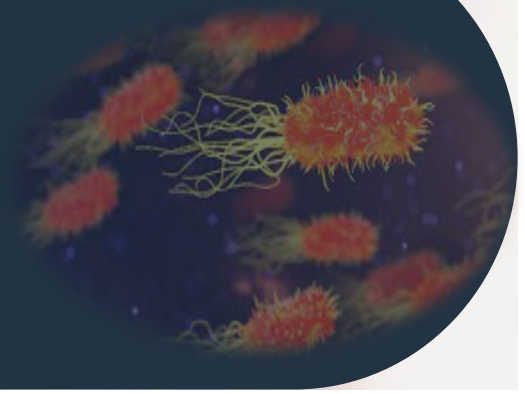
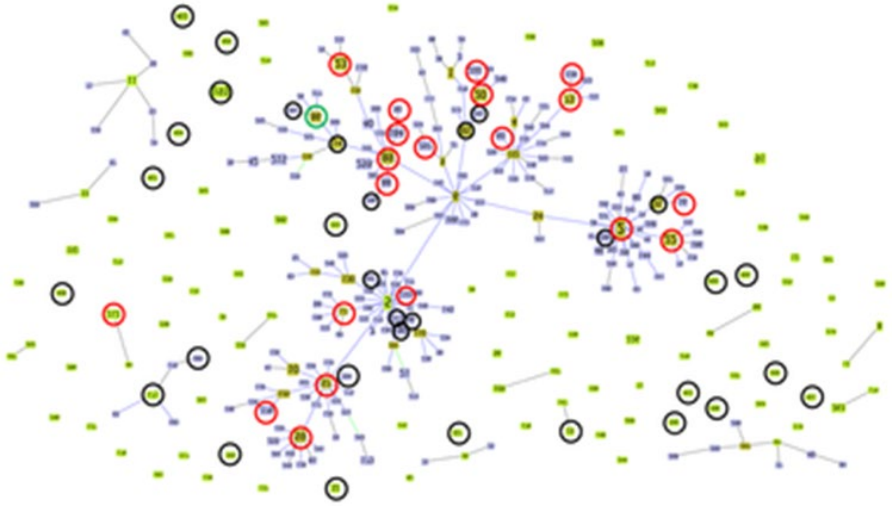
Dirençli Gram Negatif Enfeksiyon Yönetiminde Ortak Adımlar

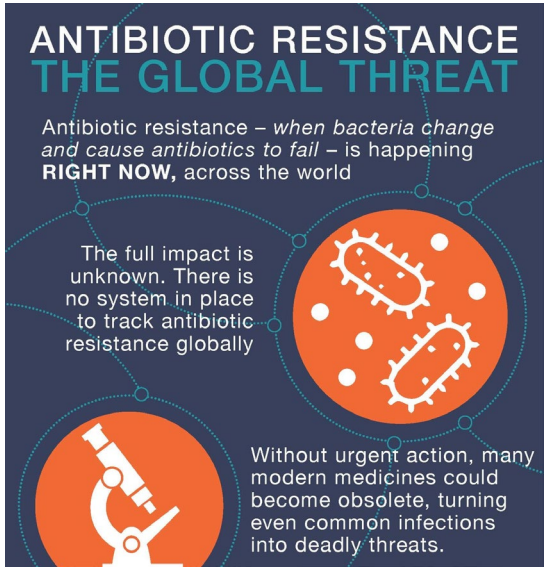


Barış Otlu



Dünyanın Problemleri

- İnsanlığın geleceğini tehdit eden en önemli üç problem;
  - İklim değişikliği
  - Silahlanma yarışı
  - Antimikrobiyal direnç

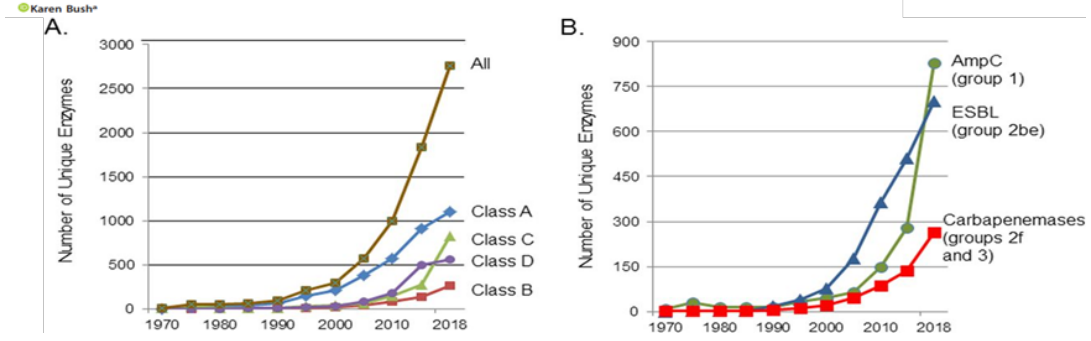


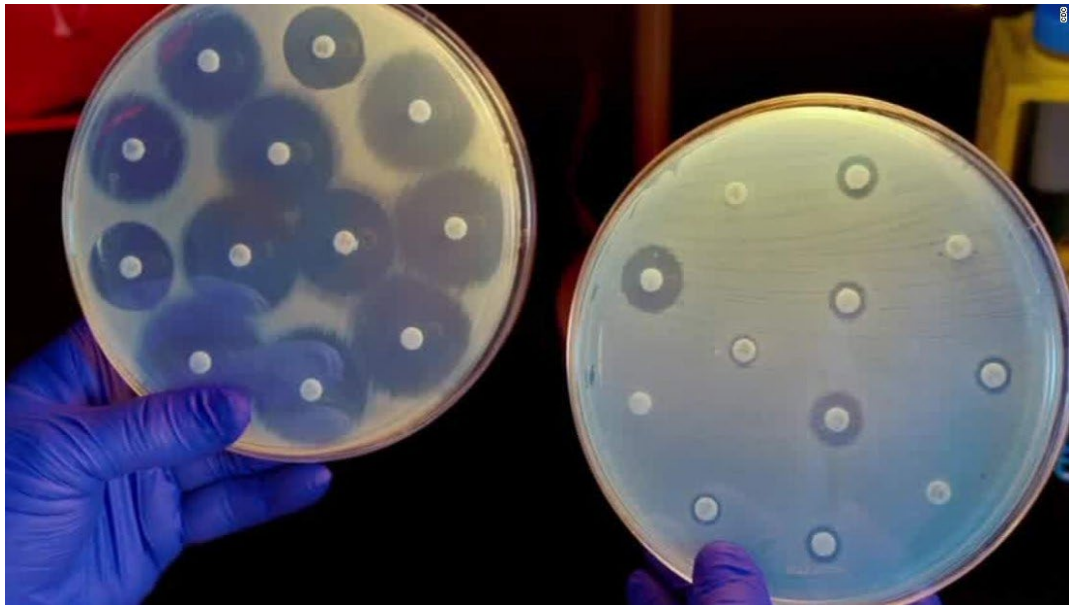
Antimicrobial Agents and Chemotherapy®

MINIREVIEW

Past and Present Perspectives on β-Lactamases

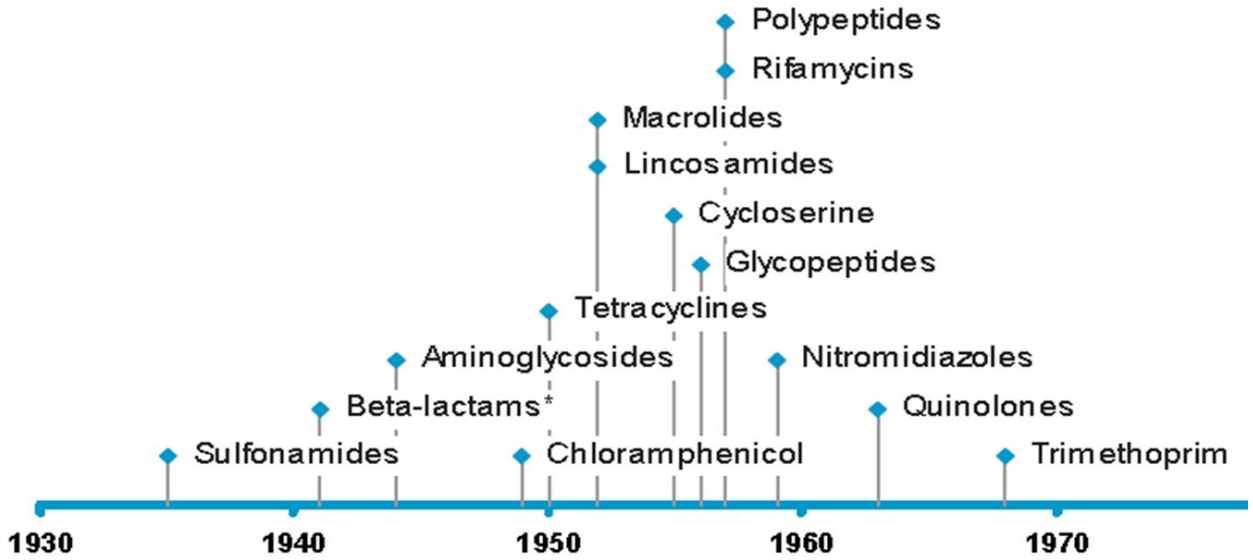
Karen Bush*





- Yeni antimikrobiyal üretilmiyor.

  Elde kalan sınırlı kaynağı daha etkin kullanmak için tüm imkanlar seferber edilmeli.



Discoveries (Craiova). 2019 Dec 31;7(4):e102. doi: 10.15190/d.2019.15.

Kazanılan her direnç mekanizması direnç havuzuna eklendi

- Antimikrobiyal direnç referans gen veri tabanı
- Patojen izolatlardan elde edilen 7185 kazanılmış direnç geni

Bacterial Antimicrobial Resistance Reference Gene Database Accession: PRJNA313047 ID: 313047

This Bioproject contains annotated sequence records for representative DNA sequences that encode proteins conferring or contributing to resistance to various antibiotics. More...

NIH U.S. National Library of Medicine
National Center for Biotechnology Information

Log in

Health > Pathogen Detection > Reference Gene Catalog Help

Search

db version: 2020-09-30.1 Changelog

Bacterial Antimicrobial Resistance Reference Gene Database

Filters

Page 1 of 360 Records per Page 20 Choose columns Download Displaying 1 - 20 of 7185

#	allele	gene family	product name	scope	type	subtype	class	subclass	refseq protein	refseq nucleoti...	genbank protein	genbank nucle...	curated refseq...
1	16S_A523C	16S	16S ribosomal RNA	core	AMR	POINT	AMINOGLYCOSIDE	STREPTOMYCIN		NC_000913.3		U00096.3	No
2	16S_G527T	16S	16S ribosomal RNA	core	AMR	POINT	AMINOGLYCOSIDE	STREPTOMYCIN		NC_000913.3		U00096.3	No
3	16S_C528T	16S	16S ribosomal RNA	core	AMR	POINT	AMINOGLYCOSIDE	STREPTOMYCIN		NC_000913.3		U00096.3	No
4	16S_A794G	16S	16S ribosomal RNA	core	AMR	POINT	AMINOGLYCOSIDE	KASUGAMYCIN		NC_000913.3		U00096.3	No
5	16S_A794T	16S	16S ribosomal RNA	core	AMR	POINT	AMINOGLYCOSIDE	KASUGAMYCIN		NC_000913.3		U00096.3	No
6	16S_G926A	16S	16S ribosomal RNA	core	AMR	POINT	AMINOGLYCOSIDE	KASUGAMYCIN		NC_000913.3		U00096.3	No
7	16S_G926C	16S	16S ribosomal RNA	core	AMR	POINT	AMINOGLYCOSIDE	KASUGAMYCIN		NC_000913.3		U00096.3	No
8	16S_G926T	16S	16S ribosomal RNA	core	AMR	POINT	AMINOGLYCOSIDE	KASUGAMYCIN		NC_000913.3		U00096.3	No
9	16S_A964G	16S	16S ribosomal RNA	core	AMR	POINT	TETRACYCLINE	TETRACYCLINE		NC_000913.3		U00096.3	No
10	16S_G1053A	16S	16S ribosomal RNA	core	AMR	POINT	TETRACYCLINE	TETRACYCLINE		NC_000913.3		U00096.3	No
11	16S_C1054T	16S	16S ribosomal RNA	core	AMR	POINT	TETRACYCLINE	TETRACYCLINE		NC_000913.3		U00096.3	No
12	16S_A1055G	16S	16S ribosomal RNA	core	AMR	POINT	TETRACYCLINE	TETRACYCLINE		NC_000913.3		U00096.3	No
13	16S_G1058C	16S	16S ribosomal RNA	core	AMR	POINT	TETRACYCLINE	TETRACYCLINE		NC_000913.3		U00096.3	No
14	16S_G1064A	16S	16S ribosomal RNA	core	AMR	POINT	AMINOGLYCOSIDE	SPECTINOMY...		NC_000913.3		U00096.3	No
15	16S_G1064C	16S	16S ribosomal RNA	core	AMR	POINT	AMINOGLYCOSIDE	SPECTINOMY...		NC_000913.3		U00096.3	No
16	16S_G1064T	16S	16S ribosomal RNA	core	AMR	POINT	AMINOGLYCOSIDE	SPECTINOMY...		NC_000913.3		U00096.3	No
17	16S_C1066T	16S	16S ribosomal RNA	core	AMR	POINT	AMINOGLYCOSIDE	SPECTINOMY...		NC_000913.3		U00096.3	No
18	16S_G1068A	16S	16S ribosomal RNA	core	AMR	POINT	AMINOGLYCOSIDE	SPECTINOMY...		NC_000913.3		U00096.3	No
19	16S_C1192A	16S	16S ribosomal RNA	core	AMR	POINT	AMINOGLYCOSIDE	SPECTINOMY...		NC_000913.3		U00096.3	No
20	16S_C1192G	16S	16S ribosomal RNA	core	AMR	POINT	AMINOGLYCOSIDE	SPECTINOMY...		NC_000913.3		U00096.3	No

Kazanılan her direnç mekanizması direnç havuzuna eklendi

- Antimikrobiyal direnç referans gen veri tabanı
- Patojen izolatlardan elde edilen 8201 kazanılmış direnç geni

Bacterial Antimicrobial Resistance Reference Gene Database

Accession: PRJNA313047 ID: 313047

This Bioproject contains annotated sequence records for representative DNA sequences that encode proteins conferring or contributing to resistance to various antibiotics. More...

Filters

Page 2 of 3 | Records per Page 20 | Choose columns | Download | Displaying 21 - 40 of 46

#	Allele	Gene family	Product name	Scope	Type	Subtype	Class	Subclass	RefSeq pr...	RefSeq nu...	GenBank p...	GenBank ...	Curated R...
21	blaOXA-788	blaOXA	OXA-48 family class D beta-lactamase OXA-788	core	AMR	AMR	BETA-LAC...	BETA-LAC...	WP_13651...	NG_06474...	QAT97596.1	MK416209.1	No
22	blaOXA-793	blaOXA	OXA-48 family class D beta-lactamase OXA-793	core	AMR	AMR	BETA-LAC...	BETA-LAC...	WP_13651...	NG_06475...	QBA86170.1	MK469978.1	No
23	blaOXA-833	blaOXA	OXA-48 family class D beta-lactamase OXA-833	core	AMR	AMR	BETA-LAC...	BETA-LAC...	WP_14042...	NG_06544...	QCY50072.1	MK976702.1	No
24	blaOXA-894	blaOXA	OXA-48 family class D beta-lactamase OXA-894	core	AMR	AMR	BETA-LAC...	BETA-LAC...	WP_14437...	NG_06675...	QFE31714.1	MN525568...	No
25	blaOXA-918	blaOXA	OXA-48 family class D beta-lactamase OXA-918	core	AMR	AMR	BETA-LAC...	BETA-LAC...	WP_17928...	NG_07018...	QJX44697.1	MT463291.1	No
26	blaOXA-920	blaOXA	OXA-48 family class D beta-lactamase OXA-920	core	AMR	AMR	BETA-LAC...	BETA-LAC...	WP_17928...	NG_07018...	QKF95718.1	MT520791.1	No
27	blaOXA-922	blaOXA	OXA-48 family class D beta-lactamase OXA-922	core	AMR	AMR	BETA-LAC...	BETA-LAC...	WP_18833...	NG_07074...	QKV50750.1	MT636504.1	No
28	blaOXA-923	blaOXA	OXA-48 family class D beta-lactamase OXA-923	core	AMR	AMR	BETA-LAC...	BETA-LAC...	WP_17928...	NG_07018...	QLC28678.1	MT675122.1	No
29	blaOXA-924	blaOXA	OXA-48 family class D beta-lactamase OXA-924	core	AMR	AMR	BETA-LAC...	BETA-LAC...	WP_17928...	NG_07018...	QLC28679.1	MT675123.1	No
30	blaOXA-929	blaOXA	OXA-48 family class D beta-lactamase OXA-929	core	AMR	AMR	BETA-LAC...	BETA-LAC...	WP_18833...	NG_07075...	QNL15887.1	MK989990.1	No
31	blaOXA-933	blaOXA	OXA-48 family class D beta-lactamase OXA-933	core	AMR	AMR	BETA-LAC...	BETA-LAC...	WP_23186...	NG_07798...	QOI60719.1	MW07310...	No
32	blaOXA-934	blaOXA	OXA-48 family class D beta-lactamase OXA-934	core	AMR	AMR	BETA-LAC...	BETA-LAC...	WP_23186...	NG_07798...	QOI60720.1	MW07310...	No
33	blaOXA-10...	blaOXA	OXA-48 family carbapenem-hydrolyzing class D beta-lactamase OXA-1038	core	AMR	AMR	BETA-LAC...	BETA-LAC...	WP_23186...	NG_07804...	UBJ91323.1	OK180617.1	No
34	blaOXA-10...	blaOXA	OXA-48 family carbapenem-hydrolyzing class D beta-lactamase OXA-1039	core	AMR	AMR	BETA-LAC...	BETA-LAC...	WP_03741...	NG_07804...	UBJ91324.1	OK180618.1	No
35	blaOXA-162	blaOXA	OXA-48 family carbapenem-hydrolyzing class D beta-lactamase OXA-162	core	AMR	AMR	BETA-LAC...	CARBAPE...	WP_06061...	NG_04946...	ADG27454.1	HM015773...	No
36	blaOXA-163	blaOXA	OXA-48 family extended-spectrum class D beta-lactamase OXA-163	core	AMR	AMR	BETA-LAC...	CEPHALO...	WP_06313...	NG_04946...	ADY06444.1	HQ700343.1	No
37	blaOXA-181	blaOXA	OXA-48 family carbapenem-hydrolyzing class D beta-lactamase OXA-181	core	AMR	AMR	BETA-LAC...	CARBAPE...	WP_01506...	NG_04948...	AEP16366.1	JN205800.1	No
38	blaOXA-199	blaOXA	OXA-48 family carbapenem-hydrolyzing class D beta-lactamase OXA-199	core	AMR	AMR	BETA-LAC...	CARBAPE...	WP_06386...	NG_04949...	AFC95894.1	JN704570.1	No
39	blaOXA-204	blaOXA	OXA-48 family carbapenem-hydrolyzing class D beta-lactamase OXA-204	core	AMR	AMR	BETA-LAC...	CARBAPE...	WP_03249...	NG_04950...	AFU91598.1	JQ809466.1	No
40	blaOXA-232	blaOXA	OXA-48 family carbapenem-hydrolyzing class D beta-lactamase OXA-232	core	AMR	AMR	BETA-LAC...	CARBAPE...	WP_04390...	NG_04952...	AGD91915.1	JX423831.1	No

Link to Protein

Feedback

Kazanılan her direnç mekanizması direnç havuzuna eklendi

- Antimikrobiyal direnç referans gen veri tabanı
- Patojen izolatlardan elde edilen 9342 kazanılmış direnç geni. (41.TMC Kongresi)

Bacterial Antimicrobial Resistance Reference Gene Database Accession: PRJNA313047 ID: 313047

This Bioproject contains annotated sequence records for representative DNA sequences that encode proteins conferring or contributing to resistance to various antibiotics. More...

Filters

Page 1 of 468 | Records per Page 20 | Choose columns | Download | Displaying 1 - 20 of 9341

#	Allele	Gene family	Product name	Scope	Type	Subtype	Class	Subclass	RefSeq pr...	RefSeq nu...	GenBank p...	GenBank ...	Curated R...	Links
1		aac(2')-I(A...	aminoglycoside N-acetyltransferase AAC(2')-I(A267)	core	AMR	AMR	AMINOGLY...	GENTAMI...	WP_02529...	NG_24215...	CDI94966.1	HG530068.1	No	
2		aac(2')-IIa	kasugamycin N-acetyltransferase AAC(2')-IIa	core	AMR	AMR	AMINOGLY...	KASUGAM...	WP_06383...	NG_04722...	BAM16262.1	AB669090.1	No	
3		aac(2')-IIb	kasugamycin N-acetyltransferase AAC(2')-IIb	core	AMR	AMR	AMINOGLY...	KASUGAM...	WP_07122...	NG_05567...	APB03221.1	KX531051.1	No	
4		aac(2')-Ia	aminoglycoside N-acetyltransferase AAC(2')-Ia	core	AMR	AMR	AMINOGLY...	GENTAMI...	WP_00491...	NG_04722...	AAA03550.1	L06156.2	No	PubChem
5		aac(2')-Ib	aminoglycoside N-acetyltransferase AAC(2')-Ib	core	AMR	AMR	AMINOGLY...	GENTAMI...	WP_00388...	NG_04722...	AAC44793.1	U41471.1	No	PubChem
6		aac(2')-Ic	aminoglycoside N-acetyltransferase AAC(2')-Ic	core	AMR	AMR	AMINOGLY...	GENTAMI...	WP_00389...	NG_04722...	AAB17563.1	U72714.1	No	PubChem
7		aac(2')-Id	aminoglycoside N-acetyltransferase AAC(2')-Id	core	AMR	AMR	AMINOGLY...	GENTAMI...	WP_01172...	NG_04723...	AAB41701.1	U72743.1	No	PubChem
8		aac(2')-Ie	aminoglycoside N-acetyltransferase AAC(2')-Ie	core	AMR	AMR	AMINOGLY...	GENTAMI...	WP_01090...	NG_05058...	CAR72650.1	FM211192.1	No	
9		aac(3)-C1...	aminoglycoside N-acetyltransferase AAC(3)-C1264	core	AMR	AMR	AMINOGLY...	GENTAMI...	WP_03400...	NG_24215...	EKW62215...	ABKGBU0...	No	
10		aac(3)-C322	aminoglycoside N-acetyltransferase AAC(3)-C322	core	AMR	AMR	AMINOGLY...	GENTAMI...	WP_04406...	NG_24215...	ECI266226...	AAIUPV01...	No	
11		aac(3)-I	AAC(3)-I family aminoglycoside 3-N-acetyltransferase	core	AMR	AMR	AMINOGLY...	GENTAMI...	WP_06384...	NG_04723...	AAK12088.1	AF318077.1	No	
12		aac(3)-I	AAC(3)-I family aminoglycoside 3-N-acetyltransferase	core	AMR	AMR	AMINOGLY...	GENTAMI...	WP_01127...	NG_04723...	CAI46944.1	AJ877225.1	No	
13		aac(3)-I	AAC(3)-I family aminoglycoside 3-N-acetyltransferase	core	AMR	AMR	AMINOGLY...	GENTAMI...	WP_06384...	NG_04724...	CBI71176.1	FN640465.1	No	
14		aac(3)-IIIa	aminoglycoside N-acetyltransferase AAC(3)-IIIa	core	AMR	AMR	AMINOGLY...	GENTAMI...	WP_06384...	NG_04724...	CAA39184.1	X55652.1	No	PubChem
15		aac(3)-IIIb	aminoglycoside N-acetyltransferase AAC(3)-IIIb	core	AMR	AMR	AMINOGLY...	GENTAMI...	WP_05817...	NG_05174...	KSC15183.1	LLLC0100...	No	
16		aac(3)-IIIc	aminoglycoside N-acetyltransferase AAC(3)-IIIc	core	AMR	AMR	AMINOGLY...	GENTAMI...	WP_06384...	NG_04724...	AAA25683.1	L06161.1	No	
17		aac(3)-IIa	aminoglycoside N-acetyltransferase AAC(3)-IIa	core	AMR	AMR	AMINOGLY...	GENTAMI...	WP_06384...	NG_04724...	CAA31895.1	X13543.1	No	
18		aac(3)-IIb	aminoglycoside N-acetyltransferase AAC(3)-IIb	core	AMR	AMR	AMINOGLY...	GENTAMI...	WP_03314...	NG_04724...	AAA26548.1	M97172.1	No	PubChem
19		aac(3)-IIc	aminoglycoside N-acetyltransferase AAC(3)-IIc	core	AMR	AMR	AMINOGLY...	GENTAMI...	WP_06384...	NG_04725...	CAA38525.1	X54723.1	No	
20		aac(3)-IId	aminoglycoside N-acetyltransferase AAC(3)-IId	core	AMR	AMR	AMINOGLY...	GENTAMI...	WP_00055...	NG_04725...	AAN87703.1	AF550415.2	No	

Prefix A7J11

Kazanılan her direnç mekanizması direnç havuzuna eklendi

- Antimikrobiyal direnç referans gen veri tabanı
- Patojen izolatlardan elde edilen 1085 kazanılmış direnç geni. (Bugün)

Bacterial Antimicrobial Resistance Reference Gene Database Accession: PRJNA313047 ID: 313047

This Bioproject contains annotated sequence records for representative DNA sequences that encode proteins conferring or contributing to resistance to various antibiotics. More

db version: 2024-12-18.1 Changelog

Bacterial Antimicrobial Resistance Reference Gene Database

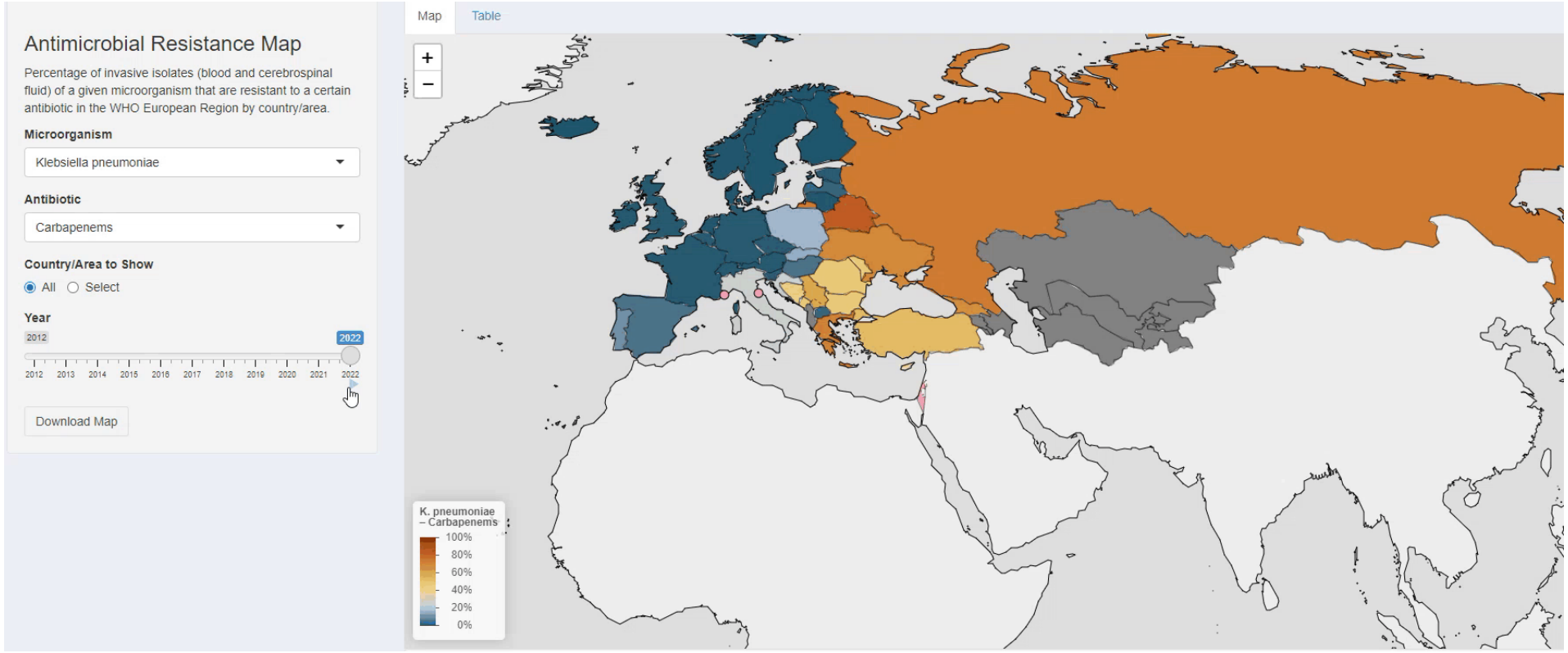
Filters

Page 1 of 543 | Records per Page 20 | Choose columns | Download | Displaying 1 - 20 of 10850

#	Allele	Gene family	Product name	Scope	Type	Subtype	Class	Subclass	RefSeq protein	RefSeq nucle...	GenBank prot...	GenBank nucl...	Curated RefS...	Links
1		aac(2')-I(A267)	aminoglycoside N-acetyltransferase AAC(2')-I(A267)	core	AMR	AMR	AMINOGLYCO...	GENTAMICIN/...	WP_0252979...	NG_242157.1	CDI94966.1	HG530068.1	No	
2		aac(2')-IIa	kasugamycin N-acetyltransferase AAC(2')-IIa	core	AMR	AMR	AMINOGLYCO...	KASUGAMYCIN	WP_0638398...	NG_047225.1	BAM16262.1	AB669090.1	No	
3		aac(2')-IIb	kasugamycin N-acetyltransferase AAC(2')-IIb	core	AMR	AMR	AMINOGLYCO...	KASUGAMYCIN	WP_0712240...	NG_055672.1	APB03221.1	KX531051.1	No	
4		aac(2')-Ia	aminoglycoside N-acetyltransferase AAC(2')-Ia	core	AMR	AMR	AMINOGLYCO...	GENTAMICIN/...	WP_0049183...	NG_047226.1	AAA03550.1	L06156.2	No	PubChem
5		aac(2')-Ib	aminoglycoside N-acetyltransferase AAC(2')-Ib	core	AMR	AMR	AMINOGLYCO...	GENTAMICIN/...	WP_0038816...	NG_047227.1	AAC44793.1	U41471.1	No	PubChem
6		aac(2')-Ic	aminoglycoside N-acetyltransferase AAC(2')-Ic	core	AMR	AMR	AMINOGLYCO...	GENTAMICIN/...	WP_0038998...	NG_047229.1	AAB17563.1	U72714.1	No	PubChem
7		aac(2')-Id	aminoglycoside N-acetyltransferase AAC(2')-Id	core	AMR	AMR	AMINOGLYCO...	GENTAMICIN/...	WP_0117269...	NG_047230.1	AAB41701.1	U72743.1	No	PubChem
8		aac(2')-Ie	aminoglycoside N-acetyltransferase AAC(2')-Ie	core	AMR	AMR	AMINOGLYCO...	GENTAMICIN/...	WP_0109089...	NG_050581.1	CAR72650.1	FM211192.1	No	
9		aac(3)-C1264	aminoglycoside N-acetyltransferase AAC(3)-C1264	core	AMR	AMR	AMINOGLYCO...	GENTAMICIN/...	WP_0340005...	NG_242158.1	EML4797591.1	ABKGBU0300...	No	
10		aac(3)-C322	aminoglycoside N-acetyltransferase AAC(3)-C322	core	AMR	AMR	AMINOGLYCO...	GENTAMICIN/...	WP_0440617...	NG_242159.1	ECI2662265.1	AAIUPV01000...	No	
11		aac(3)-I	AAC(3)-I family aminoglycoside 3-N-acetyltransferase	core	AMR	AMR	AMINOGLYCO...	GENTAMICIN	WP_0638402...	NG_047235.1	AAK12088.1	AF318077.1	No	
12		aac(3)-I	AAC(3)-I family aminoglycoside 3-N-acetyltransferase	core	AMR	AMR	AMINOGLYCO...	GENTAMICIN	WP_0112701...	NG_047237.1	CAI46944.1	AJ877225.1	No	
13		aac(3)-I	AAC(3)-I family aminoglycoside 3-N-acetyltransferase	core	AMR	AMR	AMINOGLYCO...	GENTAMICIN	WP_0638402...	NG_047240.1	CBI71176.1	FN640465.1	No	
14		aac(3)-IIIa	aminoglycoside N-acetyltransferase AAC(3)-IIIa	core	AMR	AMR	AMINOGLYCO...	GENTAMICIN	WP_0638402...	NG_047241.1	CAA39184.1	X55652.1	No	PubChem
15		aac(3)-IIIb	aminoglycoside N-acetyltransferase AAC(3)-IIIb	core	AMR	AMR	AMINOGLYCO...	GENTAMICIN	WP_0581799...	NG_051746.1	KSC15183.1	LLLC0100004...	No	
16		aac(3)-IIIc	aminoglycoside N-acetyltransferase AAC(3)-IIIc	core	AMR	AMR	AMINOGLYCO...	GENTAMICIN	WP_0638402...	NG_047243.1	AAA25683.1	L06161.1	No	
17		aac(3)-IIa	aminoglycoside N-acetyltransferase AAC(3)-IIa	core	AMR	AMR	AMINOGLYCO...	GENTAMICIN	WP_0638402...	NG_047245.1	CAA31895.1	X13543.1	No	
18		aac(3)-IIb	aminoglycoside N-acetyltransferase AAC(3)-IIb	core	AMR	AMR	AMINOGLYCO...	GENTAMICIN	WP_0331470...	NG_047249.1	AAA26548.1	M97172.1	No	PubChem
19		aac(3)-IIc	aminoglycoside N-acetyltransferase AAC(3)-IIc	core	AMR	AMR	AMINOGLYCO...	GENTAMICIN	WP_0638402...	NG_047250.1	CAA38525.1	X54723.1	No	
20		aac(3)-IId	aminoglycoside N-acetyltransferase AAC(3)-IId	core	AMR	AMR	AMINOGLYCO...	GENTAMICIN	WP_0005574...	NG_047251.1	AAN87703.1	AF550415.2	No	

Sürekli Artan Direnç

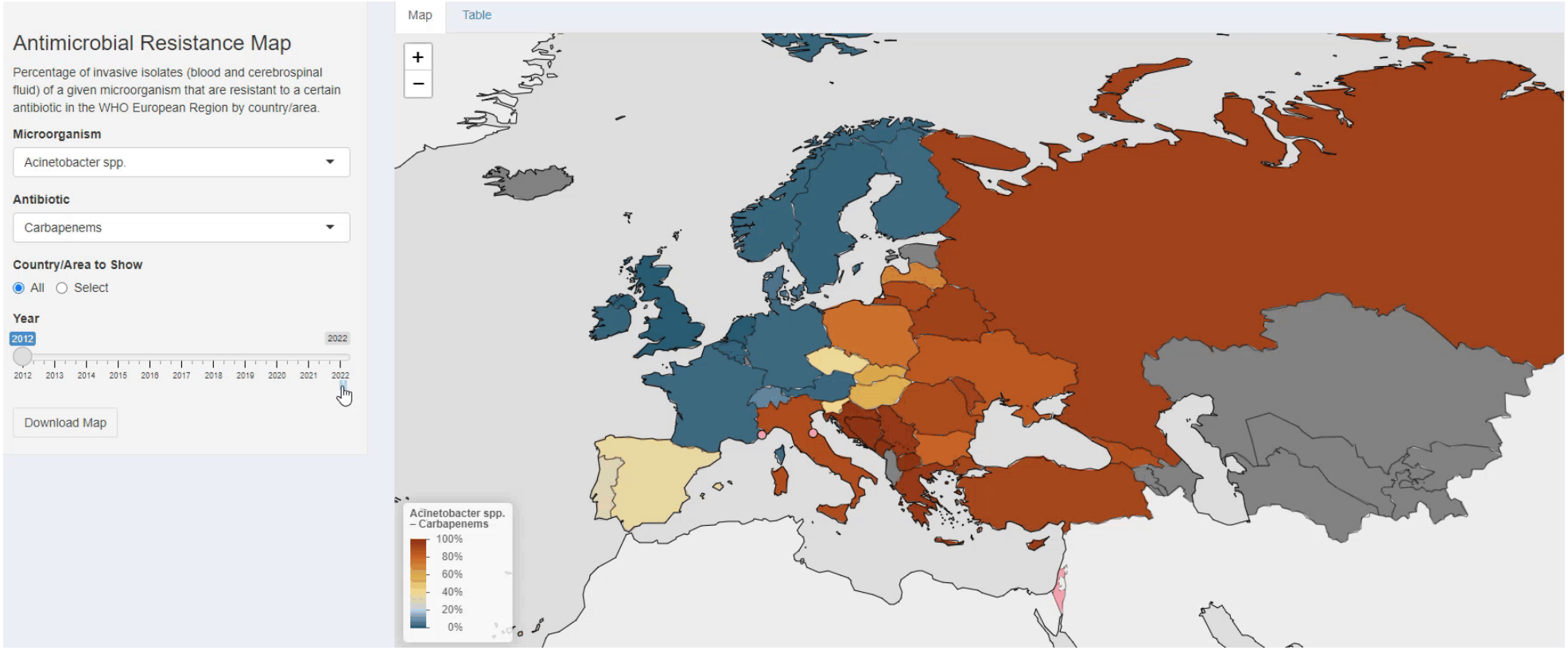
- Antimikrobiyal direnç haritası



Sürekli Artan Direnç

- Antimikrobiyal direnç haritası,

  Acinetobacter spp.'de karbapenem direnci

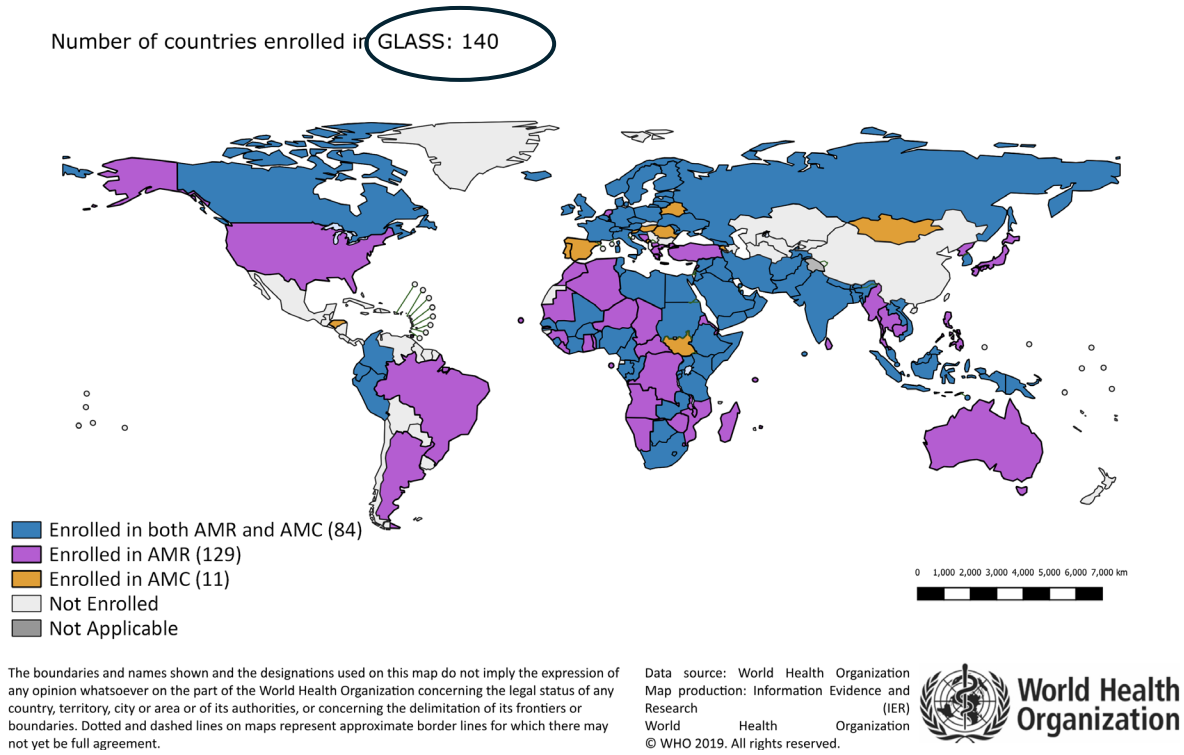


World Health Organization

- GLASS, 2015 yılında WHO tarafından başlatılmış — dünya çapında antimikrobiyal direnç (AMR) izleme ve antimikrobiyal kullanım (AMU) verilerini standart biçimde toplama, analiz etme, paylaşma amaçlı küresel bir sistem.
- Amaç;
  - farklı ülkelerden gelen verileri harmonize etmek
  - direnç yayılımını izlemek
  - antimikrobiyal kullanım trendlerini takip etmek
  - halk sağlığı politikalarını ve kontrol stratejilerini bu verilerle desteklemek.

World Health Organization

GLASS Enrolment Map October 2024

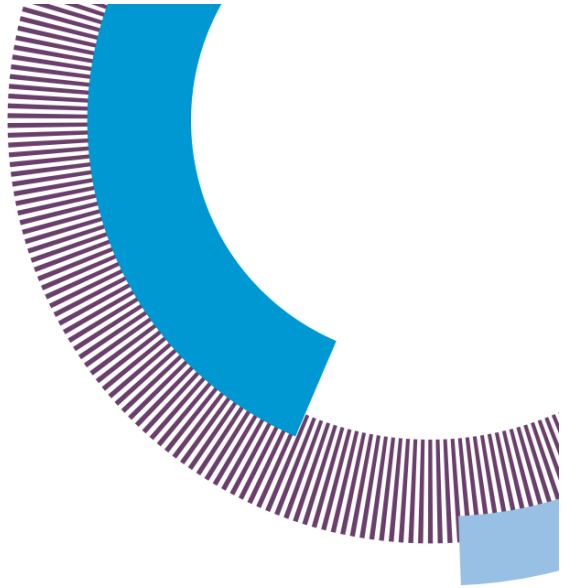


The boundaries and names shown and the designations used on this map do not imply the expression of any opinion whatsoever on the part of the World Health Organization concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. Dotted and dashed lines on maps represent approximate border lines for which there may not yet be full agreement.

Data source: World Health Organization
Map production: Information Evidence and Research (IER)
World Health Organization

World Health Organization

- 2022 sonu itibarıyla 127 ülke, bölge ve alan GLASS'a katılmaktadır.
- Ülkeler, laboratuvar altyapıları oldukça farklı olsa bile, GLASS'e katılmak için antimikrobiyal direnç / kullanım verisi göndermeye başlamadan önce resmi bir mektup ile kayıt yaptırabiliyor
- GLASS'e katılım, hem ülkelerde AMR/AMU izlemesini kurmayı hem de küresel anlamda karşılaştırılabilir, güvenilir veriler üretmeyi amaçlıyor.



Global antibiotic resistance surveillance report 2025

WHO Global Antimicrobial Resistance and Use Surveillance System (GLASS)

World Health Organization

World Health Organization (WHO) tarafından yayımlanan Global Antibiotic Resistance Surveillance Report 2025, 104 ülkenin 2023 verilerini içeren aktif bir analiz sunuyor.

- Toplamda > 23 milyon bakteriyolojik olarak doğrulanmış enfeksiyon vakası üzerinden analiz yapılmış.
- 8 öncelikli patojen ve 22 antibiyotik üzerinden modelleme yapılmış.

Acinetobacter spp.

Escherichia coli

Klebsiella pneumoniae

Neisseria gonorrhoeae

*Salmonella spp.**

Shigella spp.

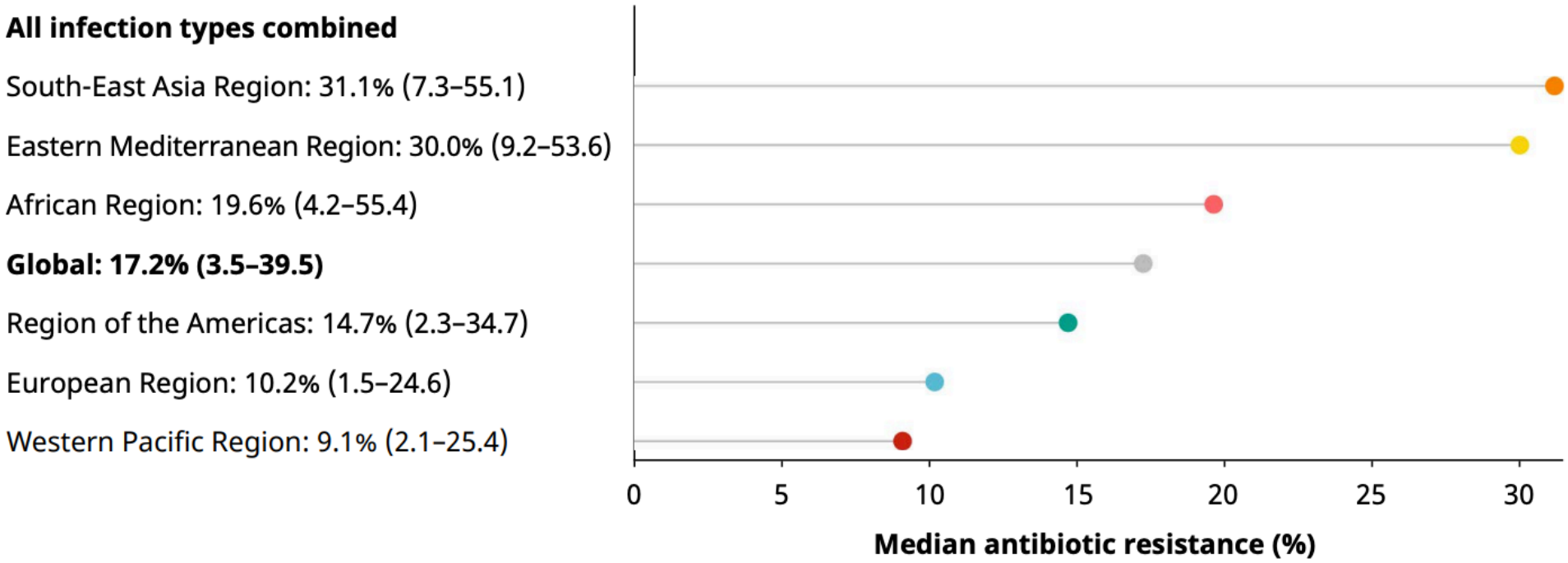
Staphylococcus aureus

Streptococcus pneumoniae

- 2023’te her 6 laboratuvar-onaylı enfeksiyondan yaklaşık 1’i antibiyotiklere dirençli durumda
- Direnç oranları coğrafi bölgelere göre büyük farklılıklar gösteriyor:

  Örneğin Güney-Asya ve Doğu Akdeniz Bölgelerinde oran ~1/3 seviyesinde, Avrupa’da ise yaklaşık 1/10 civarında

Figure 2. Median AMR in 93 infection type–bacterial pathogen–antibiotic combinations, by WHO region, 2023



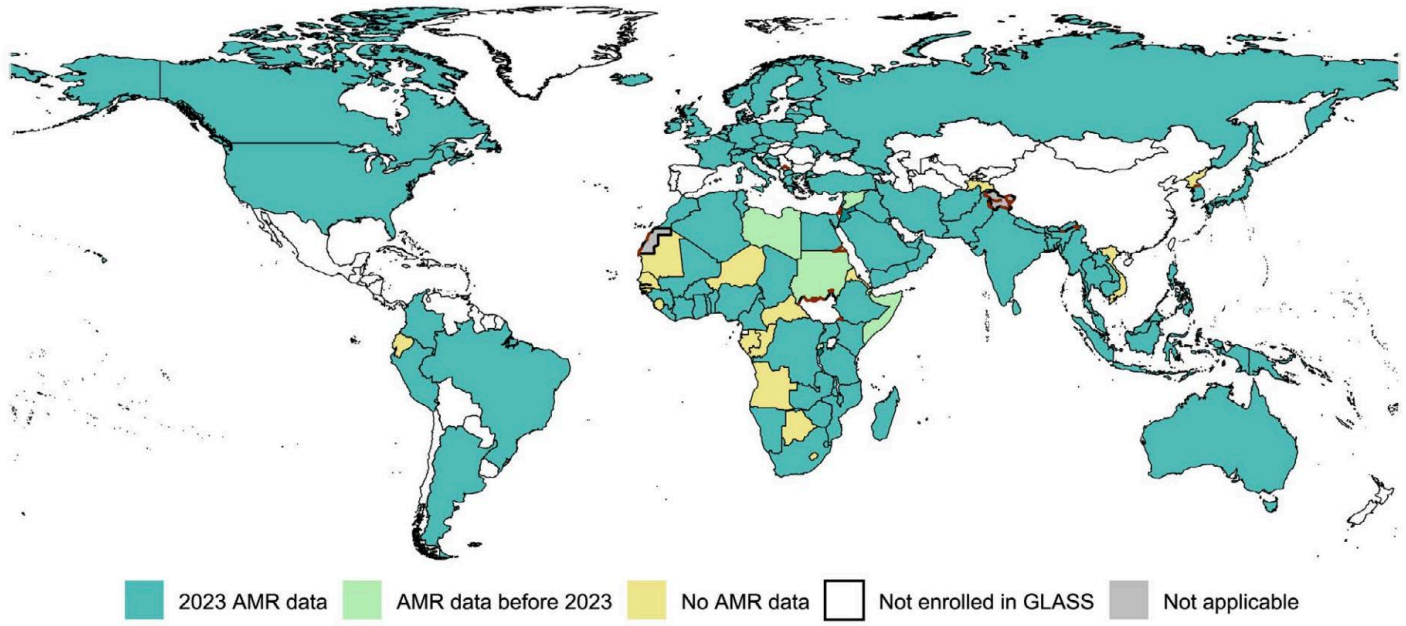
- Kullanıcılar ülke/bölge, patojen ve antibiyotik düzeyinde filtreleyebiliyor;

  23 antibiyotik, 11 antibiyotik sınıfı verisi içeriyor ve > 23 milyon enfeksiyon vakasına dayalı.

- Bu araç sayesinde örneğin bir ülkedeki artış anomalileri ya da

  belirli bir patojen-antibiyotik kombinasyonundaki trendler doğrulanabilir.

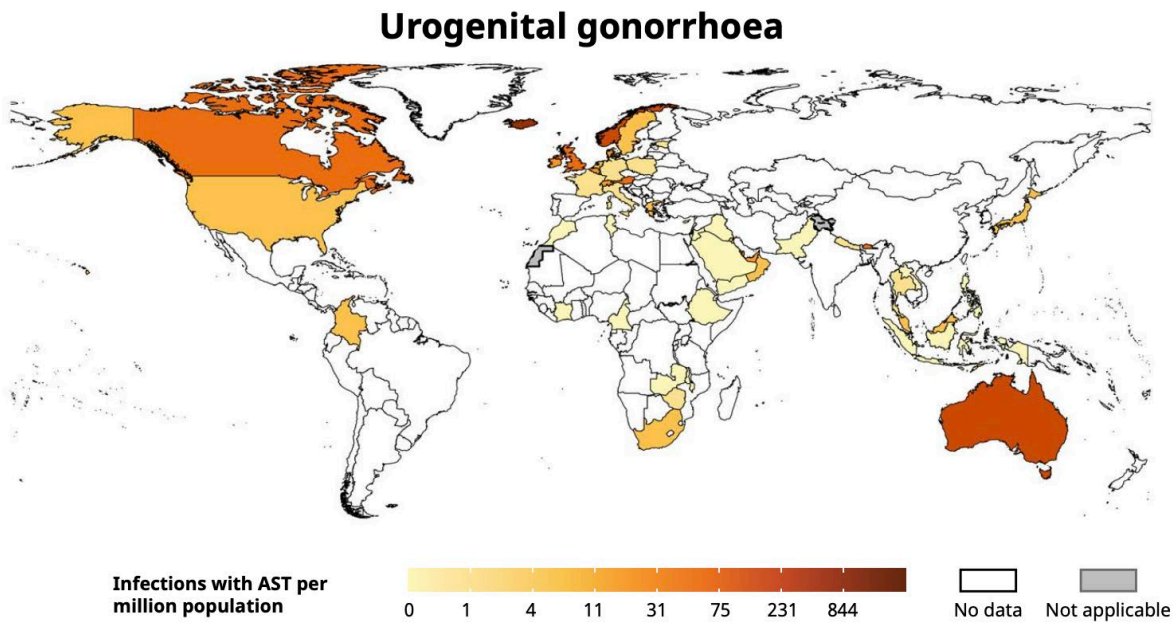
Figure 2.1. Countries reporting AMR data to WHO GLASS for at least one calendar year, 2016–2023



A country is considered to have reported AMR data if it has submitted AST results for at least one surveillance-defined infection type, pathogen and antibiotic combination under surveillance for at least one calendar year.

- Bu harita ülkelerin vakalarında kaç örnekte antibiyotik duyarlılık testi yaptığını gösteriyor.
- Dünya genelinde veri girişi eşit değil, birçok ülkede hiç veri yok.

Figure. 2.3. Numbers of infection episodes with AST results per million population, 2023



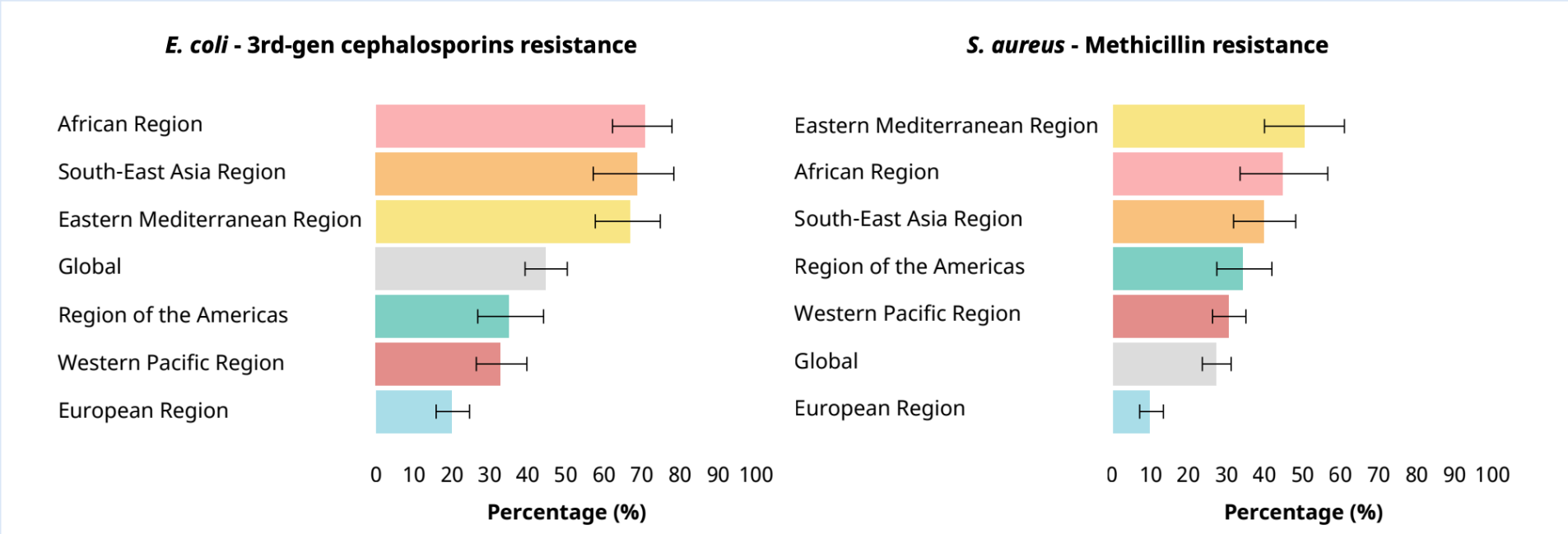
Maps show unadjusted (actual) number of infections with AST per million population.

- Bu figür kan dolaşımı enfeksiyonlarında antibiyotik direncinin küresel dağılımını gösteriyor.
- Özellikle Güneydoğu Asya, Doğu Akdeniz ve Afrika'da üçüncü kuşak sefalosporin, florokinolon ve karbapenem direnci çok yüksek.

Figure 3.1. Percentage AMR in bloodstream infections: global and regional estimates, 2023

- Küresel düzeyde *E. coli*'de 3. kuşak sefalosporin direnci %35–45 aralığında. Ancak Afrika, SEARO ve EMRO bölgelerinde %60'a kadar çıkıyor.
- MRSA oranları da özellikle Doğu Akdeniz ve Afrika'da en yüksek seviyelerde.

Figure 3.2. Percentage resistance to third-generation cephalosporins in *E. coli* and MRSA: global and regional estimates, 2023



Error bars represent 95% CrI. For methods, see Annex 1.

Figure 3.3. National percentage resistance to selected antibiotics in bloodstream infections, 2023

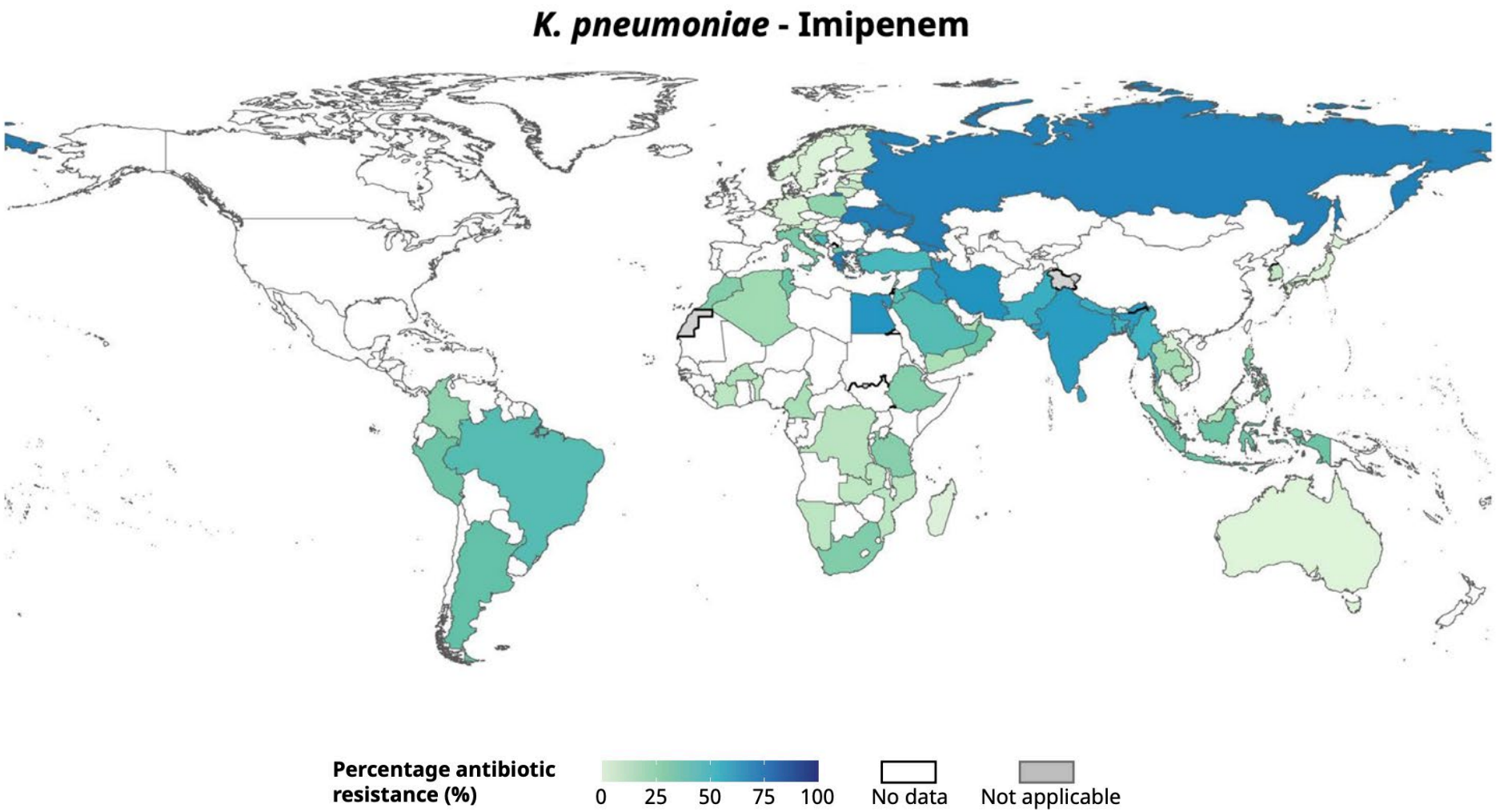
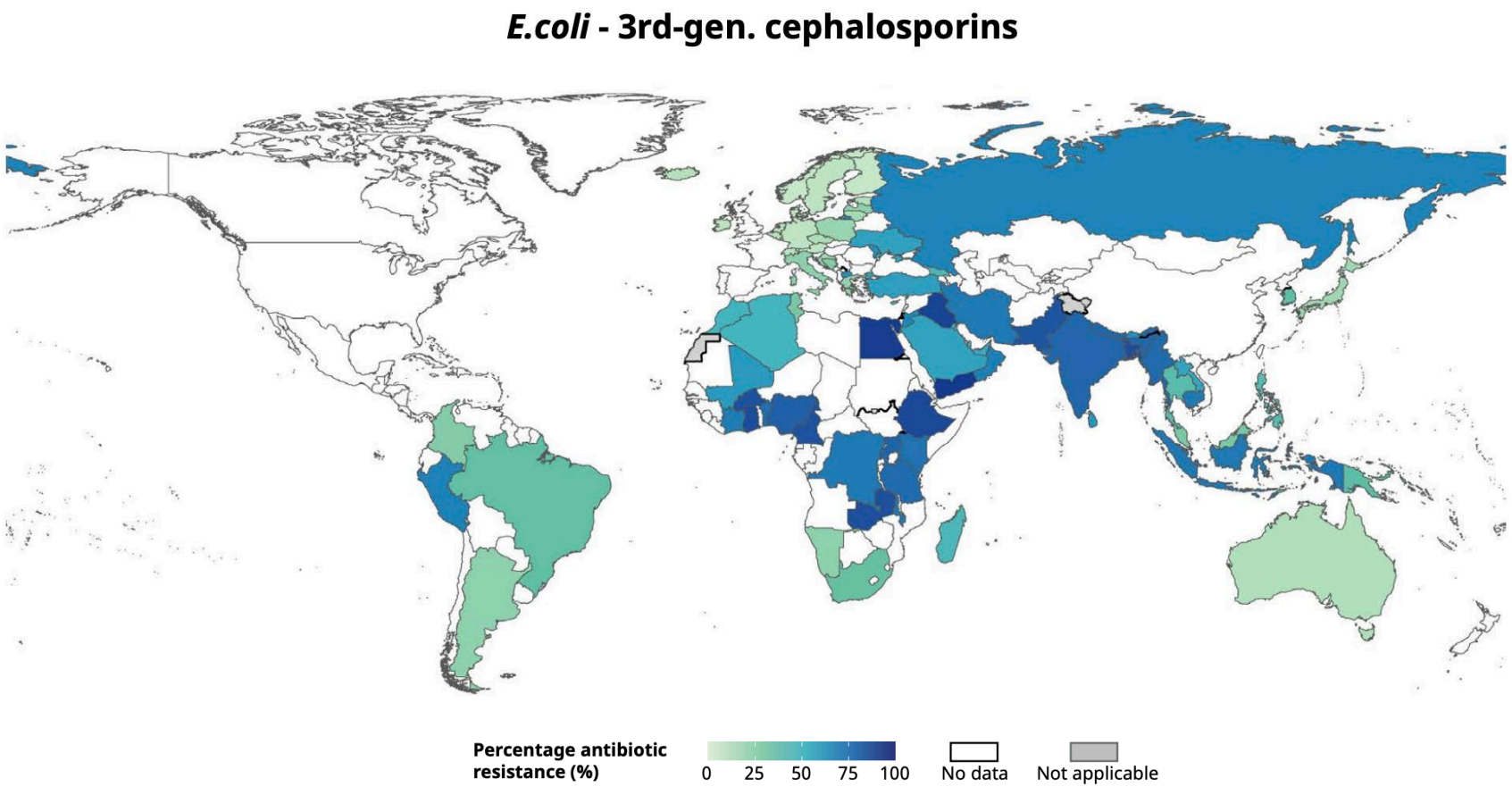
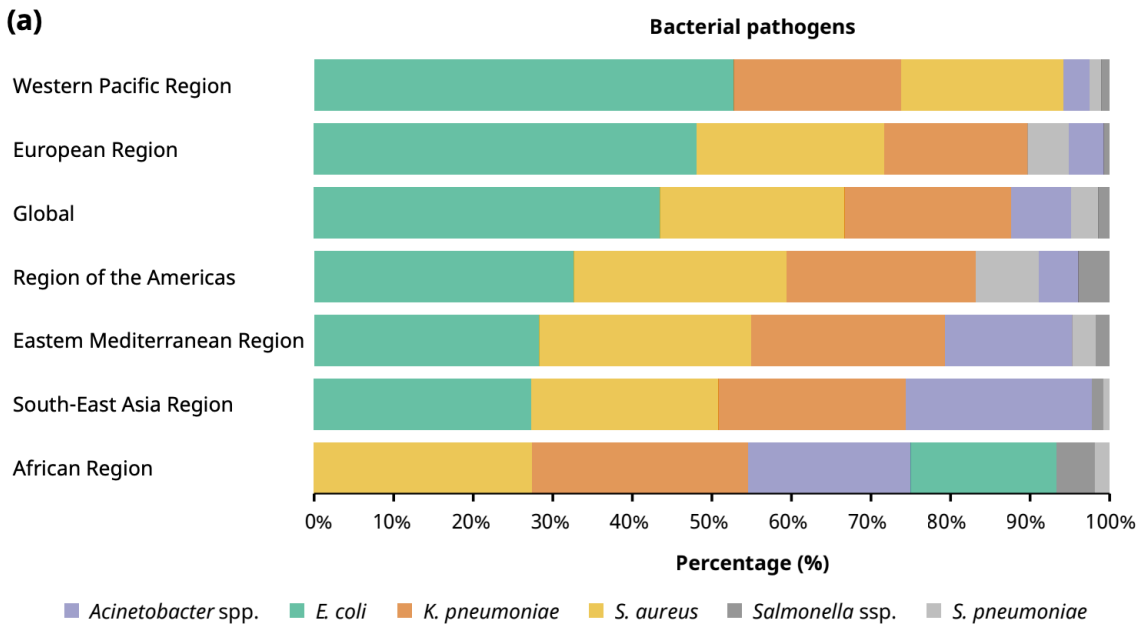


Figure 3.4. National percentage resistance to third-generation cephalosporins in *E. coli* and MRSA bloodstream infections, 2023



Adjusted AMR estimates are presented only for countries that reported data for the specific pathogen–antibiotic combination in 2023. Estimates are derived from multilevel Bayesian regression analyses that incorporate data from previous years to improve the accuracy of 2023 estimates. For further details of the method, see Annex 1.

Figure 3.5. Percentage distribution of bacterial pathogens (a) and the 10 most common antibiotic-resistant bacterial pathogens (b) in bloodstream infections, by WHO region, 2023



- Kan dolaşımı enfeksiyonlarında patojen dağılımı belirgin bölgesel farklılık gösteriyor.
- *E. coli* çoğu bölgede baskın etkenken, Afrika Bölgesi'nde Klebsiella spp. ve Acinetobacter spp. yüksek paya sahip.
- Doğu Akdeniz'de ise Klebsiella'nın belirgin baskınlığı dikkat çekiyor.
- Bu varyasyonlar, ampirik tedavi protokollerinin bölgeye özel uyarlanması gerektiğini ortaya koyuyor.

Box 3.1. WHO AWaRe classification

Effective treatment of infections depends on appropriate AMU. The AWaRe classification provides a structured framework for antibiotic selection and for national essential medicines lists and treatment guidelines. By categorizing antibiotics into Access, Watch and Reserve groups according to their spectrum of activity, resistance potential and clinical indications, it promotes appropriate prescribing and helps to safeguard last-resort antibiotics.

- "Access" antibiotics are recommended as empirical first- or second-choice treatment for a wide range of common infections. These agents usually have a narrow spectrum of activity, cost less, have favourable safety profiles and generally have low resistance potential. Examples include amoxicillin, penicillin, co-trimoxazole, first-generation cephalosporins and most aminoglycosides. Their widespread availability and appropriate use are essential to ensuring effective treatment while minimizing the development of resistance.
- "Watch" antibiotics are broader-spectrum agents that generally cost more and are at greater risk of resistance selection. They are recommended as first-choice options only in specific clinical situations, such as severe infections or when the causative pathogens are likely to be resistant to "Access" antibiotics. This group includes third- and fourth-generation cephalosporins (e.g. ceftriaxone and cefepime), fluoroquinolones (e.g. ciprofloxacin), carbapenems (e.g. meropenem) and glycopeptides (e.g. vancomycin). Their use should be carefully monitored and restricted to appropriate indications within an antibiotic stewardship programme.
- "Reserve" antibiotics are last-resort agents used in the treatment of confirmed or suspected infections caused by multidrug-resistant organisms. These antibiotics, such as colistin, tigecycline, cefiderocol and novel beta-lactam–beta-lactamase inhibitor combinations (e.g. meropenem–vaborbactam, ceftazidime–avibactam and ceftolozane–tazobactam), are used only when necessary and under strict clinical oversight. Their use should be guided by microbiological diagnostics and specialist consultation.

AWaRe, direnç yönetiminde dünyanın en kritik çerçevesi "Antibiyotikleri Access, Watch ve Reserve olarak sınıflamak; küresel reçete pratiğini yönlendiren en önemli stratejik araçtır."

Reserve grubu 'son savunma hattı'

Colistin

Tigecycline

Cefiderocol

Yeni BL-BLI ajanları:

- ✔ meropenem–vaborbactam
- ✔ ceftazidime–avibactam (CAZ-AVI)
- ✔ ceftolozane–tazobactam

Bu çok önemli bir mesaj:

GLASS 2025, yeni β-laktamaz inhibitör kombinasyonlarını artık küresel politikaların merkezine koyuyor.

CAZ-AVI artık sadece klinik bir tedavi seçeneği değil, küresel sağlık güvenliği stratejisinin bir parçası.

Tracking Resistance Beyond Phenotype

Fenotipin Ötesinde Direncin İzlenmesi: Kan Kültürlerinden İzole Edilen Karbapenem Dirençli Enterobacterales Suşlarının Moleküler Epidemiyolojisi –

KARMA Çok Merkezli Çalışması

GÜNİDER
GÜNEYDOĞU NÖROLOJİ VE İNFEKSİYON HASTALIKLARI DERNEĞİ

αÇG

"Alfa Çalışma Grubu" **Tracer Anatolia**

- Dr. Çiğdem Mermutluoğlu
  cigdemmermut@gmail.com

- Dr. Elif Seren Tanrıverdi
  seren.tanriverdi@inonu.edu.tr

Tracking Resistance Beyond Phenotype

Fenotipin Ötesinde Direncin İzlenmesi: Kan Kültürlerinden İzole Edilen Karbapenem Dirençli Enterobacterales Suşlarının Moleküler Epidemiyolojisi –

KARMA Çok Merkezli Çalışması

Prospektif Moleküler Epidemiyolojik Araştırma

- Karbapenemaz geni alt tiplerinin dağılımının belirlenmesi
- Klonal ilişki ve salgın kümelerinin tanımlanması
- Tedaviye yanıtla genotipik özelliklerin eşleştirilmesi
- Kolay uygulanabilir moleküler tanı algoritmalarının geliştirilmesi
- Epidemiyolojik trendlerin zamansal ve bölgesel analizi

Tracking Resistance Beyond Phenotype

Fenotipin Ötesinde Direncin İzlenmesi: Kan Kültürlerinden İzole Edilen Karbapenem Dirençli Enterobacterales Suşlarının Moleküler Epidemiyolojisi –

KARMA Çok Merkezli Çalışması

- Retrospektif verilerin yararı kısıtlı!

Microbial Drug Resistance, AHEAD OF PRINT | Epidemiology

Hospital Outbreak of a Colistin-Resistant, NDM-1- and OXA-48-Producing *Klebsiella pneumoniae*: High Mortality from Pandrug Resistance

Guducuoglu Huseyin, Gursoy Nafia Canan, Yakupogullari Yusuf, Parlak Mehmet, Karasin Gokhan, Sunnetcioglu Mahmut, and Otlu Baris

Published Online: 21 Dec 2017 | https://doi.org/10.1089/mdr.2017.0173

Tools Share

Abstract

Colistin resistance causes substantial problems in the treatment of serio negative bacteria. In this study, we report a fatal hospital outbreak from *pneumoniae* clone. An outbreak investigation was conducted after consi strains from eight patients in two intensive care units of a university hos resistance genes were investigated with PCR, clonal relationships of isol electrophoresis, and multilocus sequence types were determined. The o Genotyping showed a predominant CR-Kp clone consisting of seven stra type, an international high-risk clone. They were resistant to all antimicro OXA-48 carbapenemases, but negative for plasmid-borne colistin resista remaining five died due to the infection within mean 12 days. No environ outbreak was stopped by augmenting infection-control measures. Colist the hospital setting, and this spread might be associated with high mort option. Immediate implementation of infection-control measures may b spread of such incurable pathogens.

Antimicrobial Original Research Paper

Molecular characterization of carbapenem-resistant *Enterobacteriaceae* yields increasing rates of NDM-1 carbapenemases and colistin resistance in an OXA-48- endemic area

Zeynep Cizmeci[1], Elif Aktas[2], Baris Otlu[3], Ozlem Acikgoz[1], Seyhan Ordekci[1]

[1]Clinical Microbiology Laboratory, Bakırkoy Dr. Sadi Konuk Tr

Microbial Drug Resistance, Vol. 23, No. 3 | Epidemiology

VIM-1, VIM-2, and GES-5 Carbapenemases Among *Pseudomonas aeruginosa* Isolates at a Tertiary Hospital in Istanbul, Turkey

Malkoçoğlu Gülşah, Aktaş Elif, Bayraktar Banu, Otlu Barış, and Bulut Mehmet Emin

Published Online: 1 Apr 2017 | https://doi.org/10.1089/mdr.2016.0012

View Article Tools Share

Contents lists available at ScienceDirect

Journal of Infection and Public Health

journal homepage: http://www.elsevier.com/locate/jiph

Detection of bla_{OXA-48} and clonal relationship in carbapenem resistant *K. pneumoniae* isolates at a tertiary care center in Western Turkey

Gulfem Ece[a,*], Emine Tunc[b], Baris Otlu[b], Deniz Aslan[c], Cem Ece[d]

[a] Medicalpark Izmir Hospital, Department of Medical Microbiology, Izmir, Turkey
[b] Inonu University School of Medicine, Department of Medical Microbiology, Malatya, Turkey
[c] Medicalpark Izmir Hospital, Department of Anesthesiology and Reanimation, Izmir, Turkey
[d] Cigli Regional Education Hospital, Department of Anesthesiology and Reanimation, Izmir, Turkey

ARTICLE INFO ABSTRACT

Klebsiella pneumoniae is an important nosocomial pathogen that can lead to high morbidity ESBL and carbapenamase producing strains may cause epidemic situations. The aim of to investigate the molecular epidemiology and clonal relationship between carbapenem *pneumoniae* strains isolated from our hospital during a three month period. ween carbapenem resistant *K. pneumoniae* strains isolated during April 1st–June 30th 2013. The identification and the antibiotic susceptibility of the strains were studied by Vitek 2 erieux, France) system. The carbapenemase production of the isolates were investigated dge assay. The bla_{OXA} of the strains was investigated by in house PCR. The clonal rela- ween the isolates were studied by pulsed-field gel electrophoresis (PFGE) and automatized genic palindromic PCR (Rep-PCR, DiversiLab sistemi, Biomerieux, France) methods. *pneumoniae* isolates were carbapenem resistant; they were all susceptible to gentamycin of them had bla_{OXA-48}. The genotyping analysis revealed that eight isolates were in the th by Rep-PCR (similarity border ≥95%) and PFGE (Tennover criteriae) analysis. The other belong to any other clusters. The strains that are in the same cluster are isolated from ogy Intensive Care Unit during a three month period. The cluster ration by both methods

K. pneumoniae strains possessed bla_{OXA-48}. The clonal spreading was particularly thesiology Intensive Care Unit. Molecular epidemiological monitorization of nosocomial or Health Sciences. This is an open access article under the CC BY-NC-ND license (http:// creativecommons.org/licenses/by-nc-nd/4.0/).

pathogens

MDPI

Article

An Intensive Care Outbreak Caused by *Burkholderia cepacia* from Bacterial Filters

Özlem Aytaç [1,*], Elif Seren Tanrıverdi [2], Ömür Gündağ [3], Feray Ferda Şenol [1], Gülden Eser Karlıdağ [4] and Barış Otlu [2]

[1] Medical Microbiology, Elazığ Fethi Sekin City Hospital, 23280 Elazığ, Türkiye
[2] Department of Medical Microbiology, Faculty of Medicine, Inonu University, 44000 Malatya, Türkiye
[3] Infectious Diseases and Clinic Microbiology Department, Elazığ Fethi Sekin City Hospital, 23280 Elazığ, Türkiye
[4] Infectious Diseases and Clinical Microbiology Clinic, Elazığ Fethi Sekin City Hospital, Health Sciences University, 23280 Elazığ, Türkiye
* Correspondence: ozlemozlem5@hotmail.com

Abstract: Background: We report a hospital outbreak caused by *Burkholderia cepacia* that occurred in 16 patients admitted to intensive care units in Elazığ, Türkiye, between 19 March and 23 April 2024. Methods: The outbreak investigation was initiated on 23 March 2024, four days after *B. cepacia* was detected in four different patients. Environmental samples were collected from various parts of the hospital to find the source of the outbreak. Arbitrarily Primed Polymerase Chain Reaction (AP-PCR) was performed to determine the genetic relationship between environmental and patient samples. Results: In total, 16 of 18 *B. cepacia* isolates were obtained from tracheal aspirate culture. A total of 10 of 16 patients developed hospital-acquired pneumonia due to *B. cepacia*. Among the environmental cultures in the intensive care units, only the respirator bacterial filter grew. The isolate obtained here was in the same cluster as the isolate obtained from patient samples, resulting in a dominant clustering rate of 94.4%. Conclusions: Improper and inappropriate use of respirators and equipment can lead to outbreaks. Early detection of the outbreak, identification of the source, and taking appropriate measures quickly to contain the outbreak are key.

TÜBİTAK

Turkish Journal of Medical Sciences

http://journals.tubitak.gov.tr/medical/

Research Article

Turk J Med Sci (2025) 55: 265-270 © TÜBİTAK doi:10.55730/1300-0144.5967

Outbreak of bacteremia caused by *Ralstonia insidiosa* isolated from a contaminated blood gas syringe

Elif Ayça ŞAHİN[1,*], Özge ÖZGEN TOP[2], Pınar AYSERT YILDIZ[2], Elif Seren TANRIVERDİ[3], Hasan Selçuk ÖZGER[2], Barış OTLU[3], Özlem GÜZEL TUNÇCAN[2], Murat DİZBAY[2], Ayşe KALKANCI[1], Kayhan ÇAĞLAR[1]

[1]Department of Medical Microbiology, Faculty of Medicine, Gazi University, Ankara, Turkiye
[2]Department of Infectious Disease, Faculty of Medicine, Gazi University, Ankara, Turkiye
[3]Department of Medical Microbiology, Faculty of Medicine, Inonu University, Malatya, Turkiye

Received: 10.10.2024 • **Accepted/Published Online:** 23.12.2024 • **Final Version:** 18.02.2025

Background/aim: *Ralstonia* species are opportunistic, waterborne microorganisms known for their ability to survive and proliferate in a wide range of water-based environments. They can contaminate solutions used for patient care and cause hospital outbreaks due to contaminated solutions. The aim of this study was to investigate the source and clonal relationship of *Ralstonia insidiosa* bacteremia detected in 28 patients between August and December 2021, as part of an unusual outbreak.
Materials and methods: Active prospective surveillance studies were conducted, and environmental samples, including saline, antiseptic, and antibiotic solutions, injectors, arterial blood gas syringes, tap water, and hand soap, were collected from wards to determine the source of the outbreak. An arbitrary-primed polymerase chain reaction (AP-PCR) genotyping method was used to determine the clonal relationship between the isolates.
Results: All the samples were cultured, and *R. insidiosa* was isolated from arterial blood gas syringes with the same location and time-based identifier (LOT number). All the arterial blood gas syringes were recalled from the hospital departments and sent back to the manufacturer. The outbreak was reported to the national health authorities. Clonal analysis between isolates from the patients and the blood gas syringes was performed using AP-PCR. It was observed that the *R. insidiosa* isolates were monoclonal and identical.
Conclusion: It was concluded that these contaminated arterial blood gas syringes caused the *R. insidiosa* bacteremia, especially in immunocompromised patients.

medicina

MDPI

Article

An Outbreak of Vancomycin-Resistant Enterococci in a City Hospital Intensive Care Unit: Molecular Characterization of Resistance

Feray Ferda Şenol [1,*], Elif Seren Tanrıverdi [2,*], Özlem Aytaç [1], Zulal Aşçı Toraman [3] and Barış Otlu [4]

[1] Microbiology Laboratory Unit, Elazığ Fethi Sekin City Hospital, 23280 Elazığ, Turkey; ozlemozlem5@hotmail.com
[2] Microbiology Laboratory Unit, Malatya Training and Research Hospital, 44210 Malatya, Turkey
[3] Department of Microbiology, Faculty of Medicine, Firat University, 23200 Elazığ, Turkey; zulalasci@gmail.com
[4] Department of Medical Microbiology, Faculty of Medicine, Inonu University, 44280 Malatya, Turkey; boliu@yahoo.com
* Correspondence: drferdasenol@yahoo.com (F.F.Ş.); seren.tanriverdi@inonu.edu.tr (E.S.T.)

Abstract: *Background and Objectives:* Vancomisin-resistant *Enterococci* (VRE), is a resistant microorganism that colonizes and causes infections in hospitalized patients. The aim of this study was to show the spread of vancomycin-resistant *Enterococcus faecium* (VREfm) step-by-step in all intensive care units, which started with the growth of VREfm on 2 December 2021 in the blood culture of a patient hospitalized in the anesthesia intensive care unit of our hospital and was found to have reached epidemic size in the surveys. *Materials and Methods:* Rectal swab samples were taken from all patients hospitalized in intensive care units, VRE colonization was determined, the *VanA* and *VanB* resistance genes associated with the vancomycin resistance of VREfm isolates were determined by PCR method, and clonal association analysis was performed by Arbitrarily Primed-PCR (AP-PCR) and PFGE (pulsed-field gel electrophoresis). *Results:* In our study, VRE were detected in 61 of 2601 rectal swab samples. In total, fifty-four (85.52%) of the VRE isolates were *Enterococcus faecium*, three (4.91%) was *Enterococcus fucalis*, three (4.91%) was *Enterococcus gallinorum*, and one (1.63%) was *Enterococcus casseliflavus*. It was determined that all of the 54 VREfm isolates, which were the most detected among all VRE isolates, carried the *vanA* gene. In the clonal association analysis of the isolates by AP-PCR and PFGE methods, it was found that they had 12 different genotypes, 48 of them were included in any cluster, the clustering rate was 88.8%, and the largest cluster was the genotype 1 cluster, with 36 isolates. Of the 54 patients with VREfm isolated recently, 18.51 percent of the clinical samples were isolated before the survey, and 9.25% were isolated after the survey. It was determined that 100% of VREfm isolates were resistant to ampicillin, levofloxacin, ciprofloxacin, high-level gentamicin, trimethoprimsulfamethoxazole, and teicoplanin, 7.4% to tigecycline, and 1.85% to linezolid. *Conclusions:* In our study, in the clonal association analysis performed by isolating VREfm in rectal swab samples, it was found that 88.8% of the samples were indistinguishably similar, and that the increase in the number of VREfm infections after the index case in our hospital was associated with the epidemic. VREfm infections cause long-term hospitalization, costs and also deaths, which shows the seriousness of the event, and the importance of the combination of epidemiological and molecular analysis in epidemic research.

check for updates

Citation: Şenol, F.F.; Tanrıverdi, E.S.; Aytaç, Ö.; Aşçı Toraman, Z.; Otlu, B. An Outbreak of Vancomycin-Resistant Enterococci in a City Hospital Intensive Care Unit: Molecular Characterization of Resistance. *Medicina* **2023**, *59*, 2081. https://doi.org/10.3390/medicina59122081

Academic Editors: Carlo Torti and Ionil Marincu

Received: 11 September 2023
Revised: 21 October 2023
Accepted: 21 November 2023
Published: 27 November 2023

Tracking Resistance Beyond Phenotype

Fenotipin Ötesinde Direncin İzlenmesi: Kan Kültürlerinden İzole Edilen Karbapenem Dirençli Enterobacterales Suşlarının Moleküler Epidemiyolojisi –

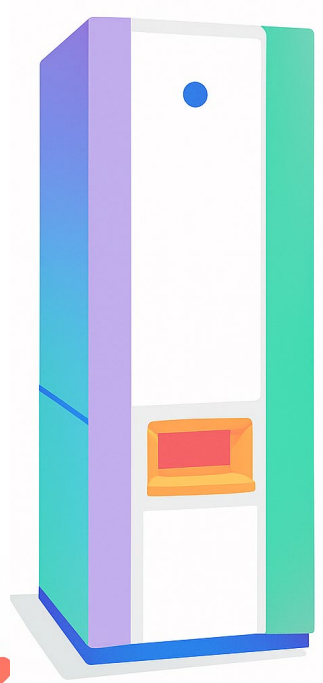
KARMA Çok Merkezli Çalışması

- Çalışmanın tasarımı
  - Kan kültürlerinden izole edilen karbapenem dirençli Enterobacterales türleri, proje koordinasyon merkezine gönderilecektir.
  - Her merkez belirlenen sayıda ardışık izolatı (en az 10-50) uygun taşıma koşullarında iletecektir.
  - İzolatlara ait klinik ve epidemiyolojik veriler kaydedilecektir.
  - Örnekler koordinasyon merkezine ulaştıktan 2-5 gün arasında ilgili merkez sonuçlara ulaşabilecek.
  - Proje süresi 1 yıl

Tracking Resistance Beyond Phenotype

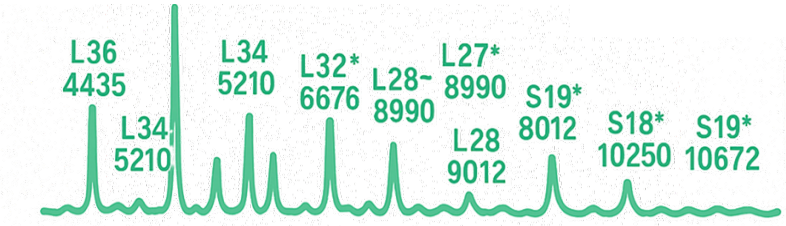
Fenotipin Ötesinde Direncin İzlenmesi: Kan Kültürlerinden İzole Edilen Karbapenem Dirençli Enterobacterales Suşlarının Moleküler Epidemiyolojisi –

KARMA Çok Merkezli Çalışması



Fenotipik Doğrulama Testleri

Gönderilen her örnek MALDI-TOF MS ile tür düzeyinde yeni tiplendirilecek.



Tracking Resistance Beyond Phenotype

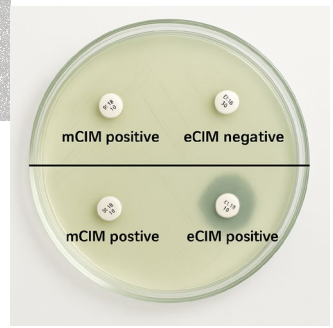
Fenotipin Ötesinde Direncin İzlenmesi: Kan Kültürlerinden İzole Edilen Karbapenem Dirençli Enterobacterales Suşlarının Moleküler Epidemiyolojisi –

KARMA Çok Merkezli Çalışması

Antimikrobiyal duyarlılık testleri

- Ceftazidime/Avibactam (CAZ/AVI)
- Aztreonam/Avibactam (AZT/AVI)

Karbapenemaz aktivite testi



Ceftazidime/
Avibactam

Tracking Resistance Beyond Phenotype

Fenotipin Ötesinde Direncin İzlenmesi: Kan Kültürlerinden İzole Edilen Karbapenem Dirençli Enterobacterales Suşlarının Moleküler Epidemiyolojisi –

KARMA Çok Merkezli Çalışması

Antimikrobiyal direnç genlerinin tespiti

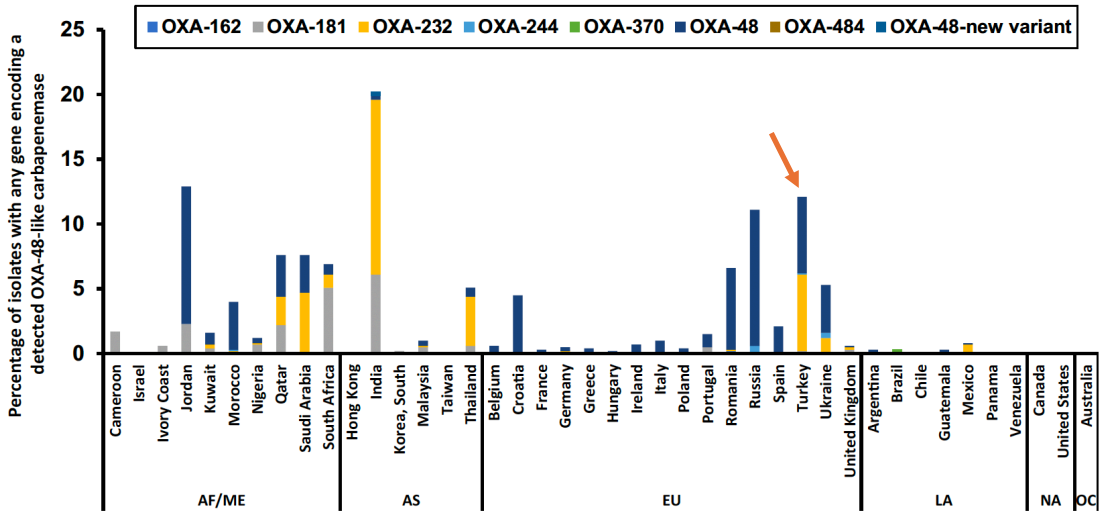
- OXA-48 like
  - OXA-162
  - OXA-181
  - OXA-232
  - OXA-244
  - OXA-370
  - OXA-48
  - OXA-484
  - OXA-48-new variant
- KPC
- NDM
- IMP
- VIM

J Antimicrob Chemother 2024; **79**: 1581–1589
https://doi.org/10.1093/jac/dkae140 Advance Access publication 17 May 2024

Journal of Antimicrobial Chemotherapy

Global epidemiology and antimicrobial resistance of Enterobacterales harbouring genes encoding OXA-48-like carbapenemases: insights from the results of the Antimicrobial Testing Leadership and Surveillance (ATLAS) programme 2018–2021

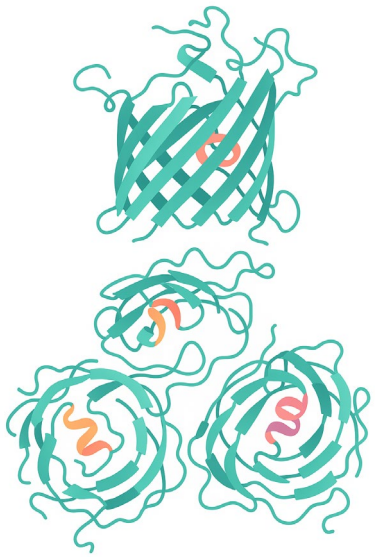
Yu-Lin Lee [1,2,3], Wei-Yao Wang[1,3], Wen-Chien Ko[4] and Po-Ren Hsueh [5,6,7,8]*



Tracking Resistance Beyond Phenotype

Fenotipin Ötesinde Direncin İzlenmesi: Kan Kültürlerinden İzole Edilen Karbapenem Dirençli Enterobacterales Suşlarının Moleküler Epidemiyolojisi –

KARMA Çok Merkezli Çalışması



Karbapenemaz nedenli olmayan direnç

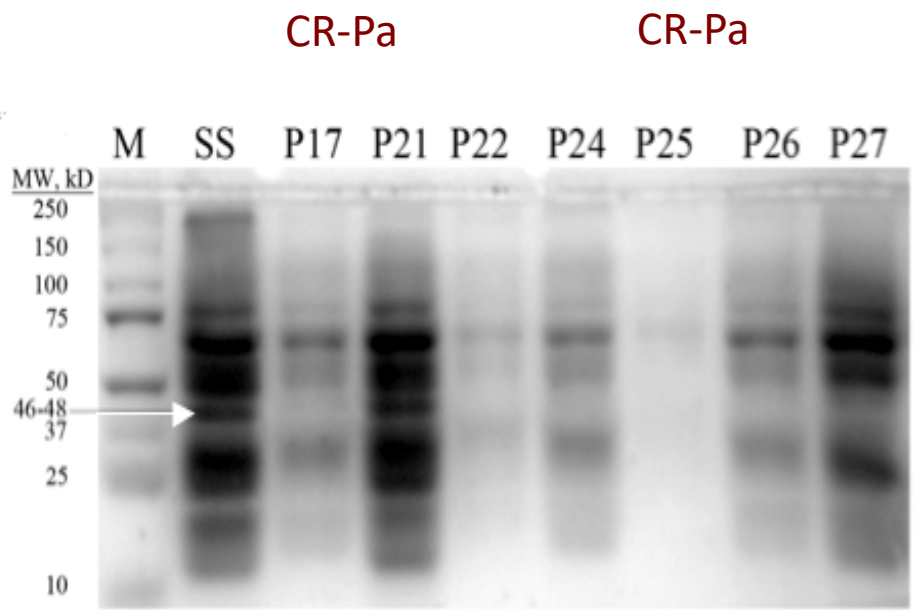
- Porin Kaybına Bağlı Karbapenem Direnci

  OprD, OmpC/OmpF porinleri

- Atım Pompaları ile Gelişen Direnç

  AcrAB-TolC sistemi (*E. coli, K. pneumoniae*)

  mexA, mexB mRNA düzeyi

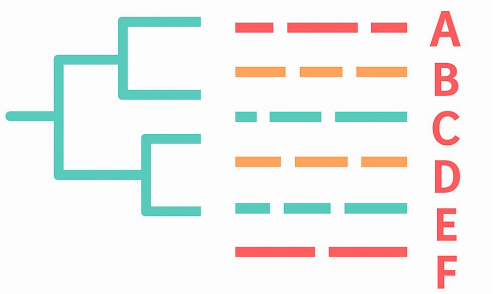


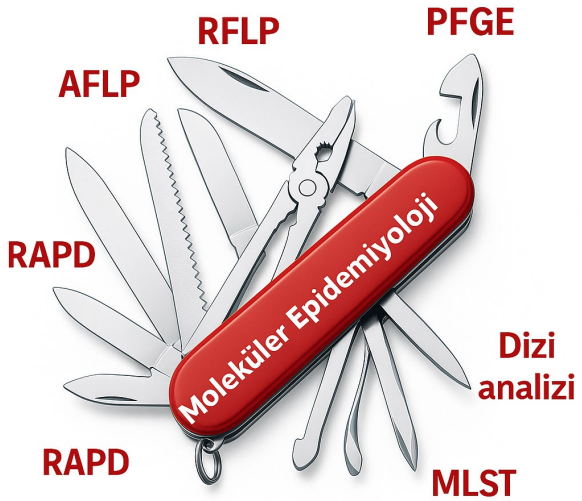
Tracking Resistance Beyond Phenotype

Fenotipin Ötesinde Direncin İzlenmesi: Kan Kültürlerinden İzole Edilen Karbapenem Dirençli Enterobacterales Suşlarının Moleküler Epidemiyolojisi –

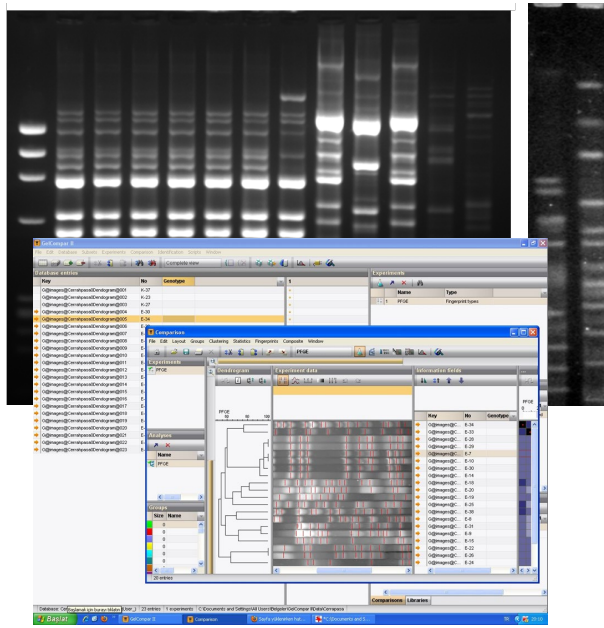
KARMA Çok Merkezli Çalışması

İzolatlar arası klonal ilişki analizi

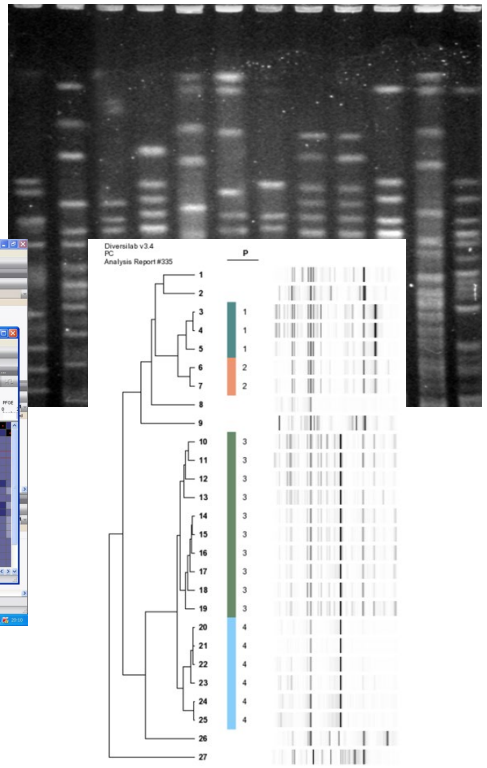




AP-PCR



PFGE



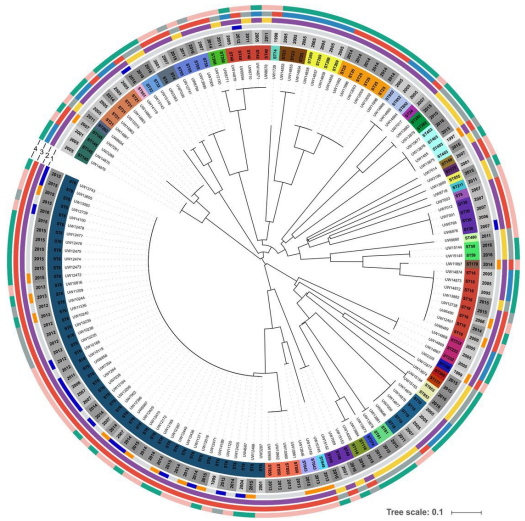
Tracking Resistance Beyond Phenotype

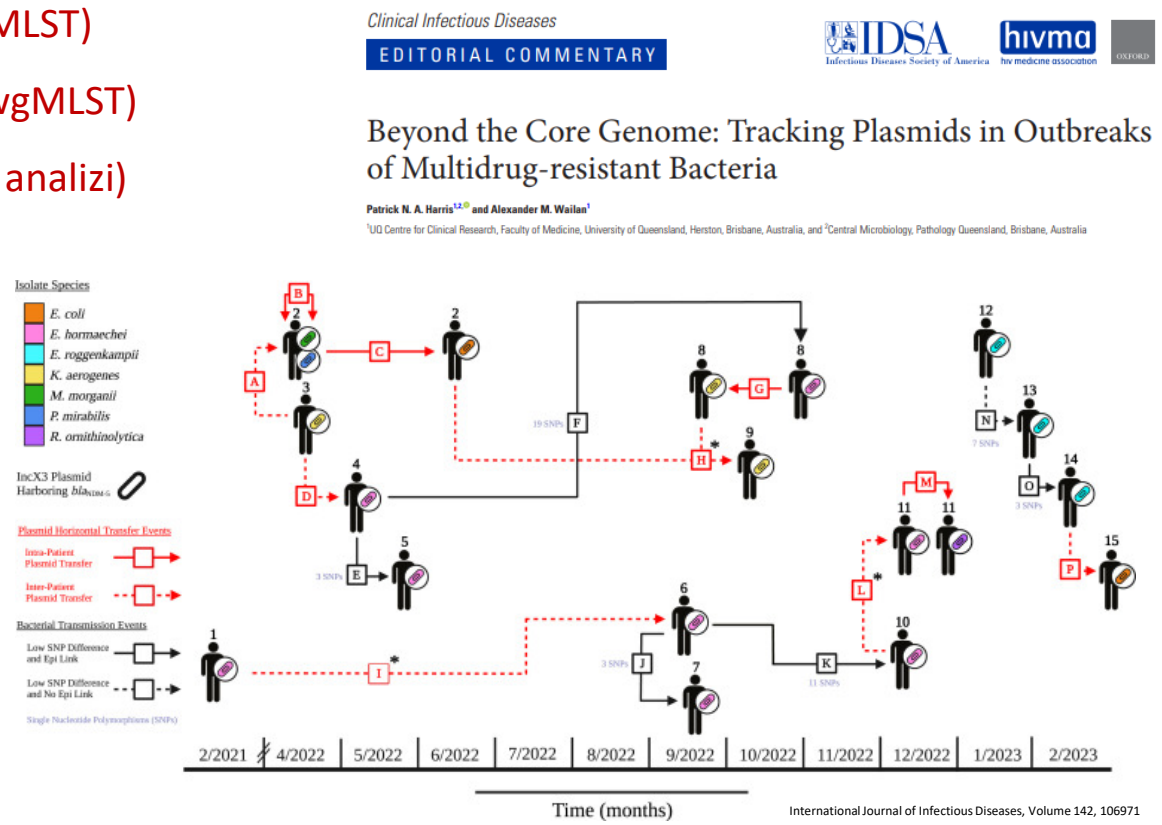
Fenotipin Ötesinde Direncin İzlenmesi: Kan Kültürlerinden İzole Edilen Karbapenem Dirençli Enterobacterales Suşlarının Moleküler Epidemiyolojisi –

KARMA Çok Merkezli Çalışması

Tüm genom dizi analizi

- Core Genome Multilocus Sequence Typing (cgMLST)
- Whole Genome Multilocus Sequence Typing (wgMLST)
- Single Nucleotide Polymorphism Analysis (SNP analizi)





Clinical Infectious Diseases
EDITORIAL COMMENTARY

Beyond the Core Genome: Tracking Plasmids in Outbreaks of Multidrug-resistant Bacteria

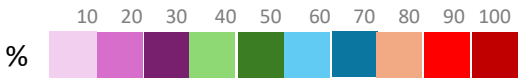
Patrick N. A. Harris and Alexander M. Wailan
UQ Centre for Clinical Research, Faculty of Medicine, University of Queensland, Herston, Brisbane, Australia, and Central Microbiology, Pathology Queensland, Brisbane, Australia

International Journal of Infectious Diseases, Volume 142, 106971

KARMA Çalışması Takip Ekranı

İL Seçimi

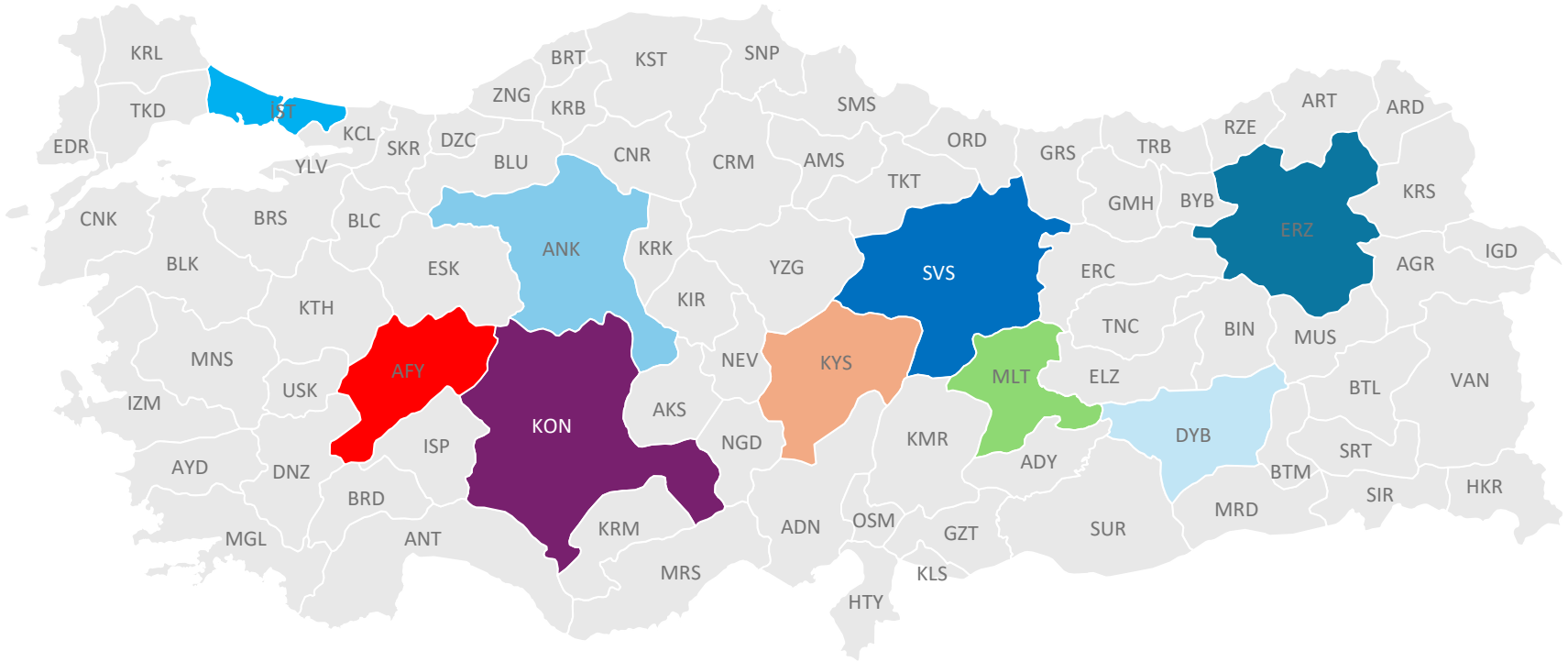
- Adana
- Adıyaman
- Afyonkarahisar
- Ağrı
- Aksaray
- Amasya
- Ankara
- Antalya
- Ardahan
- Artvin
- Aydın
- Balıkesir
- Bartın

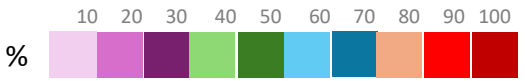


KARMA Çalışması Takip Ekranı

İL Seçimi

- Adana
- Adıyaman
- Afyonkarahisar
- Ağrı
- Aksaray
- Amasya
- Ankara
- Antalya
- Ardahan
- Artvin
- Aydın
- Balıkesir
- Bartın

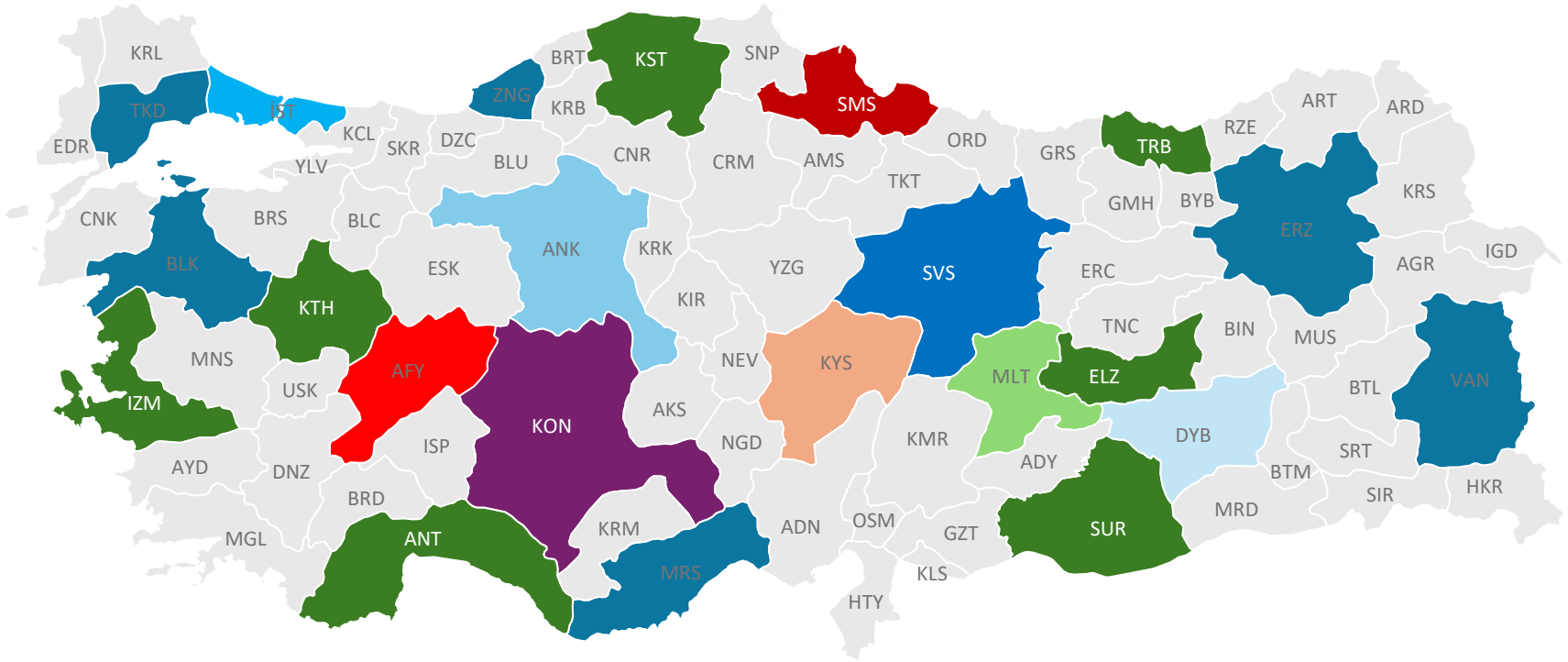


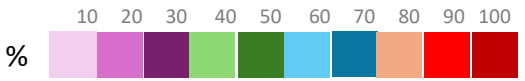


KARMA Çalışması Takip Ekranı

İL Seçimi

- Adana
- Adıyaman
- Afyonkarahisar
- Ağrı
- Aksaray
- Amasya
- Ankara
- Antalya
- Ardahan
- Artvin
- Aydın
- Balıkesir
- Bartın



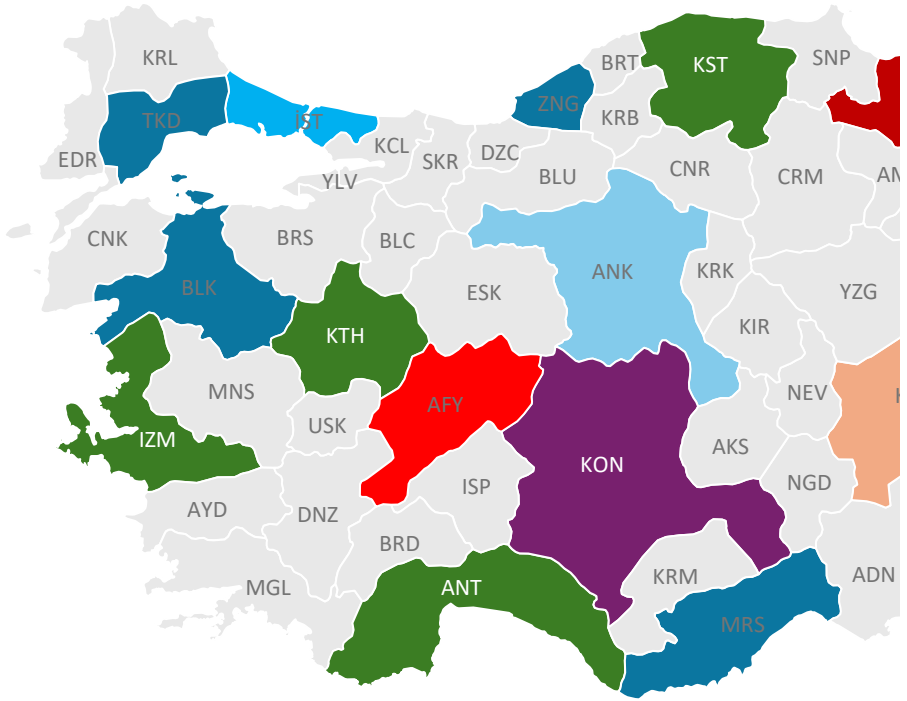


KARMA Çalışması Takip Ekranı

Tüm Merkezler

İL Seçimi

- Adana
- Adıyaman
- Afyonkarahisar
- Ağrı
- Aksaray
- Amasya
- Ankara
- Antalya
- Ardahan
- Artvin
- Aydın
- Balıkesir
- Bartın



Duyarlılık

Gönderilen izolat sayısı	CAZ/AVI	AZT/AVI	MEM/VAB	CFDC
K. pneumoniae: 550	10/41	2/41	6/41	18/41
E. coli: 240	18/41	10/41	20/41	24/41
K. oxytoca: 20	2/2	2/2	1/2	2/2
M. morganii: 10	0/1	1/1	1/1	1/1

Direnç Geni (+)

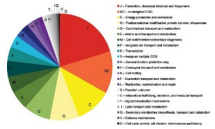
	OXA-48	NDM	KPC	IMP	VIM
K. pneumoniae: 550	10/41	2/41	6/41	1/41	0/41
E. coli: 240	18/24	10/24	20/24	0/24	0/24
K. oxytoca: 20	2/2	2/2	1/2	0/2	0/2
M. morganii: 10	0/1	1/1	1/1	1/1	0/1

Porin/Eflüks

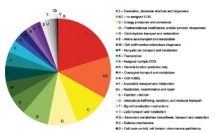
	OprD	OmpC/OmpF	ArcAB/TolC
K. pneumoniae: 550	10/41	2/41	6/41
E. coli: 240	18/41	10/41	20/41
K. oxytoca: 20	2/2	2/2	1/2
M. morganii: 10	0/1	1/1	1/1

Klonalite

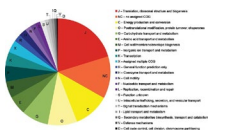
K. pneumoniae



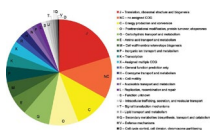
E. coli

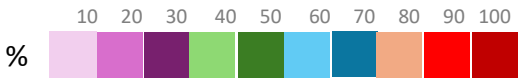


K. oxytoca



M. morganii

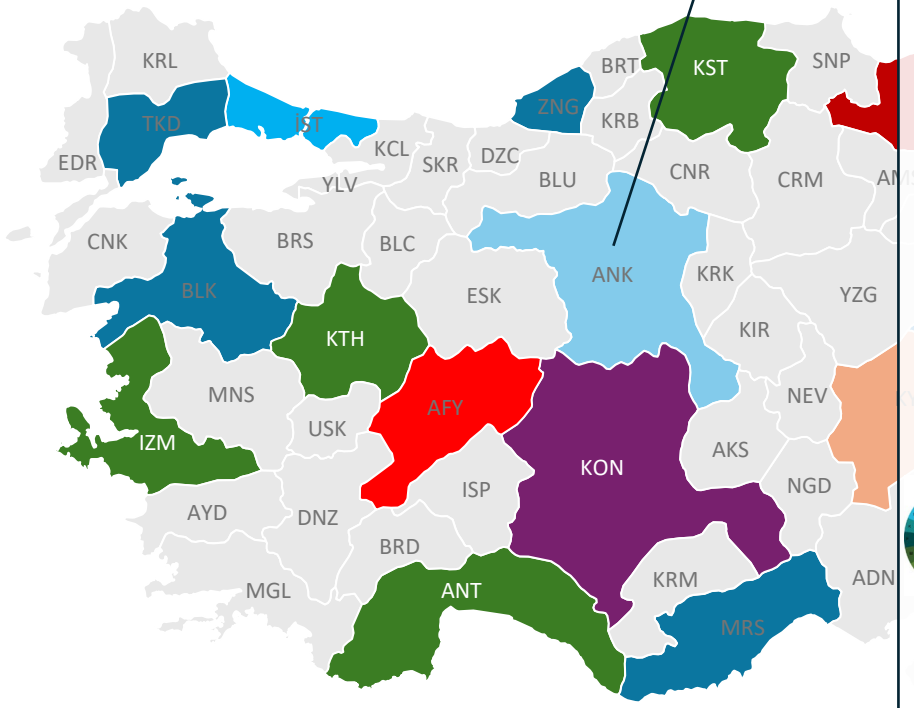




KARMA Çalışması Takip Ekranı

İL Seçimi

- Adana
- Adıyaman
- Afyonkarahisar
- Ağrı
- Aksaray
- Amasya
- Ankara
- Antalya
- Ardahan
- Artvin
- Aydın
- Balıkesir
- Bartın



Duyarlılık

Gönderilen izolat sayısı	CAZ/AVI	AZT/AVI	MEM/VAB	CFDC
K. pneumoniae: 55	10/41	2/41	6/41	18/41
E. coli:24	18/41	10/41	20/41	24/41
K. oxytoca: 2	2/2	2/2	1/2	2/2
M. morganii: 1	0/1	1/1	1/1	1/1

Direnç Geni (+)

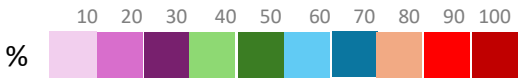
	OXA-48	NDM	KPC	IMP	VIM
K. pneumoniae: 55	10/41	2/41	6/41	1/41	0/41
E. coli:24	18/24	10/24	20/24	0/24	0/24
K. oxytoca: 2	2/2	2/2	1/2	0/2	0/2
M. morganii: 1	0/1	1/1	1/1	1/1	0/1

Porin/Eflüks

	OprD	OmpC/OmpF	ArcAB/TolC
K. pneumoniae: 55	10/41	2/41	6/41
E. coli:24	18/41	10/41	20/41
K. oxytoca: 2	2/2	2/2	1/2
M. morganii: 1	0/1	1/1	1/1

Klonalite

K. pneumoniae | E. coli | K. oxytoca | M. morganii



KARMA Çalışması Takip Ekranı

İL Seçimi

İstanbul

Duyarlılık

Gönderilen izolat sayısı	CAZ/AVI	AZT/AVI	MEM/VAB	CFDC
K. pneumoniae: 55	10/41	2/41	6/41	18/41
E. coli:24	18/41	10/41	20/41	24/41
K. oxytoca: 2	2/2	2/2	1/2	2/2
M. morganii: 1	0/1	1/1	1/1	1/1

Direnç Geni (+)

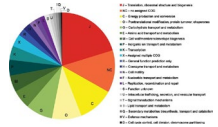
	OXA-48	NDM	KPC	IMP	VIM
K. pneumoniae: 55	10/41	2/41	6/41	1/41	0/41
E. coli:24	18/24	10/24	20/24	0/24	0/24
K. oxytoca: 2	2/2	2/2	1/2	0/2	0/2
M. morganii: 1	0/1	1/1	1/1	1/1	0/1

Porin/Eflüks

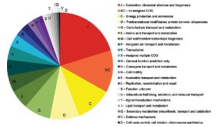
	OprD	OmpC/OmpF	ArcAB/TolC
K. pneumoniae: 55	10/41	2/41	6/41
E. coli:24	18/41	10/41	20/41
K. oxytoca: 2	2/2	2/2	1/2
M. morganii: 1	0/1	1/1	1/1

Klonalite

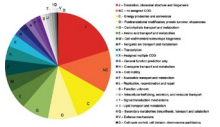
K. pneumoniae



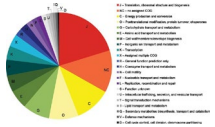
E. coli



K. oxytoca



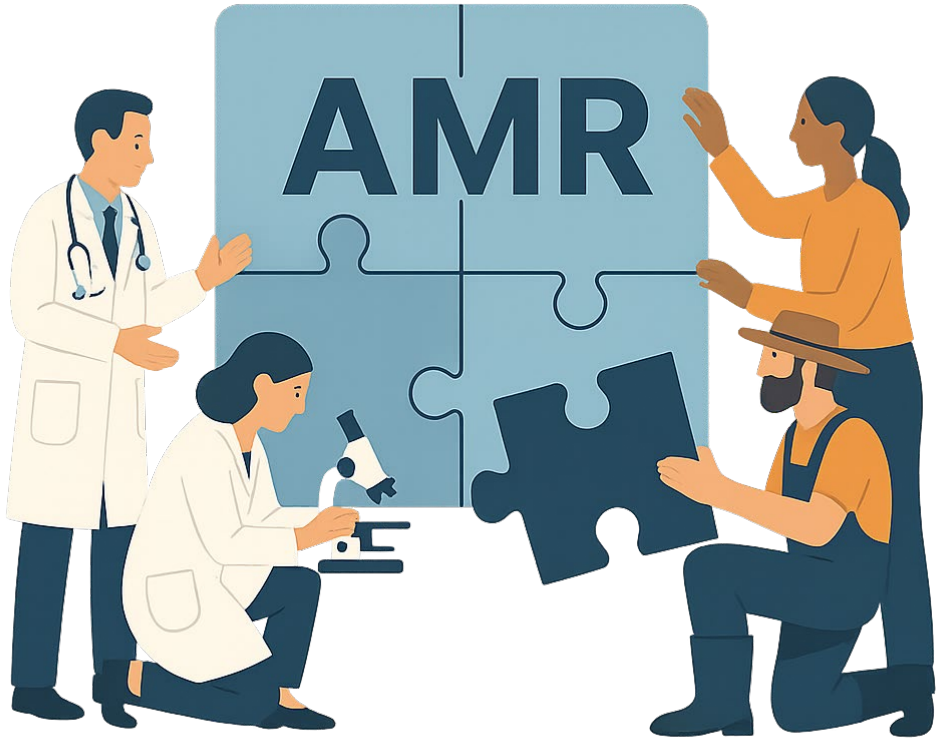
M. morganii



Tracking Resistance Beyond Phenotype

Fenotipin Ötesinde Direncin İzlenmesi: Kan Kültürlerinden İzole Edilen Karbapenem Dirençli Enterobacterales Suşlarının Moleküler Epidemiyolojisi –

KARMA Çok Merkezli Çalışması



- Dr. Çiğdem Mermutluoğlu
cigdemmermut@gmail.com

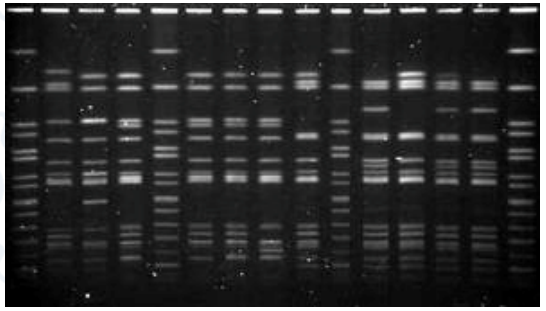
- Dr. Elif Seren Tanrıverdi
seren.tanriverdi@inonu.edu.tr

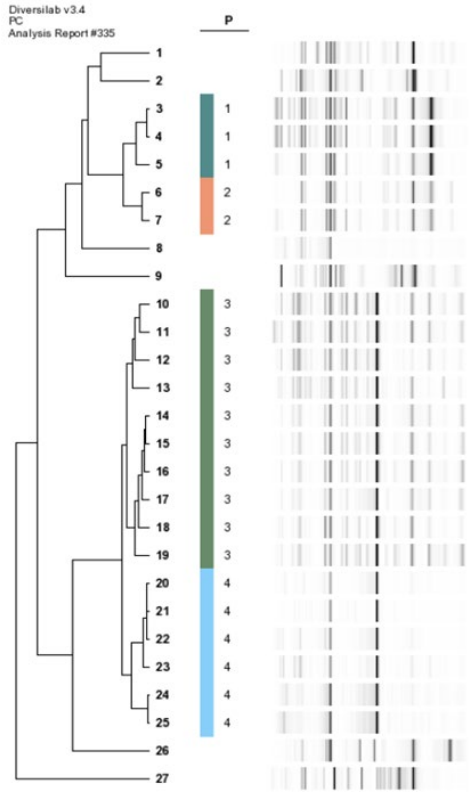
Çalışma Dışında İzolat Göndermek

- Karma çalışmasına dahil olmayacak, ancak direnç fenotipinin ve genotipinin aciliyet içerdiği durumlarda izolatlarınızı gönderebilirsiniz.
- İzolat bize geldikten sonra 24 saat içinde sonuçları e-posta adresinize ileteceğiz.

Moleküler Epidemiyoloji

- Moleküler epidemiyolojinin sınırları;
  - etken mikroorganizmanın tespiti,
  - virülanslarından sorumlu genlerin belirlenmesi,
  - bulaşma yollarının araştırılması ve
  - izolatlar arası klonal ilişkilerin araştırılmasını kapsayan geniş bir yelpazede çizilmiştir.

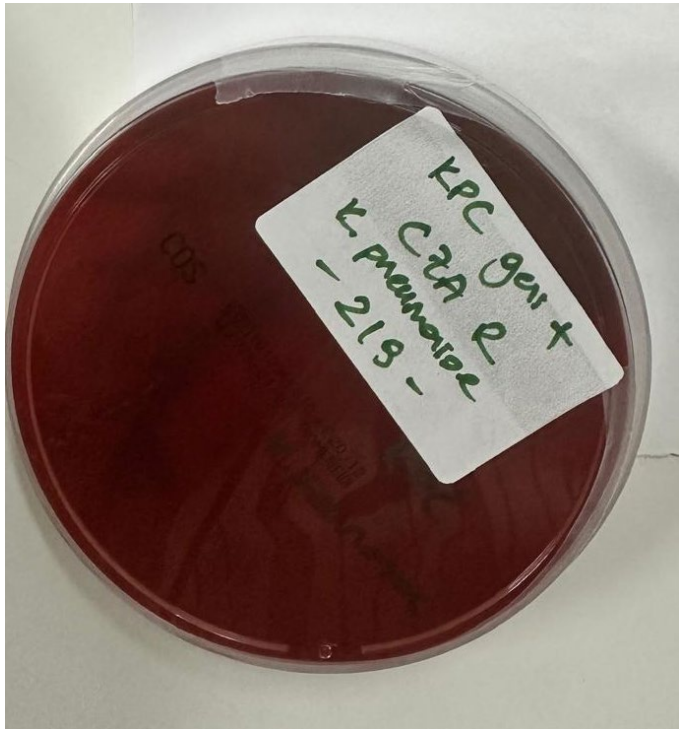




KARMA Çok Merkezli Çalışması

Potansiyel Yeni Keşifler

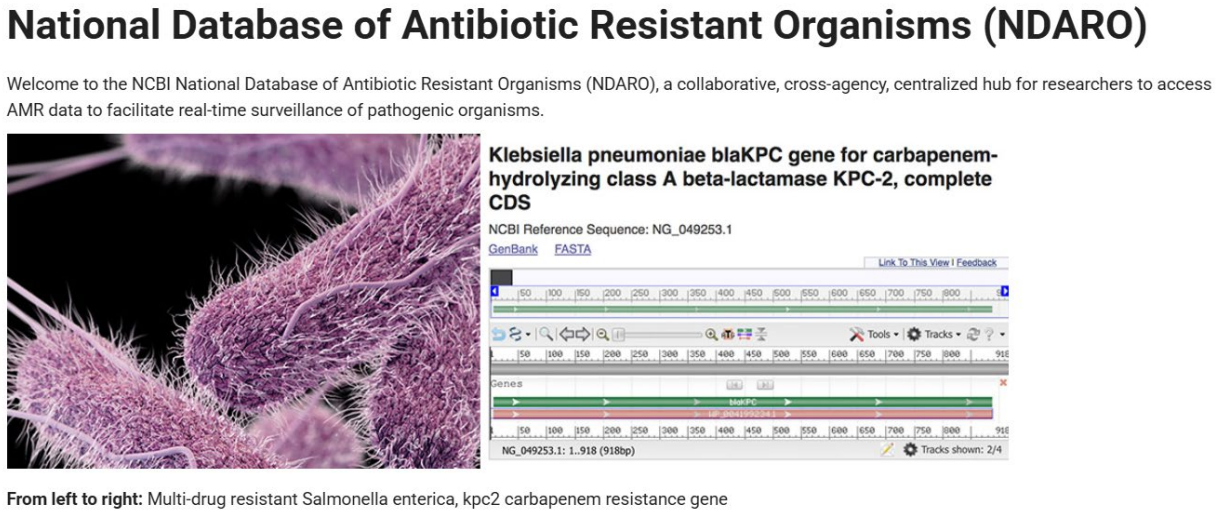
- Amikasin, gentamisin, tobramisin, kolistin (MİK: 1.0 mg/L): DUYARLI
- Levofloksasin, siprofloksasin, sefepim, sefotaksim, seftazidim, seftriakson, sefuroksim, imipenem (>64.0 mg/L), meropenem (>64.0 mg/L), ertapenem, trimetoprim-sulfametoksazol, CAZ-AVI (MİK: 16.0 mg/L): DİRENÇLİ
- PCR çalışması sonrasında KPC geni tespit edilmiştir (KPC-SE1).



- KPC-SE1; ST307 yüksek riskli klonuna aitti.
- pKpQIL benzeri IncFII(K) tipinde bir plazmid üzerinde, Tn4401a ile taşınmaktaydı.
- KPC yayılımında yüksek riskli klonların yeri önemlidir ve son yıllarda Avrupa'da başta olmak üzere ST307'de artış gözlenmektedir. Ek olarak CAZ-AVI dirençli izolatlar arasında ST307'nin azımsanmayacak kadar fazla olduğu gösterilmiştir.
- KPC'nin aynı klon içinde veya farklı klon/türlere geçişinde pKpQIL-benzeri plazmidlerin önemli bir yeri olduğu ve sıklıkla Tn4401'in bu plazmidler üzerinde KPC'nin yerleştiği klasik mobil eleman olduğu birçok sürveyans çalışmasında doğrulanmıştır.

- KPC-SE1’de, Piazza ve arkadaşlarının ilk kez 2024’te tanımladığı KPC-166’da olduğu gibi Ω-loop bölgesinde L168 delesyonu ve N169H substitüsyonu mevcuttur. Ayrıca ek olarak H179A substitüsyonu saptanmıştır.

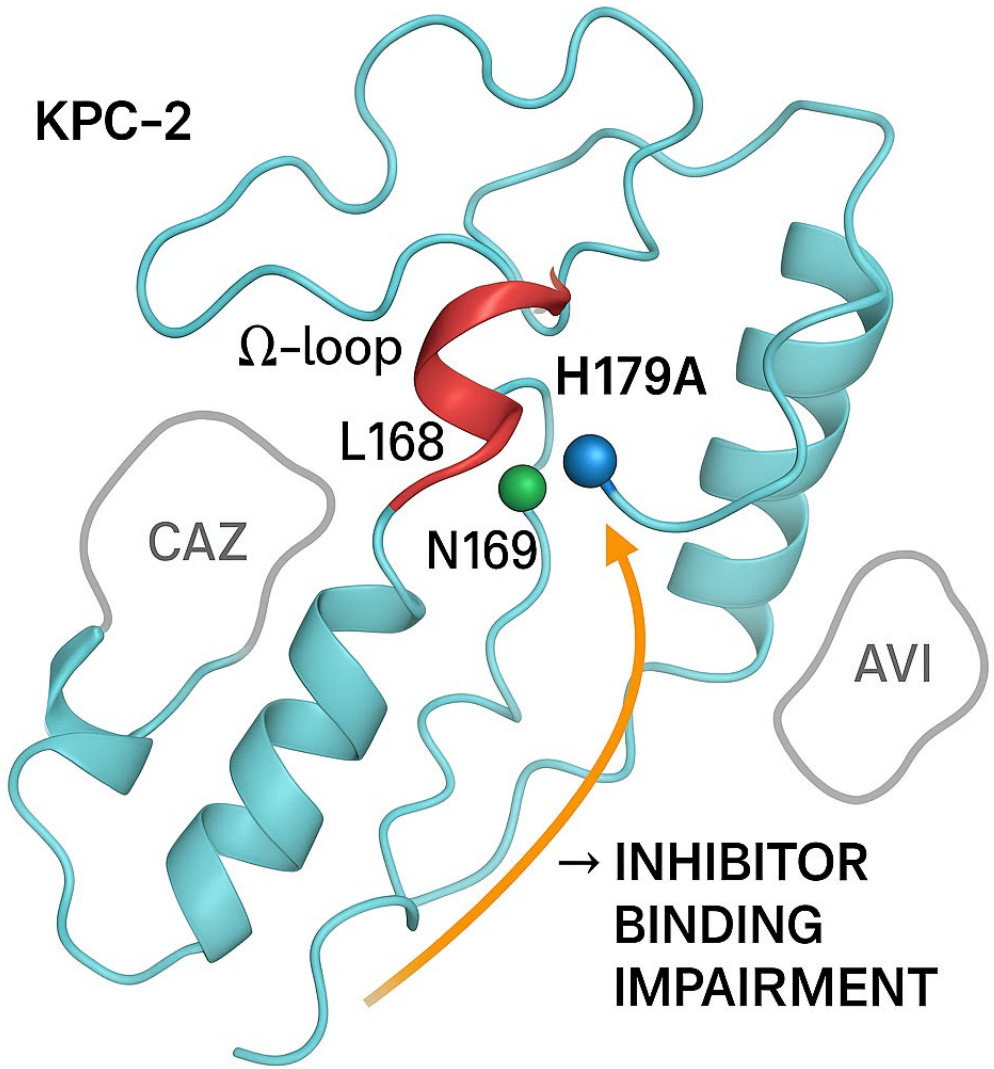
```
KPC-SE1   1 MSLYRRLVLLSCLSWPLAGFSATALTNLVAEPFAKLEQDFGGSIGVYAMDTGSGATVSYRAEERFPLCSSFKGFLAAAVL
KPC-166   1 MSLYRRLVLLSCLSWPLAGFSATALTNLVAEPFAKLEQDFGGSIGVYAMDTGSGATVSYRAEERFPLCSSFKGFLAAAVL
KPC-3     1 MSLYRRLVLLSCLSWPLAGFSATALTNLVAEPFAKLEQDFGGSIGVYAMDTGSGATVSYRAEERFPLCSSFKGFLAAAVL

KPC-SE1  81 ARSQQQAGLLDTPIRYGKNALVPWSPISEKYLTTGMTVAELSAAAVQYSDNAAANLLLKELGGPAGLTAFMRSIGDTTFR
KPC-166  81 ARSQQQAGLLDTPIRYGKNALVPWSPISEKYLTTGMTVAELSAAAVQYSDNAAANLLLKELGGPAGLTAFMRSIGDTTFR
KPC-3    81 ARSQQQAGLLDTPIRYGKNALVPWSPISEKYLTTGMTVAELSAAAVQYSDNAAANLLLKELGGPAGLTAFMRSIGDTTFR

KPC-SE1 161 LDRWELE-HSAIPGDARDTSSPRAVTESLQKLTLGSALAAPQRQQFVDWLKGNTTGNHRIRAAVPADWAVGDKTGTCGVY
KPC-166 161 LDRWELE-HSAIPGDARDTSSPRAVTESLQKLTLGSALAAPQRQQFVDWLKGNTTGNHRIRAAVPADWAVGDKTGTCGVY
KPC-3   161 LDRWELELNSAIPGDARDTSSPRAVTESLQKLTLGSALAAPQRQQFVDWLKGNTTGNHRIRAAVPADWAVGDKTGTCGVY

KPC-SE1 240 GTANDYAVVWPTGRAPIVLAVYTRAPNKDDKHSEAVIAAAARLALEGLGVNGQ 292
KPC-166 240 GTANDYAVVWPTGRAPIVLAVYTRAPNKDDKHSEAVIAAAARLALEGLGVNGQ 292
KPC-3   241 GTANDYAVVWPTGRAPIVLAVYTRAPNKDDKYSEAVIAAAARLALEGLGVNGQ 293
```



From left to right: Multi-drug resistant Salmonella enterica, kpc2 carbapenem resistance gene

- Günümüzde 260’tan fazla KPC varyantı bildirilmiştir.

- CAZ-AVI direncine sebep olan yüksek mutasyon sıklığına sahip çeşitli bölgeler tanımlanmıştır. Aktif bölgeyi çevreleyen Ω-loop (aa 164–179) bölgesi değişimin en sık gözlendiği bölgedir.



H179A → Ω-loop'un üst ucunu gevşetir → AVI'nin bağlanmasını bozar → CAZ-AVI direncini artırır.

KPC-166'daki klasik değişikliklere eklendiğinde "direnci güçlendiren dördüncü hamle" gibi davranır.

Dirençli Gram Negatif Enfeksiyon Yönetiminde Ortak Adımlar

Dr. Öğr. Üyesi Elif Seren Tanrıverdi
İnönü Üniversitesi Tıp Fakültesi
Tıbbi Mikrobiyoloji Anabilim Dalı

Merkezler

- Çalışmamız kapsamında 75 merkeze ulaştık.

Kurumlar /Bölgeler	Dr.İsmi Mikrobiyoloji	Dr.İsmi EHU
Adana Şehir Hastanesi	Uz.Dr.Nevzat Ünal	Doç.Dr. Tuğba Gülen
Adana Yüreğir Başkent Hastanesi		Prof.Dr Yusuf Ziya Demiroğlu
Adana Yüreğir Devlet Hastanesi	Uz.Dr Mustafa Cesur	Uz.Dr Nazlıgül Solmaz
Adnan Menderes Üniversitesi		Prof Dr Şerife Barçın Öztürk
Akdeniz Ünv	özlem Özyurt	ozlemozyurt@akdeniz.edu.tr
Altunizade Acıbadem	Sesin Kocagöz	Sesin Kocagoz <sesinsesin@gmail.com>
Ankara Hastanesi		Çiğdem Ataman Hatipoğlu
Antalya EAH	Hatice Nevgun Özen	nevgun@gmail.com
Antalya Şehir Hst	Elif Bilge Uysal	ebilgeuysal@gmail.com
Aydın Devlet Hst	Serkan Volkan	
B. Evler Medicalpark Hast.		Uzm. Dr. Mahmut Dülğer
Bahçelievler Medipol	Yeliz Çiçek	
Başakşehir Çam ve Sakura Şehir Hastanesi	Uz.Dr.Selda Kömeç	Doç.Dr. Ramazan Korkusuz
Bolu İzzet Baysal Köroğlu Devlet Hastanesi	Uz.Dr. Emine Zühal Kalaycı Çekin	Uz.Dr.Ayşe Torun
Bursa Şehir Hst	Umut Dağdartan	cagdasumut@yahoo.com
Bülent Ecevit Tıp Fakiltesi	Füsun Cömert	Nihal Pişkin
Cerrahpaşa Tıp Fak. Hast		Prof. Dr. Gökhan Aygün
Çukurova Üniversitesi	Doç.Dr. Hale Gümüş	Mikrobiyoloji Doç.Dr. Filiz Kibar
Dicle Üniv. Tıp Fak. Hast	Prof. Dr. Erdal Özbek	
Diyarbakır Gazi Yaşargil EAH		Muhammed Bekçibaşı
Dokuz Eylül Üniversitesi	vildan	
Doruk Nilüfer	Seval Özdemir	sevalozdemir02@gmail.com
Ege Ünv	Şöhret Aydemir	
Elazığ Fethi Sekin Şehir Hastanesi	Pınar Öner	Büşra Tanır

Merkezler

- Çalışmamız kapsamında 75 merkeze ulaştık.

Ersin Aslan EAH- Gaziantep		Uzm. Dr. Gülcan Kaplan
Eskişehir Osmangazi Üniversitesi		Fatma Erdem
Eskişehir Şehir Hastanesi		aysel Yağmuroğlu
Eskişehir Yunus Emre Devlet Hastanesi	Mustafa Kocaağa	Esra Altınsoy
Fırat Üniversitesi Tıp Fakültesi	Nuray Arı	Ayşe Sağmak Tartar
Gazi Ünv	Özge Özgen Top	
Göztepe Süleyman Yalçın Şehir Hastanesi	Esra Koçoğlu	Yasemin Çağ
Gülhane EAH		Ertuğrıu Yazıcı
Hatay Eğitim Araştırma Hastanesi	Uz.Dr.Fatma Bağcı	Uz.Dr. Tahsin Usta
Hatay Mustafa Kemal Üniversitesi		Doç.Dr Mehmet Çabalak
İnönü Üniversitesi		
İstanbul Bağcılar EAH		
İstanbul Üniversitesi Çapa Tıp Fakültesi		
İstinye Liv	Didem Taşçıoğlu	
İzmir Katip Çelebi EAH	Tuba Müderris	
İzmir Tepecik EAH	Uz Dr Duygu Tekin	Doç Dr İlkay Akbulut
Kars Kafkas Üniversitesi		Elif Özge Damar Mıdık
Kartal Lütfi Kırdar	Serap Tekol	Bülent Kaya
Kastamonu Devlet Hast	Furkan arabacı	
Kayseri Şehir Hast	esma eren	
Kocaeli Üniversitesi		Sıla Akhan, Müge toygar deniz
Konya Şehir Hst	Arzu Tarakçı Arıbaş	Şerife Yüksekkaya
Koşuyolu Kalp Damar Hastanesi		Şirin Menekşe
liv Ulus	Çağla Karakoç	
Manisa Celal Bayar Ünv	Semra Kurutepe	

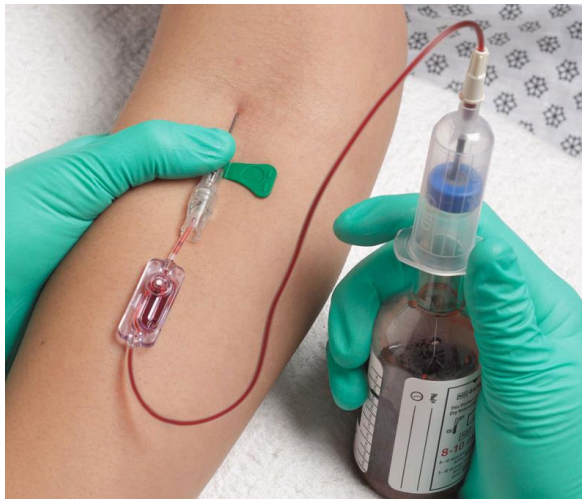
Merkezler

- Çalışmamız kapsamında 75 merkeze ulaştık.

Manisa Şehir Hastanesi		Uz Dr Sevil Sapmaz
Maslak Acıbadem	Sedef Başgönül	Serap Gencer
Medipol Mega	Meyha Şahin	Rıdvan Dumlu
Medistate Kavacık	Mücait Yemişen	
Memoral Bahçelievler	Funda Timurkaynak	
Mersin Şehir Hastanesi		Uz.Dr Mustafa Uğuz
Mersin Üniversitesi		Prof.Dr Gülden Ersöz
Muğla EAH		Alper Aksözek
Osmaniye Devlet Hastanesi	Uz.Dr. Batuhan Büyükgezgin	Uz.Dr.Fuat Yağız
Özel Anadolu Sağlık Merkezi	Melda Özdamar	
Prof. Dr. Cemil Taşcıoğlu Şehir Hast	Doç. Dr. Çiğdem Arabacı	
Recep Tayyip Erdoğan Üniversitesi	İlkay Bahçelievler	İlknur Esen Yıldız
Samsun Üniversitesi Tıp Fakültesi	Doç.Dr.Selim Görgün	Prof.Dr. Özgür Günal
Selçuk Üniversitesi		Nazlım Aktuğ Demir
Seyhan Devlet Hastanesi	Uz.Dr.Seray Tümer	Uz.Dr. Tuba Akdoğan
Seyrantepe Hamidiye Etfal EAH	senihasen@gmail.com	Seniha Şenbayrak
Sivas Cumhuriyet Üniversitesi		
Sivas Numune Hastanesi		Sevgi Baltacı
Siyami Ersek Kalp damar cerrahisi	Sinem AKKAYA IŞIK	
Süleyman Demirel Ünv	Emel Sesli	
Taksim Acıbadem		
Tekirdağ Şehir Hastanesi	Hülya Duran	
Trakya Üniversitesi Hastanesi	Prof.Dr.Hüseyin Güdücüoğlu	Habibe Tülin Elmaslar
Tuzla Devlet Hastanesi	İlvana Caklovica Küçükkaya	Pınar Elbir Kılıç
Yunus Emre Devlet	Mustafa Kocaağa	
Yüsek İhtisas		Erdem Karakaoç

Gönderim süreci

- Kan kültüründen izole edilen karbapenem dirençli *Enterobacterales* izolatları





Örnek Gönderimi

- Çalışmamız kapsamında göndereceğiniz izolatları;
  - Kanlı, EMB, çikolata, mueller hinton besiyeri
  - Taşıma besiyerleri, skim milk besiyeri gibi saklama besiyerleri



Kargo adresi: Alıcı- Elif Seren Tanrıverdi

İnönü Üniversitesi Turgut Özal tıp merkezi moleküler mikrobiyoloji laboratuvarı 3. Kat Battalgazi/Malatya

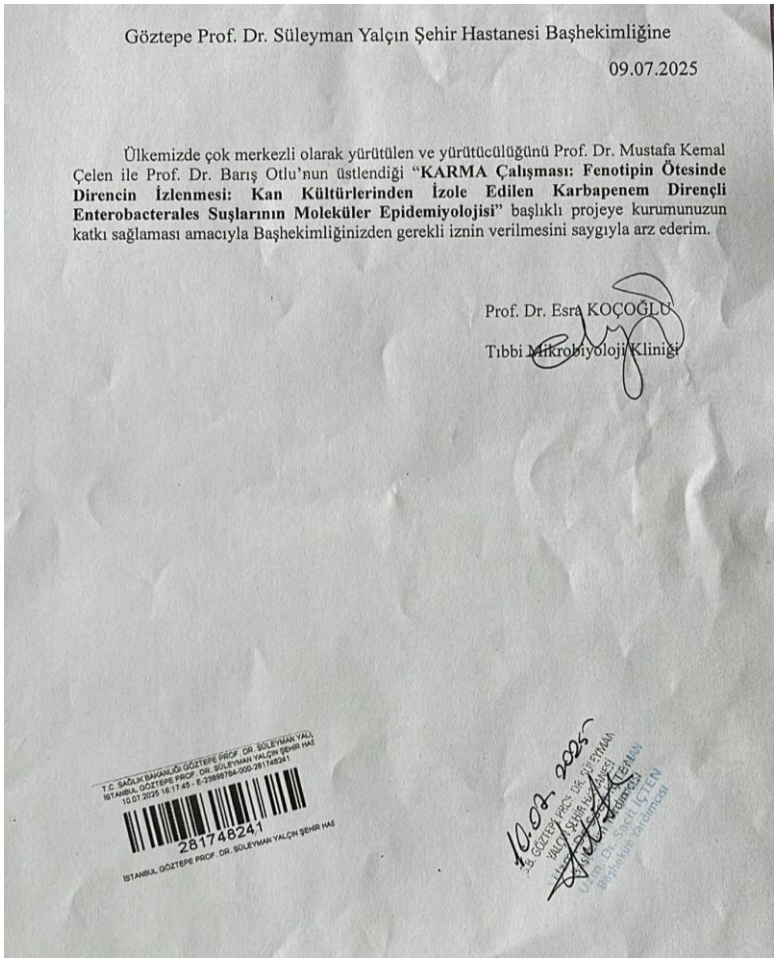
Örnek Gönderen Merkezler

- Anadolu Sağlık Merkezi
- Eskişehir Osmangazi Üniversitesi
- İzmir Katip Çelebi Üniversitesi
- Kayseri Şehir Hastanesi
- Koşuyolu Kalp Damar Hastanesi
- Samsun Eğitim ve Araştırma Hastanesi
- Sivas Numune Hastanesi

Merkezlerden 150 adet karbapenem dirençli *Enterobacterales* izolatı tarafımıza ulaştı

Etik Kurul

- Gerekli etik kurul izni koordinatör merkez tarafından alındı.
- Etik kurul için izin belgesi gönderen merkezlerimizi ekliyoruz.



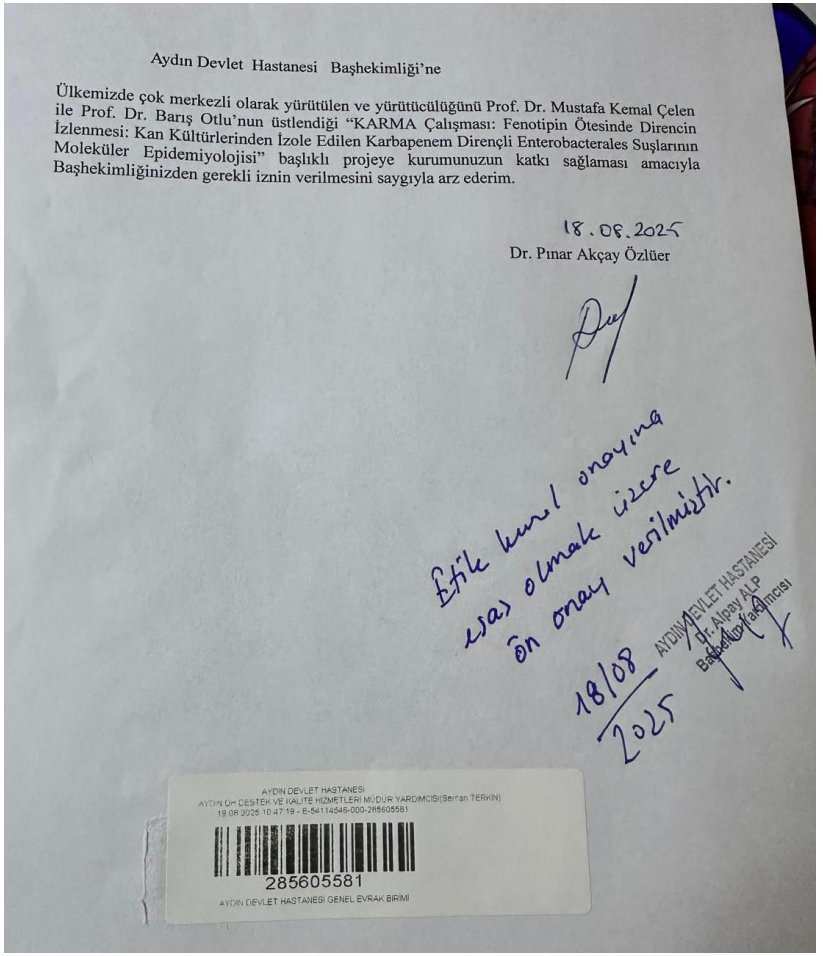
Göztepe Prof. Dr. Süleyman Yalçın Şehir Hastanesi Başhekimliğine

09.07.2025

Ülkemizde çok merkezli olarak yürütülen ve yürütücülüğünü Prof. Dr. Mustafa Kemal Çelen ile Prof. Dr. Barış Otlu'nun üstlendiği **"KARMA Çalışması: Fenotipin Ötesinde Direncin İzlenmesi: Kan Kültürlerinden İzole Edilen Karbapenem Dirençli Enterobacterales Suşlarının Moleküler Epidemiyolojisi"** başlıklı projeye kurumunuzun katkı sağlaması amacıyla Başhekimliğinizden gerekli iznin verilmesini saygıyla arz ederim.

Prof. Dr. Esra KOÇOĞLU

Tıbbi Mikrobiyoloji Kliniği



Aydın Devlet Hastanesi Başhekimliği'ne

Ülkemizde çok merkezli olarak yürütülen ve yürütücülüğünü Prof. Dr. Mustafa Kemal Çelen ile Prof. Dr. Barış Otlu'nun üstlendiği "KARMA Çalışması: Fenotipin Ötesinde Direncin İzlenmesi: Kan Kültürlerinden İzole Edilen Karbapenem Dirençli Enterobacterales Suşlarının Moleküler Epidemiyolojisi" başlıklı projeye kurumunuzun katkı sağlaması amacıyla Başhekimliğinizden gerekli iznin verilmesini saygıyla arz ederim.

18.08.2025

Dr. Pınar Akçay Özlüer

Etik kurul onayına esas olmak üzere ön onay verilmiştir.

18/08/2025

Teşekkür ederim