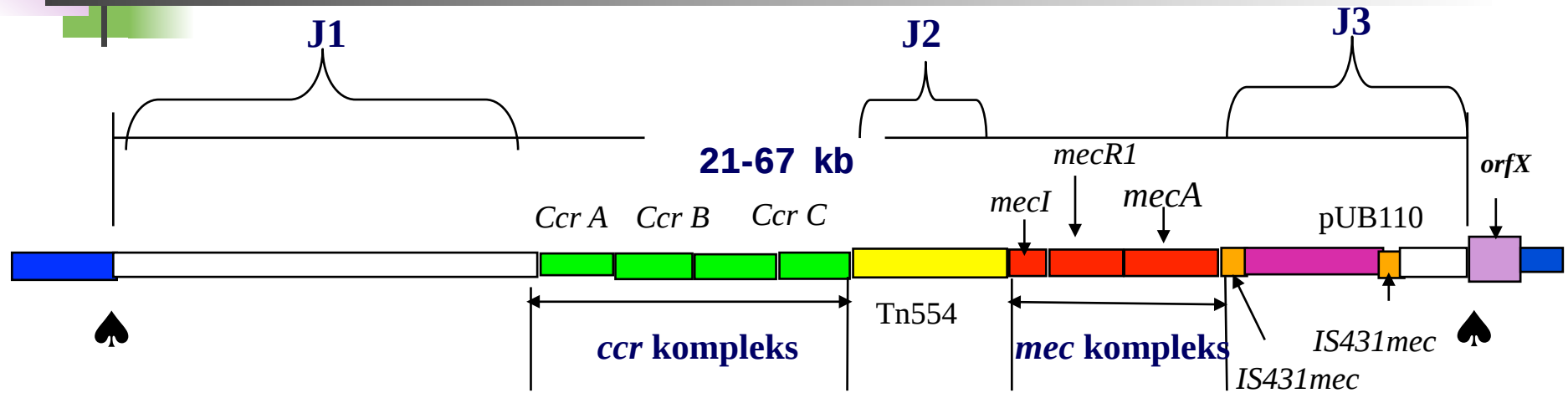
YMA^a

YMDMA

BA

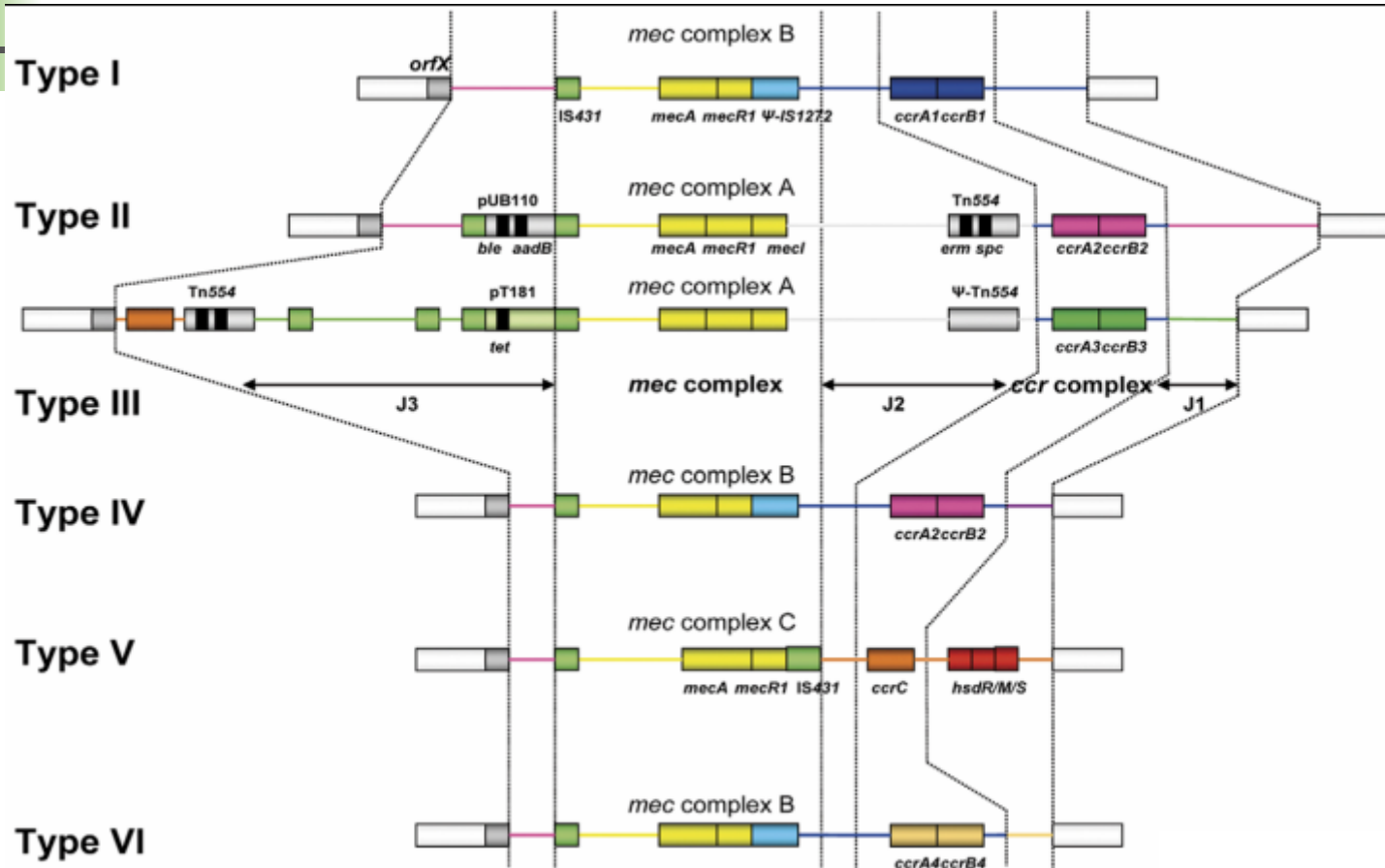
Düze

SCCmec Gen Kaset Yapısı



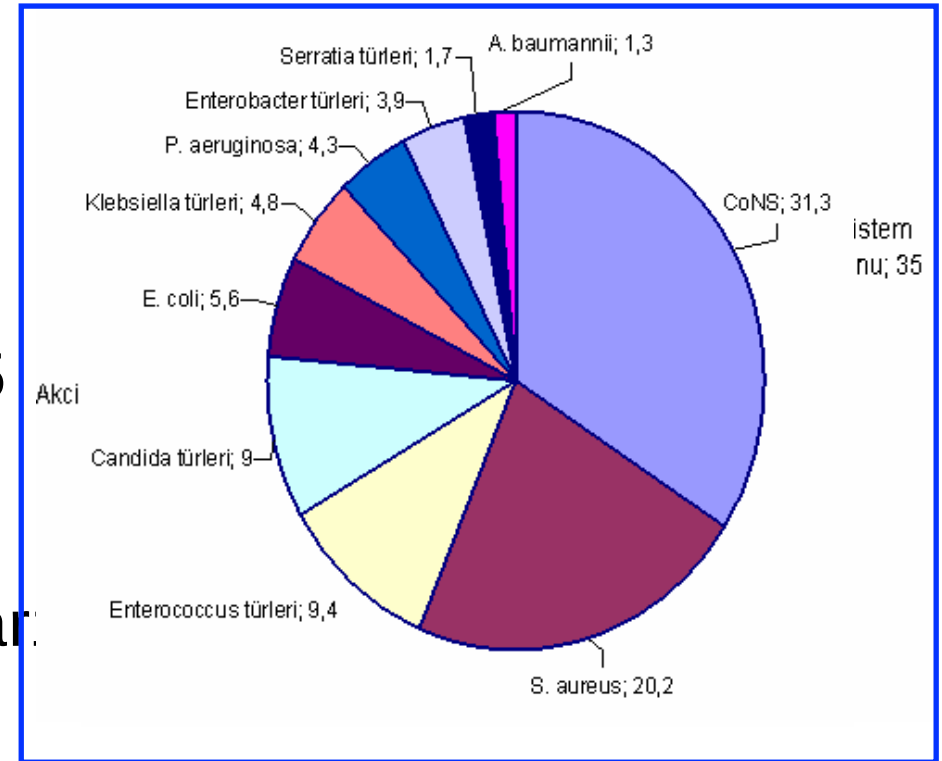
**Beta-laktam
direnci ve bu
direncin
düzenlenmesi**

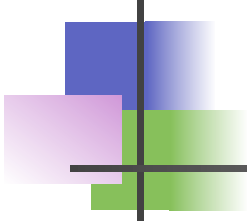
SCCmec Yap_{IS1} (I-VI)



Kan Akımı Enfeksiyonları (KAE)

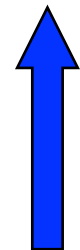
- ABD'de yıllık 250.000 vaka (Hastane enfeksiyonlarının %10'u)
- Mortalite oranı %25-30 (ilk 25 saat içinde uygun tedavi almayanlarda 2 kat fazla)
- %20'sinde *S. aureus*, %50 civarında MR





MRSA KAE

- Metisilin direnci hastanede **yatış süresini** 1.29-2 kat arttırır
- Metisilin direnci hasta **maliyetini** 1.44-3 kat arttırır
- Metisilin direnci **mortaliteyi** yaklaşık 1.5-2.6 kat arttırır
- Gecikmiş tedavi mortalite oranını 4 kat hasta **yatış süresini** 1.5 kat arttırır



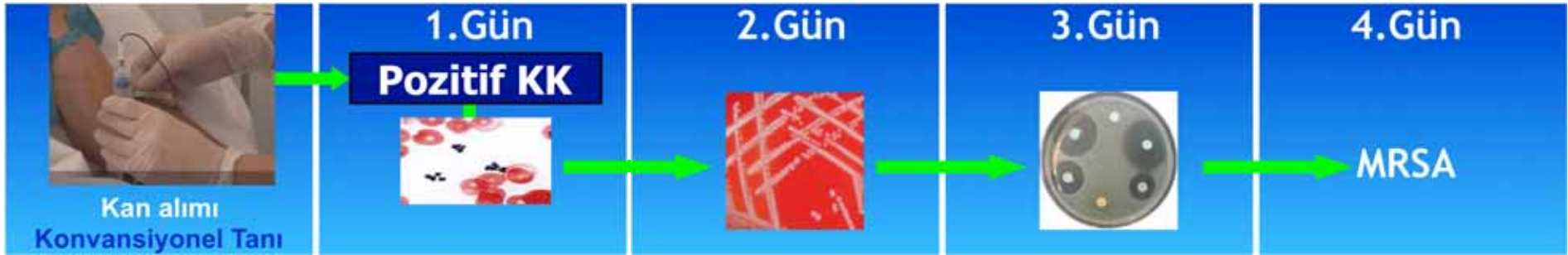
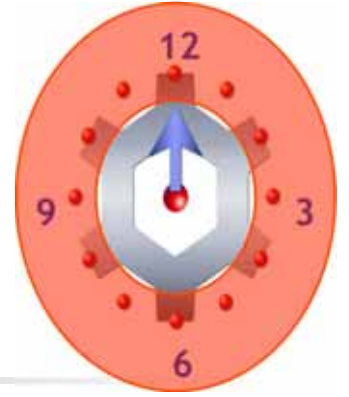
Outcomes Analysis of Delayed Antibiotic Treatment for Hospital-Acquired *Staphylococcus aureus* Bacteremia

Thomas P. Lodise,^a Peggy S. McKinnon, Linda Swiderski, and Michael J. Rybak

Anti-Infective Research Laboratory, Detroit Receiving Hospital and University Health Center, and Eugene Applebaum College of Pharmacy and Health Sciences, Wayne State University, Detroit, Michigan

The objective of this study was to determine the effect of delayed therapy on morbidity and mortality associated with nosocomial *Staphylococcus aureus* bacteremia. The study included all episodes of *S. aureus* bacteremia that developed >2 days after hospital admission during 1999 to 2001. Classification and regression tree analysis (CART) was used to select the mortality breakpoint between early and delayed treatment. During the 25-month study period, 167 patients met the inclusion criteria. The breakpoint between delayed and early treatment derived using CART was 44.75 hours. On multivariate analysis, delayed treatment was found to be an independent predictor of infection-related mortality (odds ratio, 3.8; 95% confidence interval, 1.3–11.0; $P = .01$) and was associated with a longer hospital stay than was early treatment (20.2 days versus 14.3 days; $P = .05$). These findings support the notion that delay of therapy has deleterious effects on clinical outcomes, and efforts should be made to ensure that appropriate therapy is initiated promptly.

MRSA KAE'u Laboratuvar Tanısı



Empirik Tedavi

Geniş spektrumlu AB

Uygun Tedavi



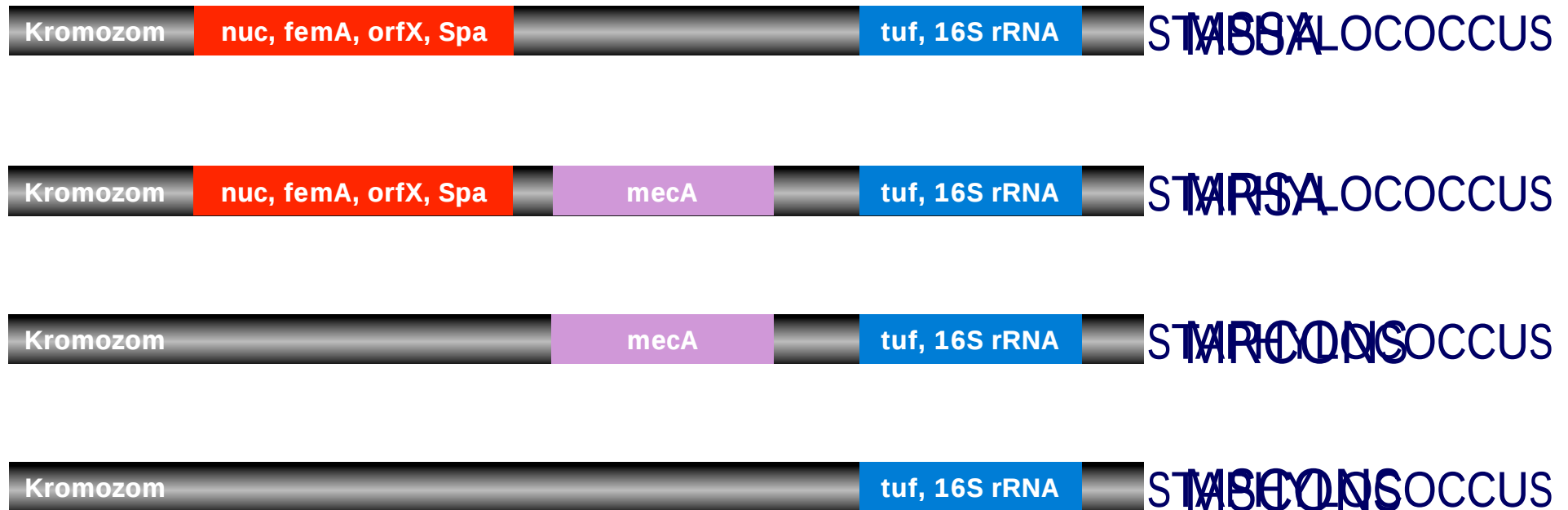
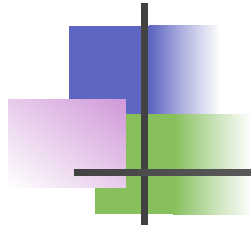
Empirik Tedavi

Uygun Tedavi

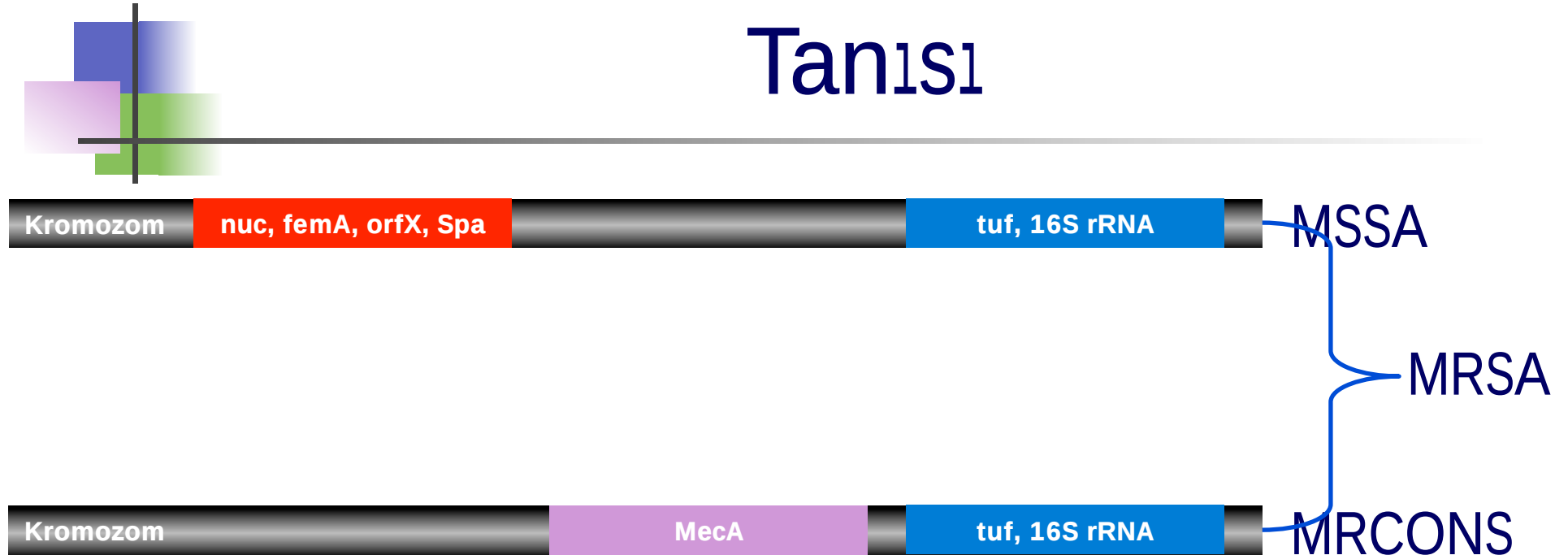
- Mortalite
- Yatış süresi
- Maliyet
- Direnç



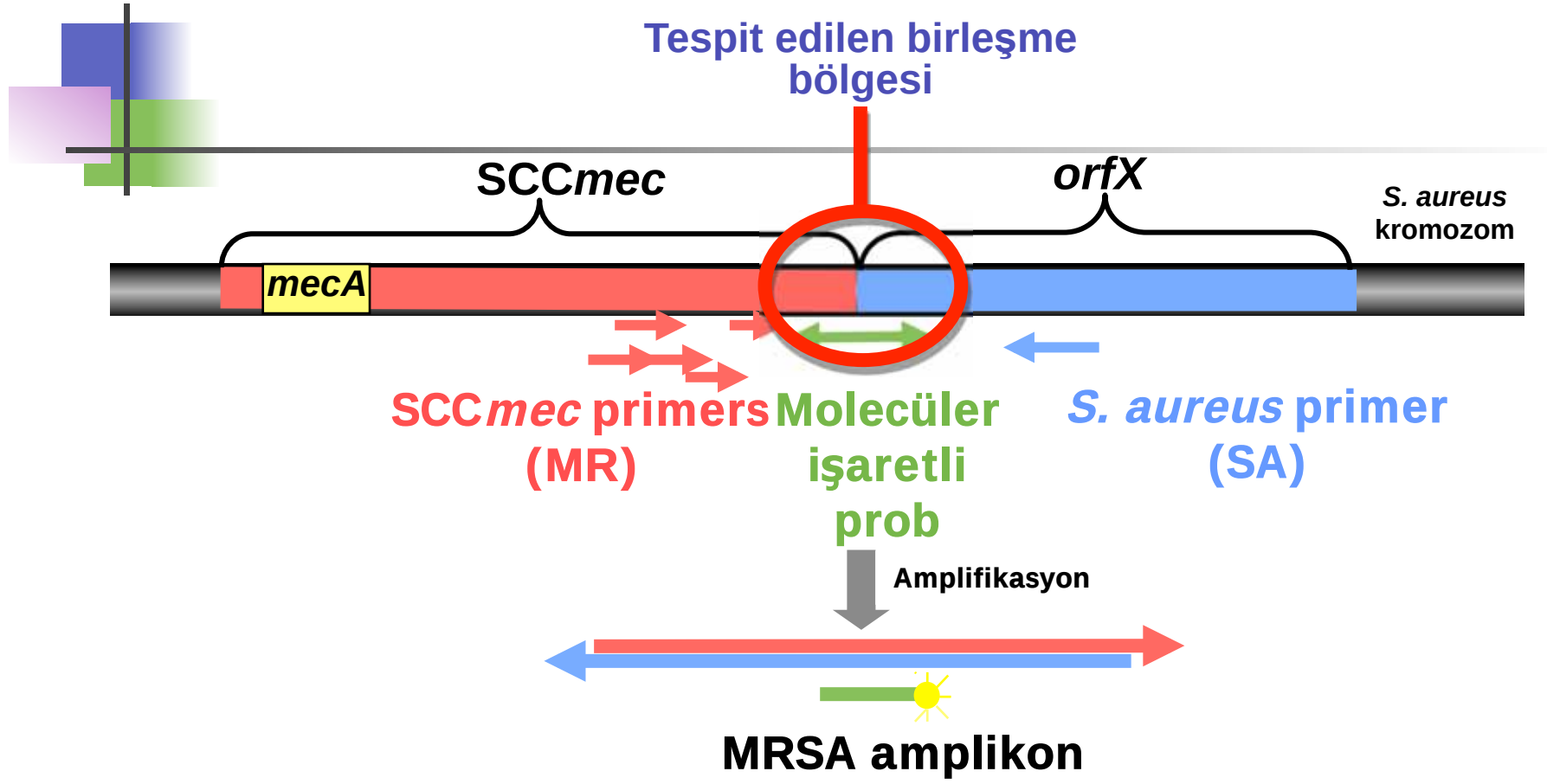
MRSA KAE'u Moleküler Tanısı



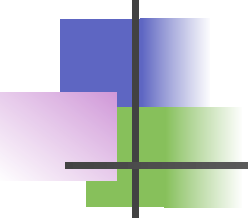
MRSA KAE'u Moleküler Tanısı



- Burun örneklerinde %3.4-4.6
- Steril örneklerde %0-2.5



FDA Onayı Almış MRSA Testleri



- **BD GeneOhm™ MRSA**
- **Xpert MRSA/SA BC**

FDA Onaylı Almış MRSA Testleri

BD GeneOhm™
MRSA



Pozitif kan
kültürü



Örnek
Hazırlama



Lizis-DNA
ekstraksiyonu



Rekonstrüksiyon



Real-time
PCR
SmartCycler

Site ID	Sample ID	Assay Result	IC Result	Warning
A1	449225	MRSA	NA	
A2	912579	MRSA	NA	
A3	557884	MRSA	NA	
A4	368713	MRSA	NA	
A5	208430	MRSA	NA	
A6	290385	MRSA	NA	
A7	449577	MRSA	NA	
A8	740956	MRSA	NA	
A9	546616	MRSA	NA	

Ekranda
kesin sonuçlar

15 örnek için 20 dk

~ 70 dk

< 2 saat

Xpert MRSA/
SA BC



Pozitif kan
kültürü



Lizis
solüsyon



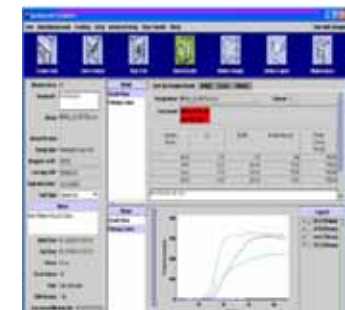
R-1



R-2



Real-time PCR
GenExpert Cihazı



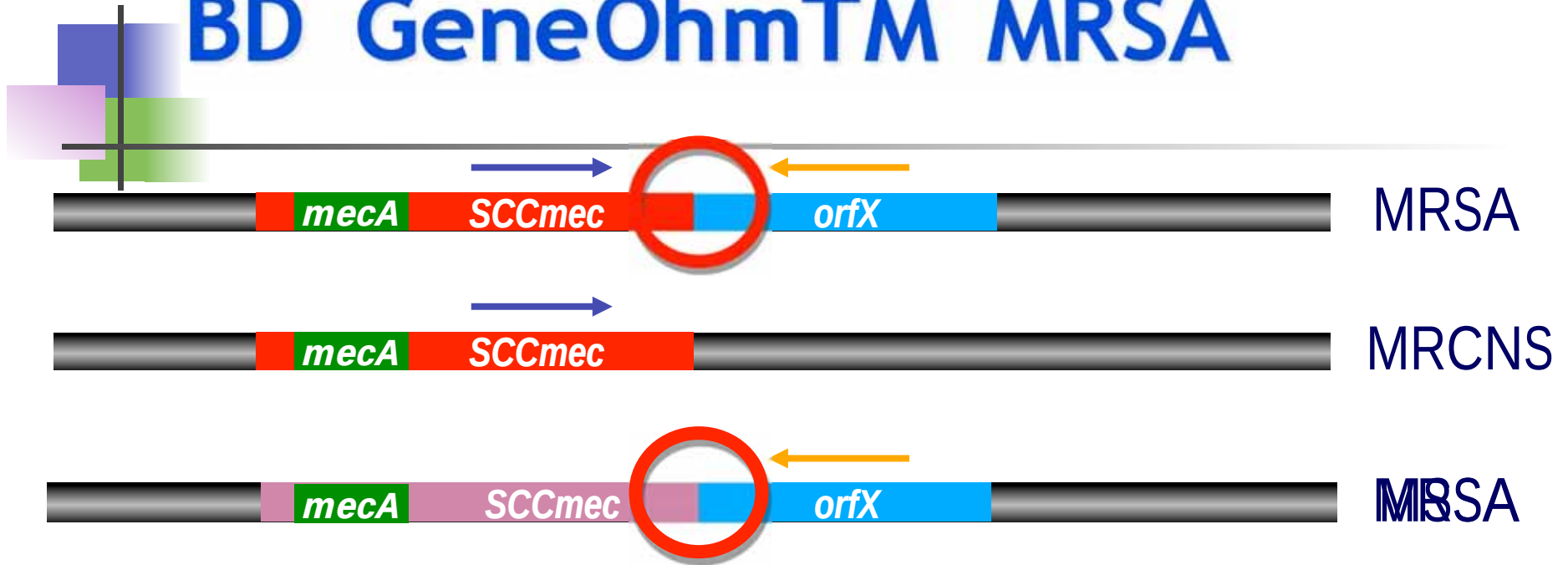
Ekranda
Kesin sonuçlar

2 dk

~ 70 dk

< 2 saat

BD GeneOhm™ MRSA



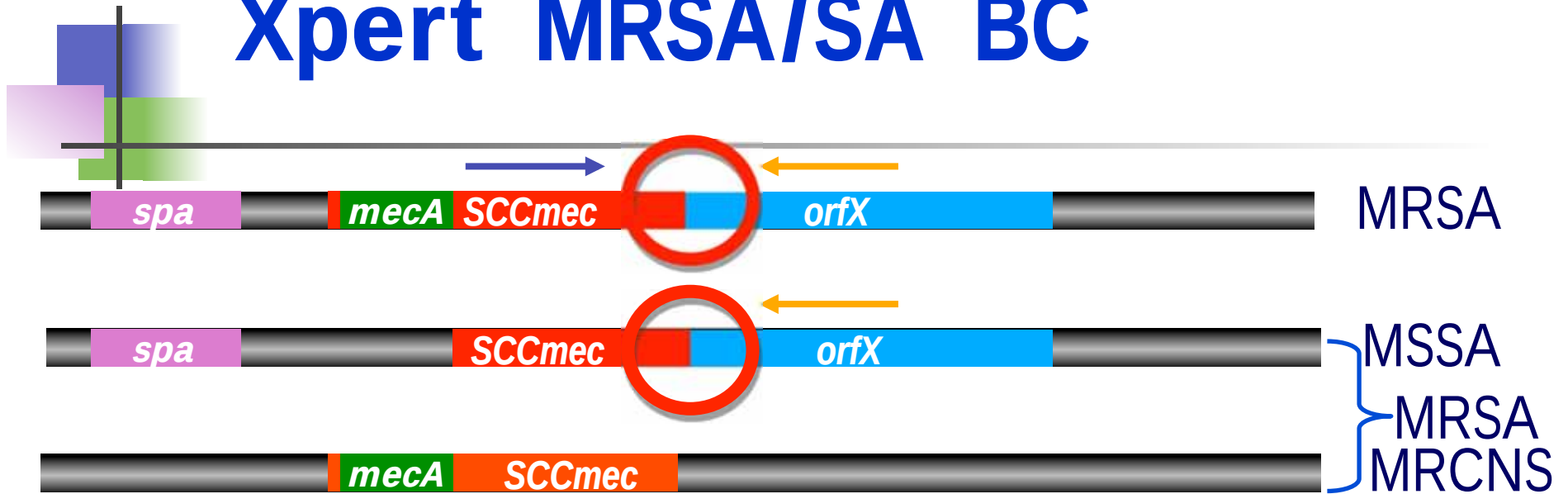
- *orfX* (*S. aureus*) and *SCCmec* gen kaset (direnç geni bölgesi) birleşim yeri
- *SCCmec* tip I - IV tespiti: Hastane ve toplum kaynaklı
 - Yalancı pozitiflik: “empty *mecA*” fenomene *mec* varyant izolatlar
 - Yalancı negatiflik: Varyant *SCCmec* birleşme bölgesi

Huletsky et al J Clin Microbiol (2004) 1875-84
Bartels et al J Clin Microbiol (2009) 1524-7
Thomas et al J Clin Microbiol (2008) 4116-7

BD GeneOhm™ MRSA

Kaynak	Duyarlılık	Özgüllük
Gröbner et al JCM 2009	%95.6 (43/45)	%95.3 (61/64)
Kimura et al RB 2009	%100 (67/67)	% 97.4 (37/38)
Snyder et al JCM 2009	%95.0 (56/59)	%97.5 (40/41)

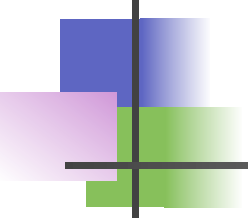
Xpert MRSA/SA BC



- *orfX* (*S. aureus*) and *SCCmec* gen kaset (direnç geni bölgesi) birleşim yeri, *spa*, *mecA*
- *SCCmec* tip I - V tespiti: Hastane ve toplum kaynaklı
 - Yalancı pozitiflik: “empty *mecA*” fenomene (*spa* ve *SCCmec*)+ MRCNS bir arada olması (*mecA*)
 - Yalancı negatiflik: Yetersiz bakteri miktarı

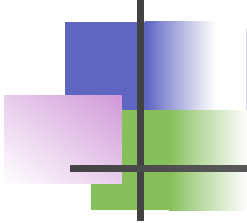
Xpert MRSA/SA BC

Kaynak	Duyarlılık	Özgüllük
Parta et al JCM 2009	% 97.9 (46/47)	% 100 (21/21)
Wolk et al JCM 2009	% 98.3 (57/58)	% 99.4 (346/348)



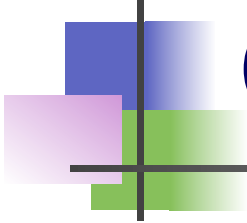
Tripleks Real-Time PCR Yöntemi ile Kan Kültürü Örneklerinden Stafilokokların ve Metisilin Direncinin Tespit Edilmesi

Amaç: KAE'una neden olan stafilokokların ve metisilin direncinin real-time PCR yöntemi ile tanımlanması



Fenotipik Yöntem

- 12 Kasım 2008-11 Ağustos 2009 arasında 341 gram pozitif kok kümesi (GPKK) görülen kan kültür örneği çalışmaya alındı
- Konvansiyonel yöntem ile
 - 22 MRSA
 - 22 MSSA
 - 230 MRCoNS
 - 54 MSCoNS
 - 13 stafilokok dışı GPKK yapmış organizma



Genotipik yöntem

Kromozom **nuc** **tuf** MSSA

Kromozom **nuc** **mecA** **tuf** MRSA

Kromozom **mecA** **tuf** MRCoNS

Kromozom **tuf** MSCoNS

Dizi

Staphylococcus aureus nuc gene

☐ sirküler
☒ lineer

Preset Oligo

Tm

PRİMER UZUNLUĞU

20

BAŞLANGIÇ YERİ

1

BİTİŞ YERİ

648

ARA

Referans Dizi No:

4

Toplam Dizi Sayısı:

12

Dizi Uzunluğu:

648

Amplikon Uzunluğu:

192

1.Primer

revers yap

3' -> 5' YAP

5' **gtacaaaggtaaccaatgacattca** 3'

Başlangıç Nükleotidi : 284

2.Primer

revers yap

3' -> 5' YAP

5' **actgataaatatggacgtggcttagc** 3'

Başlangıç Nükleotidi : 450

3.Primer

revers yap

3' -> 5' YAP

5' **tgggtgatacacctgaaacaaagcatcc** 3'

Başlangıç Nükleotidi : 319

4.Primer

revers yap

3' -> 5' YAP

5' 3'

Başlangıç Nükleotidi :

5.Primer

revers yap

3' -> 5' YAP

5' 3'

Başlangıç Nükleotidi :

6.Primer

revers yap

3' -> 5' YAP

5' 3'

Başlangıç Nükleotidi :

DİZİ ARA

DİZİ GÖSTER

PRİMER ANALİZ

HESAPLAMALAR

YENİ DİZİ GİRİŞİ

PRİMERLER

ENZİM KESİMİ

ÇIKIŞ

GTATGGCAATTGTTTCAATATTACTTATAGGGATGGCTATCAGTAATGTTTCGAAAGGGCAATACGCAAAGAGGTTTTT
 CTATTTTCGCTACTAGTTGTTTCTAGTTAACTTTAGTTGTAGTTTCAAGTCTAAGTAGCTCAGCAAATGCATCACAACAA
 GATAATGGCGTAAATAGAAAGTGTCTGAAGATCCAACAGTATATAGTGCAACTTCACTAAAAAATTACATAAAGAAC
 CTGCGACATTAATTAAAGCGATTGATGGTGATACGGTTAAATTAATgtacaaaggtaaccaatgacattcaGACTATT
 ATTggttgatacacctgaaacaaagcatccTAAAAAAGGTGTAGAGAAATATGGTCCTGAAGCAAGTGCATTTACGAAA
 AAAATGGTAGAAAATGCAAAGAAAATTGAAGTCGAGTTTGACAAAGGTCAAAGAactgataaatatggacgtggcttag
 cGTATATTTTATGCTGATGGAAGAAATGGTAAACGAAGCTTTAGTTTCGTCAAGGCTTGGCTAAAGTTGCTTTATGTTTATAA
 ACCTAACAATACACATGAACAACTTTTAAGAAAAAGTGAAGCACAAGCAAAAAAGAGAAATTAATATTTTGGAGCGAA
 GACAACGCTGATTTCAG

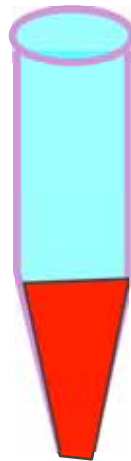


Hedef gen	Primerler	Proplar	Genbank No
<i>nuc</i>	5'-gttgcttagtgtaacttttagttgta-3', 5'-aatgtcgcaggttctttatgtaattt-3'	5'-VIC-aagtctaagtagctcagcaaagca-BHQ1-3'	EF529599 EF529596 EF529595 EF529593
<i>mecA</i>	5'-aaatattattagctgattcaggttac-3' 5'-cgtaaatattgccattattttctaatt-3'	5'-FAM-caaggtgaaatactgattaaccagta-BHQ1-3'	AB221124 AB221123 AB221122 AB221121 AB221120
<i>tuf</i>	5'-aaacaactgttactggtgtagaaatg-3' 5'-agtacggaaatagaattgtg-3'	5'-TR-tccgtaaattattagactacgctgaagc BHQ2-3'	GQ141079 EU652826 EU652822 EU652816 EU652802 EU652800 EU652794 EU652785

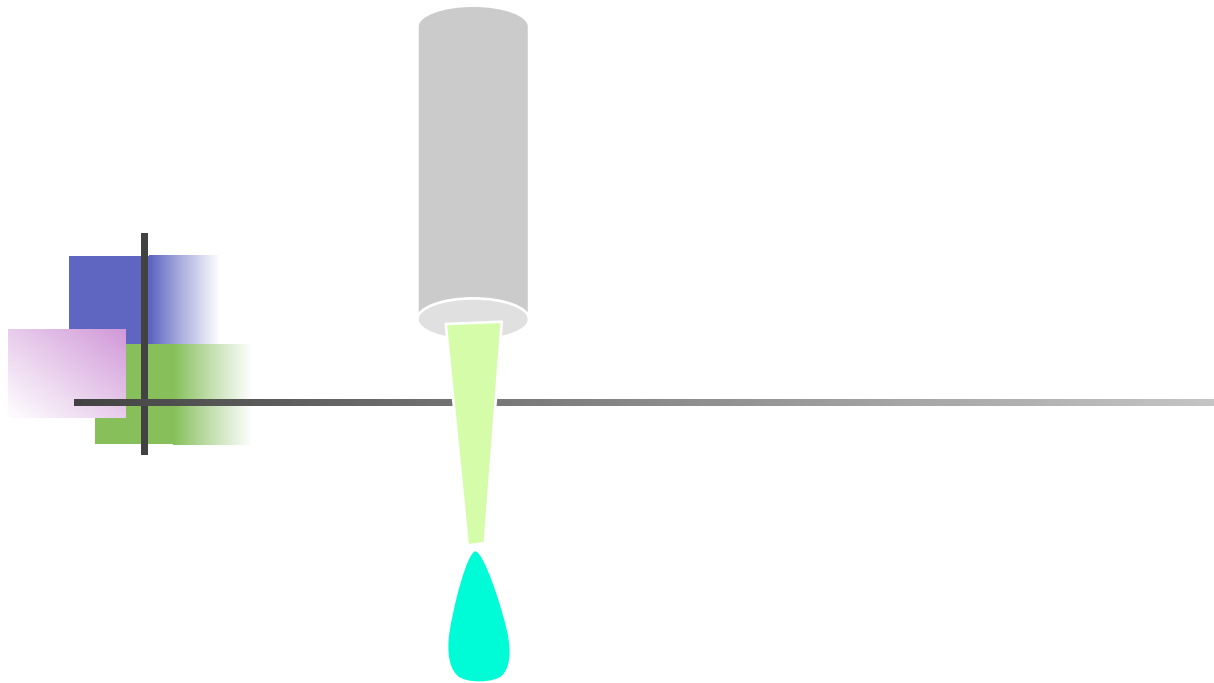


20 μl

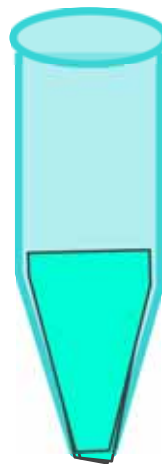
Sodium polyanetolsulfonat (SPS)



1980 μl



Prüfung (135ul)



7500 System SDS Software - [Plate1 (Standard Curve)]

FileViewToolsInstrumentAnalysisWindowHelp

Start

Stop

Disconnect

Extend...

Estimated Time Remaining (hh:mm):

Status:

Temperature

Sample:Heat Sink:

Cover:Block:

Cycle

Stage:Rep:

Time (mm:ss):Step:

State:

Thermal Cycler Protocol

Thermal Profile

Auto Increment

Ramp Rate

Stage 1

Stage 2

Reps: 1

Reps: 35

95.0

95.0

15:00

0:15

60.0

1:00

Add Cycle

Add Hold

Add Step

Add Dissociation Stage

Delete

Help

Settings

Sample Volume (µL): 25

Run Mode: Standard 7500

Data Collection: Stage 2, Step 2 (60.0 @ 1:00)

Ready

Connected

NUM

start

Removable Disk (F:)

Removable Disk (F:)

7500 System SDS Sof...

3:13 PM

7500 System SDS Software - [MRSA.sds (Standard Curve)]

FileViewToolsInstrumentAnalysisWindowHelp

Start

Stop

Disconnect

Extend...

Estimated Time Remaining (hh:mm):

01:23

Status:

Running...

Temperature

Sample:	24	Heat Sink:	29
Cover:	104	Block:	25

Cycle

Stage:	1	Rep:	1
Time (mm:ss):	00:00	Step:	1
State:	Ramping...		

Thermal Cycler Protocol

Thermal Profile

Auto Increment

Ramp Rate

Stage 1

Stage 2

Reps: 1

Reps: 35

95.0

95.0

15:00

0:15

60.0

1:00

Add Cycle

Add Hold

Add Step

Add Dissociation Stage

Delete

Help

Settings

Sample Volume (µL):

25

Run Mode

Standard 7500

Data Collection:

Stage 2, Step 2 (60.0 @ 1:00)

Ready

Running MRSA.sds

NUM

start

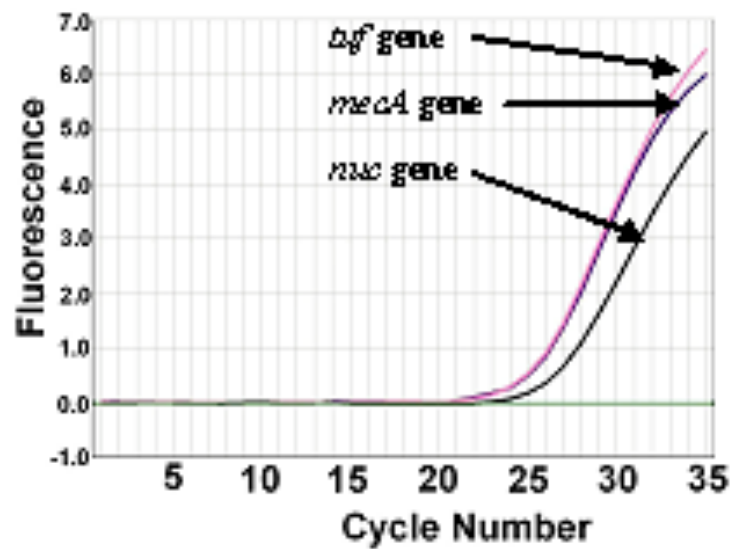
Removable Disk (F:)

Removable Disk (F:)

7500 System SDS Sof ...

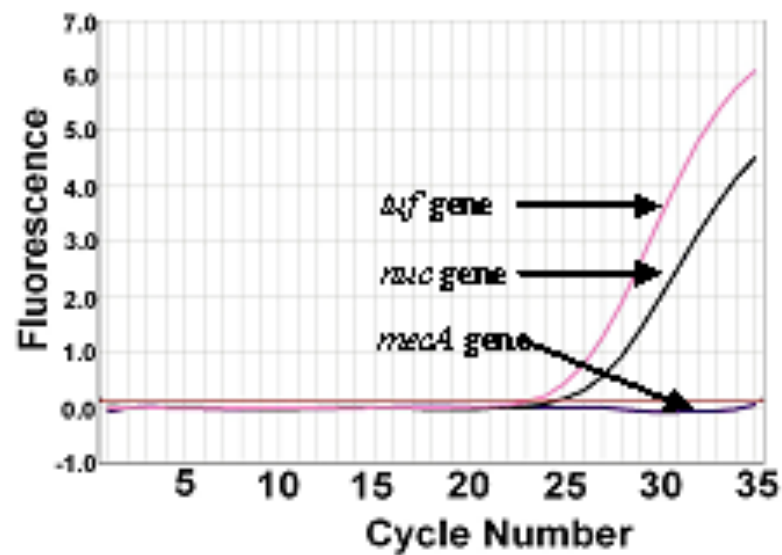
untitled - Paint

3:15 PM



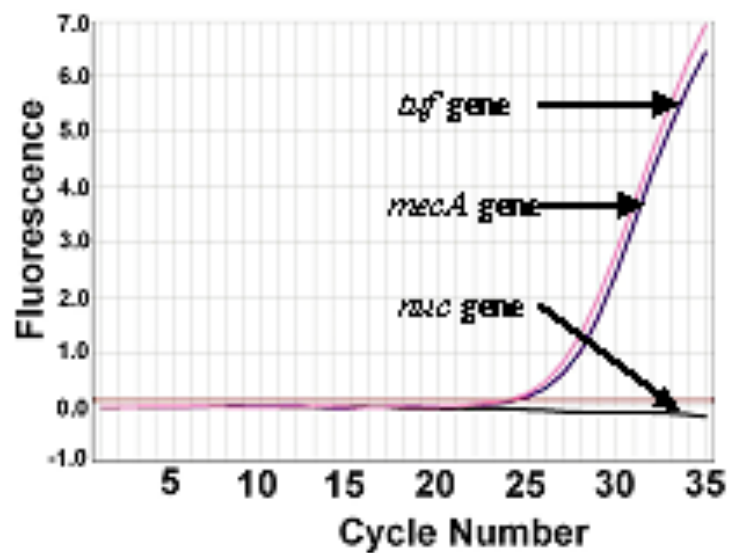
A

MRSA



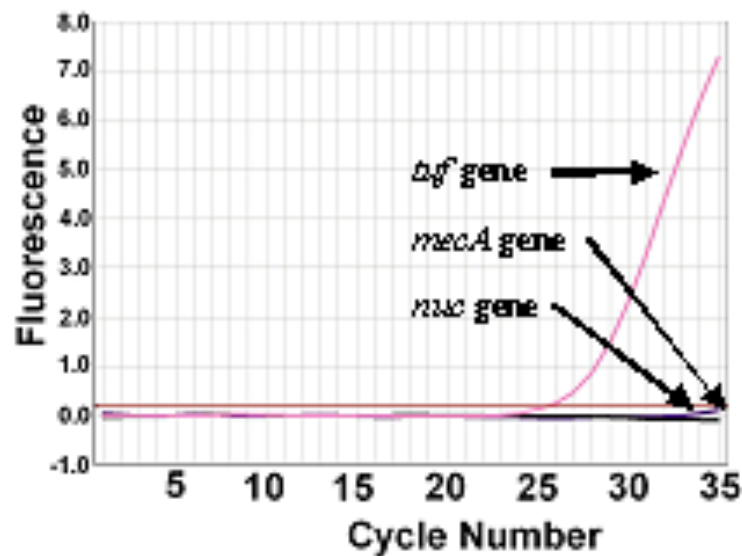
B

MSSA



C

MRCoNS



D

MSCoNS

Mikroorganizmalar

Tripleks PCR sonucu

tuf

nuc

mecA

MRSA NCTC10442, N315, 85/2082, JCSC4744, WIS (WBG8318)

+

+

+

S. aureus ATCC25923, ATCC29213

+

+

0

S. hominis ATCC700236; *S. epidermidis* ATCC35984

+

0

+

S. warneri ATCC25614; *S. simulans* ATCC27848; *S. haemolyticus* ATCC29970; *S. capitis* ATCC27840; *S. lugdunensis* ATCC43809; *S. saprophyticus* ATCC15305; *S. sciuri* ATCC29061

+

0

0

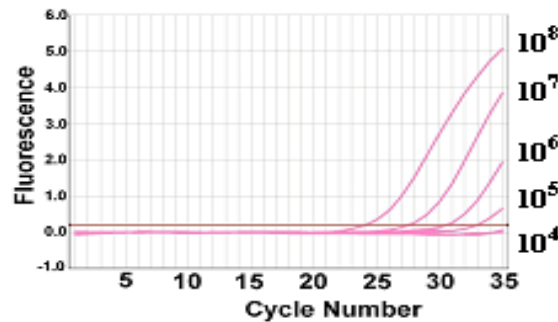
Enterococcus casseliflavus ATCC25788; *Enterococcus gallinarum* GS; *Enterococcus faecalis* ATCC27270; *Enterococcus faecium* B7641; *Streptococcus pneumoniae* NCTC12695; *Streptococcus pyogenes* NCTC12696; *Acinetobacter haemolyticus* ATCC19002; *Acinetobacter septicus* DSM19415; *Pseudomonas aeruginosa* ATCC27853; *Enterobacter aerogenes* ATCC13048; *Escherichia coli* ATCC35218; *Klebsiella pneumoniae* ATCC13883; *Salmonella typhimurium* NCTC12023

0

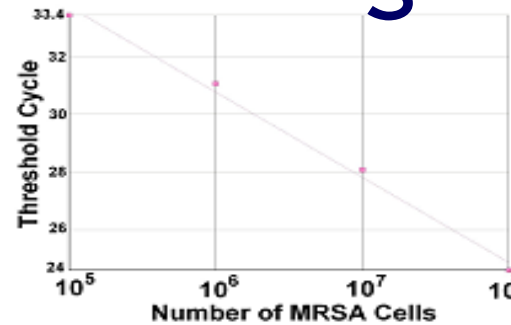
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Analitik Duyarlılık ve Reaksiyon Etkinliđi



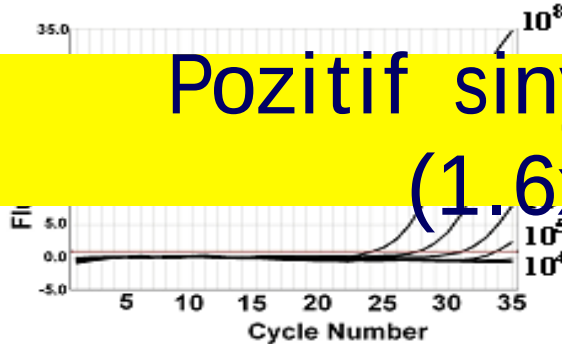
A1



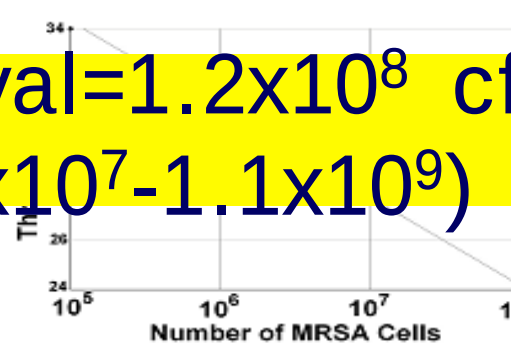
A2

$$RE (tuf) = \%120$$

Pozitif sinyal= 1.2×10^8 cfu/ml
(1.6×10^7 - 1.1×10^9)

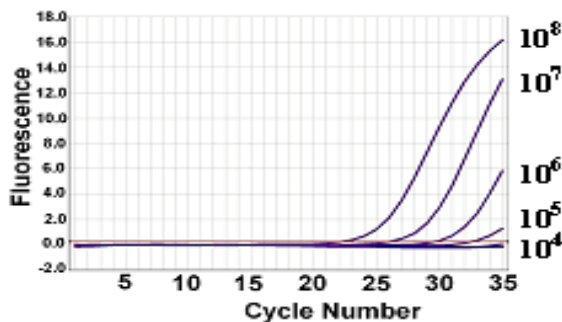


B1

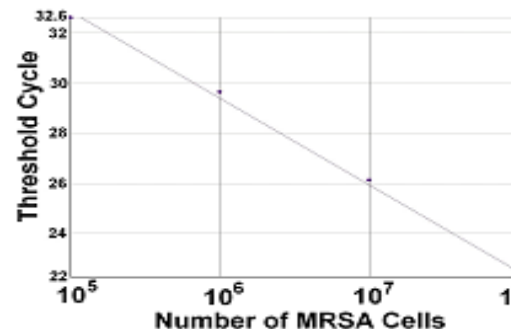


B2

$$RE (mecA) = \%90$$



C1



$$\text{Reaksiyon etkinliđi} = 10^{(-1/\text{slope})} - 1$$



Değişken	Tespit edilen örnek sayısı ^a		Toplam örnek sayısı
	Real-time PCR+	Real-time PCR-	
<i>nuc</i> gen ^b			
<i>S. aureus</i>	44	0	44
CoNS	0	284	284
Non-staphylococcal izolat ^c	0	13	13
<i>tuf</i> gen ^d			
<i>S. aureus</i>	44	0	44
CoNS	283	1	284
Non-staphylococcal izolat ^c	0	13	13

b Duyarlılık = %100; özgüllük = % 100

c 10 *Enterococcus faecalis*, 3 *Enterococcus faecium*.

d Duyarlılık = %99.7; özgüllük = % 100

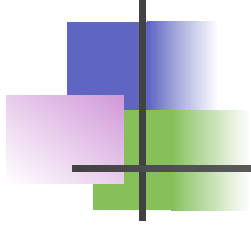


Mikroorganizma	Tespit edilen örnek sayısı ^a		Toplam örnek sayısı
	Real-time PCR+	Real-time PCR-	
Tüm staphylococci (n = 328) ^b			
methicillin-resistant	250	2	252
methicillin-susceptible	1	75	76
<i>S. aureus</i> (n = 44) ^c			
methicillin-resistant	22	0	22
methicillin-susceptible	0	22	22
CoNS (n = 284) ^d			
methicillin-resistant	228	2	230
methicillin-susceptible	1	53	54

b Duyarlılık = %99.2; özgüllük = % 98.7

c Duyarlılık = 100%; özgüllük = % 100

d Duyarlılık = %99.1; özgüllük = % 98.1



- Avantajları
 - En önemli avantajı PCR amplifikasyon öncesi zaman kaybı ve kontaminasyon riski olan DNA elde etme yöntemi olmaması
 - İkincisi her üç gen bölgesini aynı reaksiyonda tespit etmesi
- Dezavantajları
 - MSSA ve MRCoNS karışık örneklerde (kokolonizasyon) yalancı pozitiflik
 - İki CoNS izolat (*S. haemolyticus* ve *S. hominis*) örneği real-time PCR ile *mecA* negatif bulundu ve başka bir direnç mekanizmasının sorumlu olduğu düşünüldü
 - Bir vakada (*S. hominis*) *tuf* geni 1:100 dilüsyonda tespit edilemedi ve sonrasında 1:10 dilüsyonda tespit edildi

Triplex real-time polymerase chain reaction assay for simultaneous detection of *Staphylococcus aureus* and coagulase-negative staphylococci and determination of methicillin resistance directly from positive blood culture bottles

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Received 13 October 2009; accepted 23 November 2009

Abstract

We describe here a 1-step, triplex real-time polymerase chain reaction (PCR) assay for the detection and identification of staphylococci directly from signal-positive blood culture bottles containing Gram-positive cocci in clusters (GPCC). The triplex assay targeted and detected *tuf*, *nuc*, and *mecA* genes in a single tube and had a detection limit of 10^5 CFU/mL for each gene target. A total of 341 GPCC-positive blood culture bottles were collected between November 12, 2008, and August 11, 2009. Among them, 230 methicillin-resistant coagulase-negative staphylococci (CoNS), 54 methicillin-susceptible CoNS, 22 methicillin-resistant *Staphylococcus aureus*, 22 methicillin-susceptible *S. aureus*, and 13 nonstaphylococci species were identified by conventional methods. The results obtained by triplex assay were in agreement with those of conventional methods for *tuf* (99.7%), *nuc* (100.0%), and *mecA* (99.1%), respectively. The triplex assay was found to have sensitivities of 99.7%, 100%, and 99.2% and specificities of 100%, 100%, and 98.7%, respectively, for the *tuf*, *nuc*, and *mecA* gene targets. The triplex real-time PCR assay accurately detects and identifies staphylococci directly from positive blood cultures without nucleic acid extraction prior to amplification.

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KAE'unda Kontaminasyon

- CoNS tüm KAE'ların %30'undan izole edilmektedir
- İzole edilen CoNS'lerin %70-94'ü kontaminanttır
- Hastanemizde 249 epizotun 45'inde (%18.1)'inde gerçek CoNS KAE tespit edildi (GMG,2010)
- Uygunsuz AB kullanımına bağlı (%34'ünde vankomisin)
 - Maliyet
 - Hastaların hastanede kalış süresi
 - Direnç oranları
- Gerçek CoNS KAE'larının tanımlanması etkili ve uygun antibiyotik (glikopeptid) kullanılması için önemlidir



Surveillance Definitions for Primary BSIs, National Nosocomial Infections Surveillance System

Laboratory-Confirmed BSI

Should meet at least one of the following criteria:

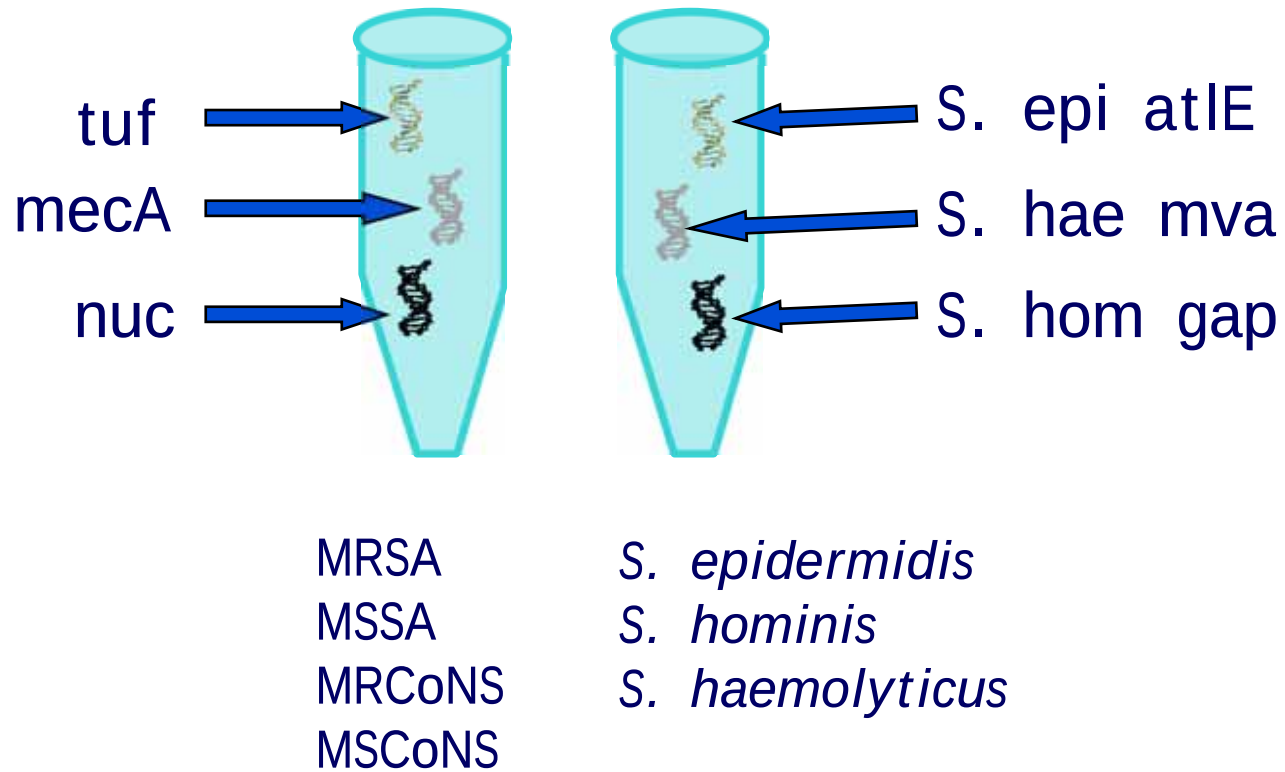
Criterion 1: Patient has a recognized pathogen cultured from one or more blood cultures, and the pathogen cultured from the blood is not related to an infection at another site.

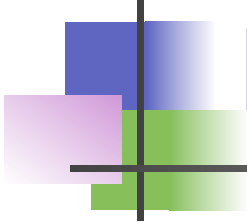
Criterion 2: Patient has at least one of the following signs or symptoms: fever ($>100.4^{\circ}\text{F}$ [$>38^{\circ}\text{C}$]), chills, or hypotension, and at least one of the following:

1. Common skin contaminant (e.g., diphtheroids, *Bacillus* spp., *Propionibacterium* spp., coagulase-negative staphylococci, or micrococci) cultured from two or more blood cultures drawn on separate occasions.
2. Common skin contaminant (e.g., diphtheroids, *Bacillus* spp., *Propionibacterium* spp., coagulase-negative staphylococci, or micrococci) cultured from at least one blood culture from a patient with an intravenous line, and the physician institutes appropriate antimicrobial therapy.
3. Positive antigen test on blood (e.g., *Hemophilus influenzae*, *Streptococcus pneumoniae*, *Neisseria meningitidis*, or group B streptococcus).

and signs and symptoms with positive laboratory results are not related to an infection at another site.

CoNS Çalışması





Fenotipik Yöntem

- 15 Ağustos 2009-11 Şubat 2010 tarihleri arasında 238 gram pozitif kok kümesi (GPKK) görülen kan kültür örneği çalışmaya alındı
- Konvansiyonel yöntem ile
 - 11 MRSA
 - 28 MSSA
 - 176 MRCoNS
 - 21 MSCoNS
 - 2 stafilokok dışı GPKK yapmış organizma

Dizi

Staphylococcus haemolyticus mva gene

☐ sirküler
☒ lineer

Preset Oligo

Tm

PRİMER UZUNLUĞU

20

BAŞLANGIÇ YERİ

1

BİTİŞ YERİ

2685015

ARA

Referans Dizi No:

2

Toplam Dizi Sayısı:

2

Dizi Uzunluğu:

2685015

Amplikon Uzunluğu:

103

1.Primer

ters yap

3' -> 5' YAP

5' gcatgatggttaacagatg 3'

Başlangıç Nükleotidi : 524799

2.Primer

düz yap

3' -> 5' YAP

5' gtgaaatgcaagatgagttc 3'

Başlangıç Nükleotidi : 524882

3.Primer

ters yap

3' -> 5' YAP

5' ctttcattatgtaccaatgggtgaacagc 3'

Başlangıç Nükleotidi : 524820

4.Primer

ters yap

3' -> 5' YAP

5' Başlangıç Nükleotidi :

5.Primer

ters yap

3' -> 5' YAP

5' Başlangıç Nükleotidi :

6.Primer

ters yap

3' -> 5' YAP

5' Başlangıç Nükleotidi :

DİZİ ARA

DİZİ GÖSTER

PRİMER ANALİZ

HESAPLAMALAR

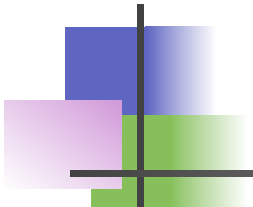
YENİ DİZİ GİRİŞİ

PRİMERLER

ENZİM KESİMİ

ÇIKIŞ

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 ATAGCTGAAAAATATGACATCACGcgtaaatgcaagatgagtttcGCAATCATTCACAAGCTAAAGCAGCTAAAG



Hedef gen	Primerler	Proplar	Genbank No
<i>atIE</i>	5'-ggaggaactaataataagttaactg -3', 5'-gtcataaacagttgtatataagcc -3'	5'-fam-ctgctaatacgtggtgttgctcaaattaa a-bhq1-3'	AJ887986 AJ887985 AJ887984 AJ887983
<i>gap</i>	5'-tagatggatctgaaacagtagtat -3' 5'-ccttcaacaataccaaattcgtc -3	5'-tr-aggtgcttcattgtactacaaactcattg -bhq1-3'	DQ321688
<i>mva</i>	5'-tatgcatgatggtttaacagatg -3' 5'-gaactcatcttgcatttcac -3'	5'-v1c-ctttcattatgtaccaatgggtgtaacagc bhq2-3'	AP006716 AF290088

7500 System SDS Software - [MRSA.sds (Standard Curve)]

FileViewToolsInstrumentAnalysisWindowHelp

Start

Stop

Disconnect

Extend...

Estimated Time Remaining (hh:mm):
01:23

Status:
Running...

Temperature

Sample:	24	Heat Sink:	29
Cover:	104	Block:	25

Cycle

Stage:	1	Rep:	1
Time (mm:ss):	00:00	Step:	1
State: Ramping...			

Thermal Cycler Protocol

Thermal Profile

Auto Increment

Ramp Rate

Stage 1

Stage 2

Reps: 1

Reps: 35

95.0

95.0

15:00

0:15

60.0

1:00

Add Cycle

Add Hold

Add Step

Add Dissociation Stage

Delete

Help

Settings

Sample Volume (µL): 25

Run Mode: Standard 7500

Data Collection: Stage 2, Step 2 (60.0 @ 1:00)

Ready

Running MRSA.sds

NUM

start

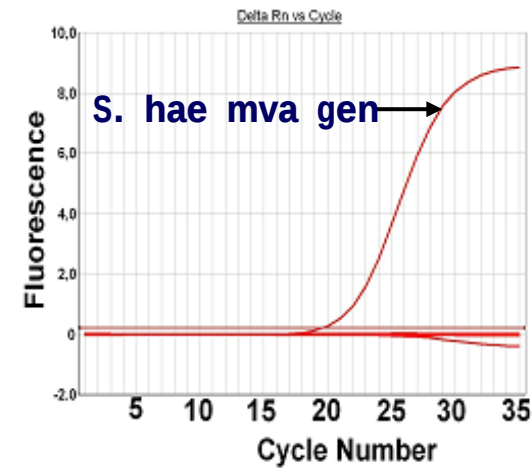
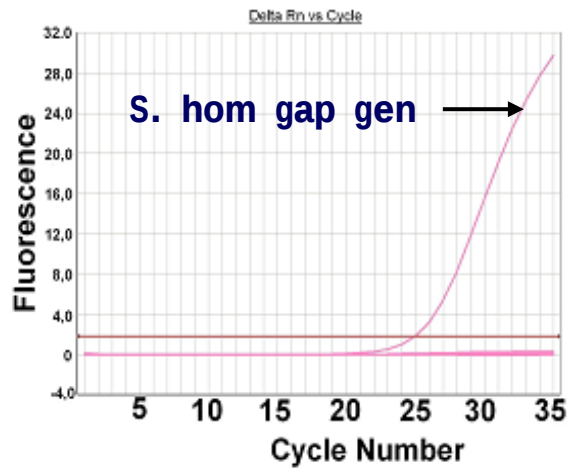
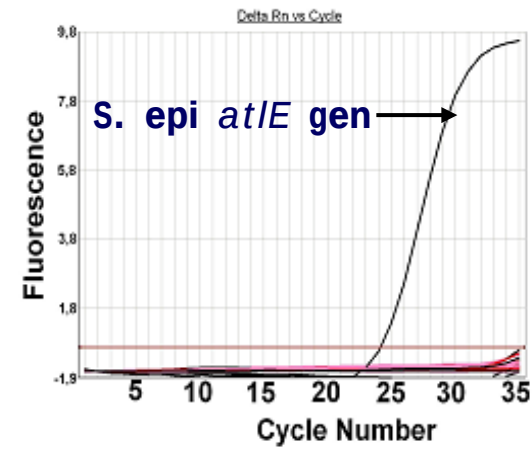
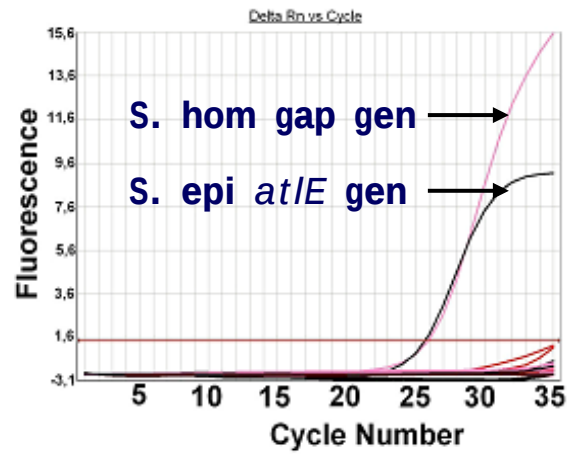
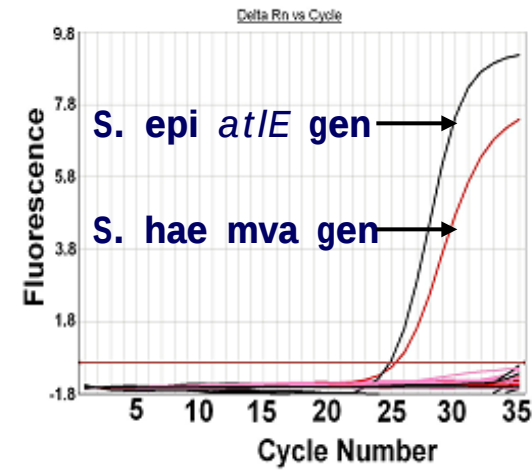
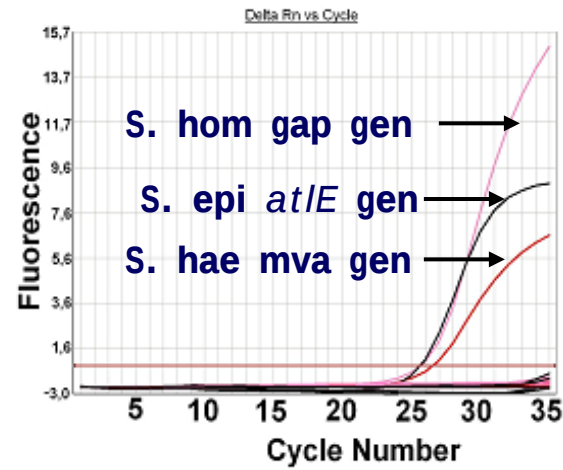
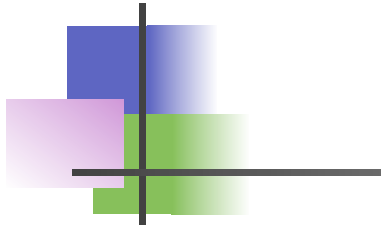
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Removable Disk (F:)

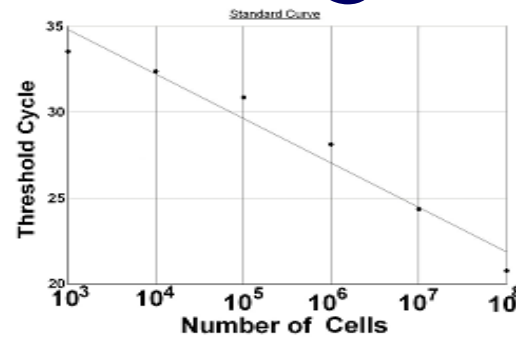
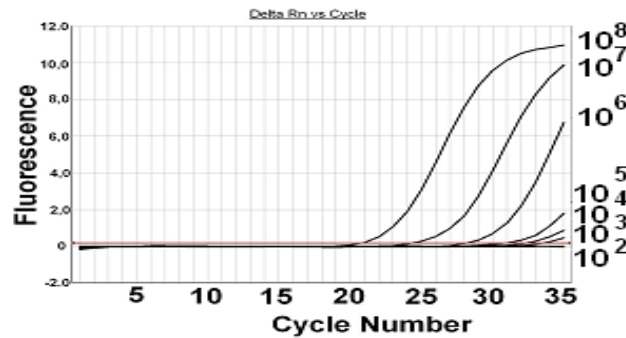
7500 System SDS Sof ...

untitled - Paint

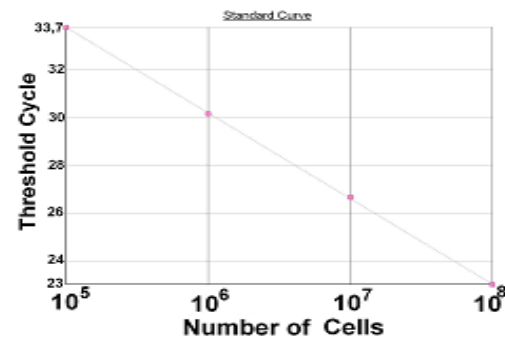
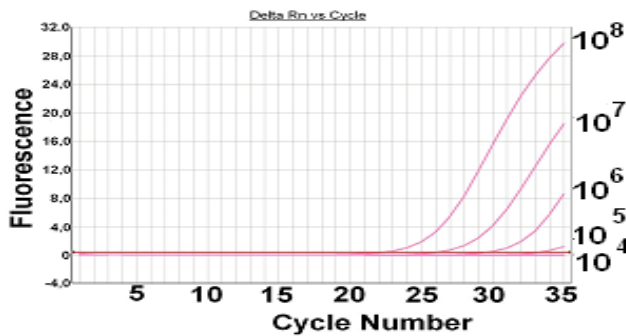
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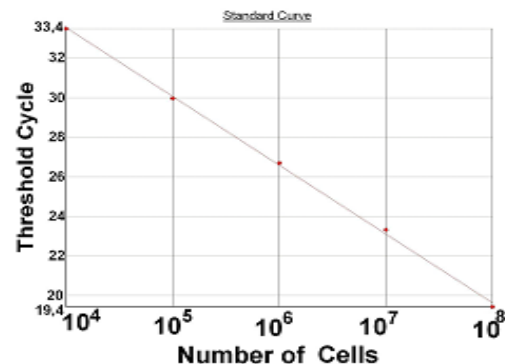
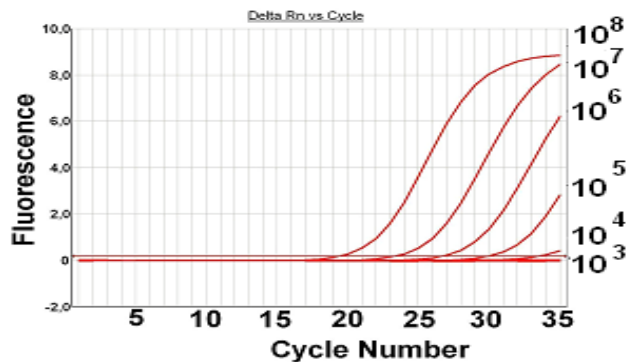
Analitik Duyarlılık ve Reaksiyon Etkinliği



$$RE (et/A) = \%143$$



$$RE (gap) = \%93$$



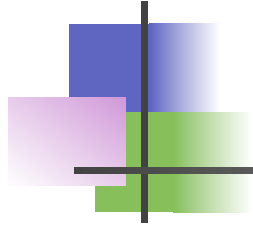
$$RE (mva) = \%90$$

$$\text{Reaksiyon etkinliği} = 10^{(-1/\text{slope})} - 1$$

Mikroorganizmalar

Tripleks PCR sonucu

	<i>atfE</i>	<i>mva</i>	<i>gap</i>
<i>S. epidermidis</i> ATCC35984	+	0	0
<i>S. hominis</i> ATCC700236	0	0	+
<i>S. haemolyticus</i> ATCC29970	0	+	0
MRSA NCTC10442, N315	0	0	0
<i>S. aureus</i> ATCC25923, ATCC29213	0	0	0
<i>S. warneri</i> ATCC25614; <i>S. simulans</i> ATCC27848; <i>S. capitis</i> ATCC27840; <i>S. lugdunensis</i> ATCC43809; <i>S. saprophyticus</i> ATCC15305; <i>S. sciuri</i> ATCC29061	0	0	0
<i>Enterococcus casseliflavus</i> ATCC25788; <i>Enterococcus gallinarum</i> GS; <i>Enterococcus faecalis</i> ATCC27270; <i>Enterococcus faecium</i> B7641; <i>Streptococcus pneumoniae</i> NCTC12695; <i>Streptococcus pyogenes</i> NCTC12696; <i>Acinetobacter haemolyticus</i> ATCC19002; <i>Acinetobacter septicus</i> DSM19415; <i>Pseudomonas aeruginosa</i> ATCC27853; <i>Enterobacter aerogenes</i> ATCC13048; <i>Escherichia coli</i> ATCC35218; <i>Klebsiella pneumoniae</i> ATCC13883	0	0	0



Mikroorganizmalar (Fenotipik Yöntem) Phenix 0.5 McFarland	<i>S. epidermidis</i> <i>atfE</i> gen		<i>S. hominis</i> <i>gap</i> gen		<i>S. haemolyticus</i> <i>mva</i> gen		Mikroroganizmalar (moleküler yöntem)
	PCR+	PCR—	PCR+	PCR—	PCR+	PCR—	
<i>S. epidermidis</i> (n=120)	107	13	21	99	2	118	<i>S.epidermidis</i> (n=107) <i>S.hominis</i> (n=11) <i>S.epidermidis</i> + <i>S.hominis</i> (n=9) <i>S.epidermidis</i> + <i>S.haemolyticus</i> (n=1) <i>S. hominis</i> + <i>S.haemolyticus</i> (n=1) Negatif (n=2)
<i>S. hominis</i> (n=64)	4	60	64	0	0	64	<i>S.hominis</i> (n=60) <i>S.hominis</i> + <i>S.epidermidis</i> (n=4)
<i>S. haemolyticus</i> (n=17)	1	16	1	16	17	0	<i>S.haemolyticus</i> (n=15) <i>S.haemolyticus</i> + <i>S.epidermidis</i> (n=1) <i>S.haemolyticus</i> + <i>S.hominis</i> (n=1)
*Diğer (n=6)	0	6	0	6	0	6	Negatif (n=6)



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0095-1137/07/\$08.00+0 doi:10.1128/JCM.01847-07
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Vol. 45, No. 12

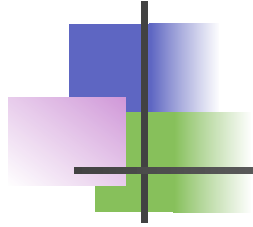
Letters to the Editor

Evaluation of the Inoculation Procedure Using a 0.25 McFarland Standard for the BD Phoenix Automated Microbiology System[▽]

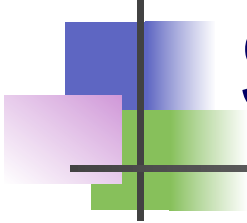
^a The 132 clinical strains were 55 *Enterobacteriaceae*, 31 *Pseudomonaceae*, 25 staphylococci, and 21 enterococci. Discordant IDs were tested by API strips (API-20E, 32-STREP, and 32-STAPH; bioMérieux, Marcy l'Etoile, France), and the API result was used to select or adjudicate the correct ID result.

The performance of the low-inoculum-density method based on presented results has allowed us to start to use this approach routinely in our laboratory.

J.-L. Donay
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Mikroorganizmalar (Fenotipik Yöntem) Phoenix 0.25 McFarland	<i>S. epidermidis</i> <i>atlE</i> gen		<i>S. hominis</i> <i>sodA</i> gen		<i>S. haemolyticus</i> <i>mva</i> gen		Mikroorganizmalar (moleküler yöntem)
	PCR+	PCR—	PCR+	PCR—	PCR+	PCR—	
<i>S. epidermidis</i> (n=109)	107	2	10	99	2	107	<i>S.epidermidis</i> (n=107) <i>S.hominis</i> (n=0) <i>S.epidermidis</i> + <i>S.hominis</i> (n=9) <i>S.epidermidis</i> + <i>S.haemolyticus</i> (n=1) <i>S. hominis</i> + <i>S.haemolyticus</i> (n=1) Negatif (n=2)
<i>S. hominis</i> (n=75)	4	71	75	0	0	75	<i>S.hominis</i> (n=71) <i>S.epidermidis</i> + <i>S.hominis</i> (n=4)
<i>S. haemolyticus</i> (n=17)	1	16	1	16	17	0	<i>S.haemolyticus</i> (n=15) <i>S.haemolyticus</i> + <i>S.epidermidis</i> (n=1) <i>S.haemolyticus</i> + <i>S.hominis</i> (n=1)
*Diğer (n=6) * <i>S.simulans</i> , <i>S.capitis</i> (n=2), <i>S.saprophyticus</i> (n=2), <i>S.equorum</i>	0	6	0	6	0	6	Negatif (n=6)



Sonuç

- İkili multipleks real-time PCR ile kan kültürü örneklerinden 83 dk'da
 - MRSA ve MSSA
 - MR *S. epidermidis* ve MS *S. epidermidis*
 - MR *S. hominis* ve MS *S. hominis*
 - MR *S. haemolyticus* ve MS *S. haemolyticus*
- Karışık örneklerin tanımlayabilmektedir
- Phoenix sistemi ile CoNS tanımlanmasında düşük inokulum daha iyi sonuç vermektedir

Gülhane Mikrobiyoloji Günleri

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