

NARMS and the Evolution of One Health Surveillance

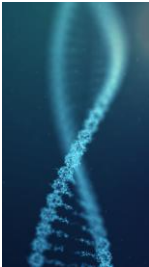
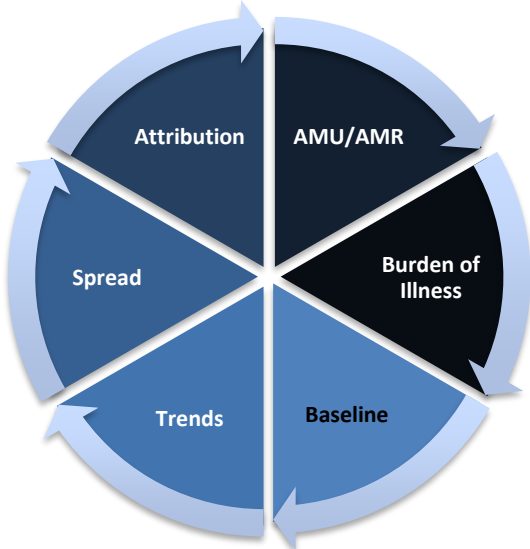
Patrick McDermott, MS, Ph.D., D(AAM)
Director, The National Antimicrobial Resistance Monitoring System
Food & Drug Administration
Center for Veterinary Medicine
Office of Research
Laurel, MD

PACCARB meeting
Dec 1, 2021

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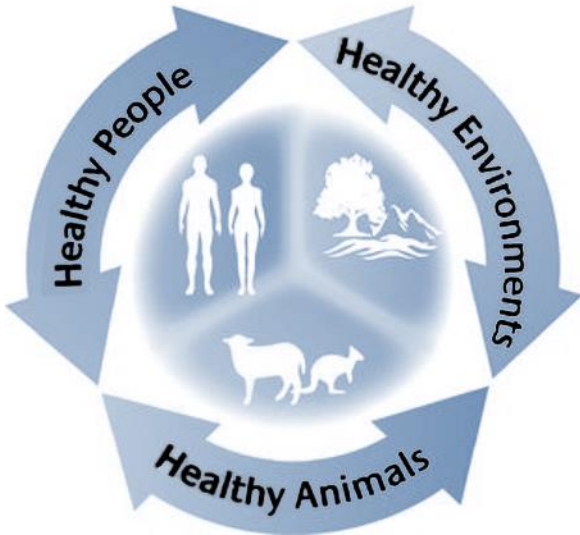
Integrated surveillance of antimicrobial resistance: **Zoonotic foodborne bacteria**

The coordinated sampling and testing of bacteria from food animals, foods, and clinically ill humans; and the subsequent evaluation of antimicrobial resistance trends throughout the food production and supply chain using harmonized methods.



One Health surveillance of antimicrobial resistance: **Human, animal, plant environment**

An integrated, unifying approach that recognizes that the health of humans, animals, plants, and our ecosystems are closely linked and inter-dependent.



GOAL 1: ENHANCE SAMPLING FOR FOODBORNE PATHOGENS WITHIN A ONE HEALTH FRAMEWORK



THE NATIONAL
ANTIMICROBIAL
RESISTANCE
MONITORING
SYSTEM

STRATEGIC PLAN
2021-2025

- *Objective 1.1:* Add select pathogens causing illness in animals
- *Objective 1.2:* Establish baseline AMR data in aquatic ecosystems
- *Objective 1.3:* Test animal feed and pet food
- *Objective 1.4:* Add seafood and explore other possible sources of AMR (minor food-producing animal species, produce, and wildlife)
- *Objective 1.5:* Explore AMR in other foodborne microorganisms

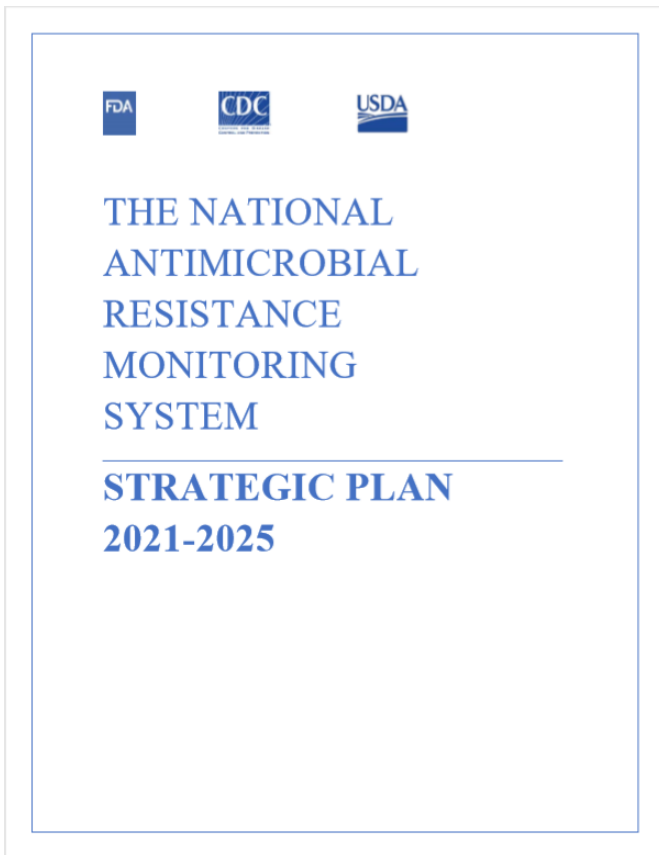
The Three Arms of NARMS - 2019

	Humans	Retail Meats	Food-Producing Animals
Agency	Centers for Disease Control and Prevention (CDC)	U.S. Food and Drug Administration (FDA)	United States Department of Agriculture (USDA)
	Health departments in 50 states	Health departments in 15 states	Food Safety and Inspection Service (FSIS)
		Universities in 7 states	Agricultural Research Service (ARS)
Source	Ill persons	Grocery Stores	Ceca and Product
		Chicken	Chickens
		Ground Turkey	Turkeys
		Ground Beef	Cattle
		Pork	Swine
Bacteria	<i>Salmonella</i>	<i>Salmonella</i>	<i>Salmonella</i>
	<i>Campylobacter</i>	<i>Campylobacter</i>	<i>Campylobacter</i>
	<i>E. coli</i> 0157	<i>Escherichia coli</i>	<i>Escherichia coli</i>
	<i>Vibrio</i>	<i>Enterococcus</i>	<i>Enterococcus</i>
	<i>Shigella</i>		

The Three+ Arms of NARMS - 2021

	Humans	Retail Meats	Food-Producing Animals	Animal Pathogens	Environment	WGS Data Repository
Agency	CDC	FDA	USDA - FSIS, ARS	Vet-LIRN, NAHLN	EPA, FDA, USDA, CDC	NIH - NCBI
Source	Ill persons	Grocery Stores	Ceca and Product	Ill Animals	Pilot Studies	Genomes
		Chicken	Chickens	Dogs	Method dev. (2021-2)	AMRFinderPlus
		Ground Turkey	Turkeys	Cats	Watersheds (2022)	
		Ground Beef	Cattle	Cattle		
		Pork	Swine	Pigs	Natl. survey (2023-4)	
		Shrimp	Veal	Poultry		
		Tilapia	Lamb			
		Salmon	Goat			
Bacteria	<i>Salmonella</i>	<i>Salmonella</i>	<i>Salmonella</i>	<i>Salmonella</i>	<i>Salmonella</i>	
	<i>Campylobacter</i>	<i>Campylobacter</i>	<i>Campylobacter</i>			
	<i>E. coli</i> 0157	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>E. coli</i>	<i>E. coli</i>	
	<i>Vibrio</i>	<i>Enterococcus</i>	<i>Enterococcus</i>	<i>Enterococcus</i>		
	<i>Shigella</i>	<i>Aeromonas</i>		<i>Other</i>	<i>Metagenome</i>	
		<i>Vibrio</i>				

GOAL 2: EMPLOY ADVANCED TECHNOLOGIES TO BETTER UNDERSTAND THE EVOLUTION AND SPREAD OF RESISTANCE AMONG FOODBORNE PATHOGENS



- *Objective 2.1:* Apply predictive resistance analytics, machine learning, and other bioinformatics tools to NARMS-related data to better understand the mechanisms, sources, and spread of resistance.
- *Objective 2.2:* Optimize *in vitro* antimicrobial susceptibility testing to identify new resistance mechanisms.
- *Objective 2.3:* Develop metagenomic approaches to characterize the resistome of animals, humans and environmental samples and to link resistance genes to their microbial source.
- *Objective 2.4:* Employ long-read DNA sequencing methods to establish a reference database of fully characterized strains and their plasmids.
- *Objective 2.5:* Conduct research to understand concomitant adaptive microbial features that might contribute to the persistence and spread of resistance (*e.g.*, colonization, stress tolerance) under different selection pressures (*e.g.*, heavy metals, antiseptics, *etc.*).

NARMS Genomes with Susceptibility Data*

Bacterium	Human	FP Animals	Retail Meats	VD Labs	Total
<i>Salmonella</i>	9,449	8,916	8,982	1,624	28,971
<i>Campy</i>	2,164	11,059	3,871		17,094
<i>E. coli</i>	566	4,314	4,569	1,690	11,139
<i>Enterococcus</i>		1,575	102		1,677
<i>S. pseudintermedius</i>				1,463	1,463
TOTAL	12,179	25,864	17,524	4,777	60,344

*As of November 24, 2021

NARMS Genotype-Phenotype Correlations

Antimicrobial Agents and Chemotherapy

Whole-Genome Sequencing for Detecting Antimicrobial Resistance in Nontyphoidal *Salmonella*

Patrick F. McDermott,^a Gregory H. Tyson,^a Claudine Kabera,^a Yuansha Chen,^a Cong Li,^a Jason P. Folster,^b Sherry L. Ayers,^a Claudia Lam,^a Heather P. Tate,^a Shaohua Zhao^a

Applied and Environmental Microbiology

Whole-Genome Sequencing Analysis Accurately Predicts Antimicrobial Resistance Phenotypes in *Campylobacter* spp.

S. Zhao,^a G. H. Tyson,^a Y. Chen,^a C. Li,^a S. Mukherjee,^a S. Young,^a C. Lam,^a J. P. Folster,^b J. M. Whichard,^b P. F. McDermott^a

JOURNALS
 investing in science

Pathogens and Disease, 76, 2018, fty018
 doi: 10.1093/femspd/fty018
 Advance Access Publication Date: 12 March 2018
 Research Article

RESEARCH ARTICLE

Whole-genome sequencing based characterization of antimicrobial resistance in *Enterococcus*

Gregory H. Tyson*, Jonathan L. Sabo, Crystal Rice-Trujillo, Jacqueline Hernandez and Patrick F. McDermott

Journal of Antimicrobial Chemotherapy

J Antimicrob Chemother 2015; **70**: 2763–2769
 doi:10.1093/jac/dkv186 Advance Access publication 3 July 2015

WGS accurately predicts antimicrobial resistance in *Escherichia coli*

Gregory H. Tyson¹, Patrick F. McDermott¹, Cong Li¹, Yuansha Chen¹, Daniel A. Tadesse¹, Sampa Mukherjee¹, Sonya Bodeis-Jones¹, Claudine Kabera¹, Stuart A. Gaines¹, Guy H. Loneragan², Tom S. Edrington³, Mary Torrence⁴, Dayna M. Harhay⁵ and Shaohua Zhao^{1*}

Antimicrobial Agents and Chemotherapy

Validating the AMRFinder Tool and Resistance Gene Database by Using Antimicrobial Resistance Genotype-Phenotype Correlations in a Collection of Isolates

Michael Feldgarden,^a Vyacheslav Brover,^a Daniel H. Haft,^a Arjun B. Prasad,^a Douglas J. Slotta,^a Igor Tolstoy,^a Gregory H. Tyson,^b Shaohua Zhao,^b Chih-Hao Hsu,^b Patrick F. McDermott,^b Daniel A. Tadesse,^b Cesar Morales,^c Mustafa Simmons,^c Glenn Tillman,^c Jamie Wasilenko,^c Jason P. Folster,^a William Klimke^a

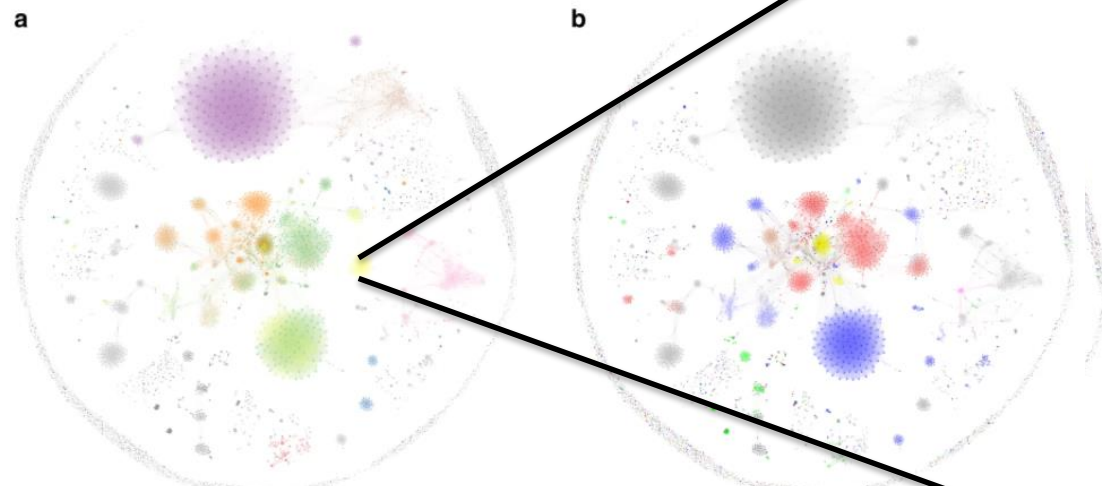
Pathways for horizontal gene transfer in bacteria revealed by a global map of their plasmids

Santiago Redondo-Salvo, Raúl Fernández-López, Raúl Ruiz, Luis Vielva, María de Toro, Eduardo P. C. Rocha, M. Pilar Garcillán-Barcia & Fernando de la Cruz

Nature Communications **11**, Article number: 3602 (2020) | [Cite this article](#)

Fig. 3: ANI_{L50} similarity network of the bacterial plasmidome.

From: [Pathways for horizontal gene transfer in bacteria revealed by a global map of their plasmids](#)

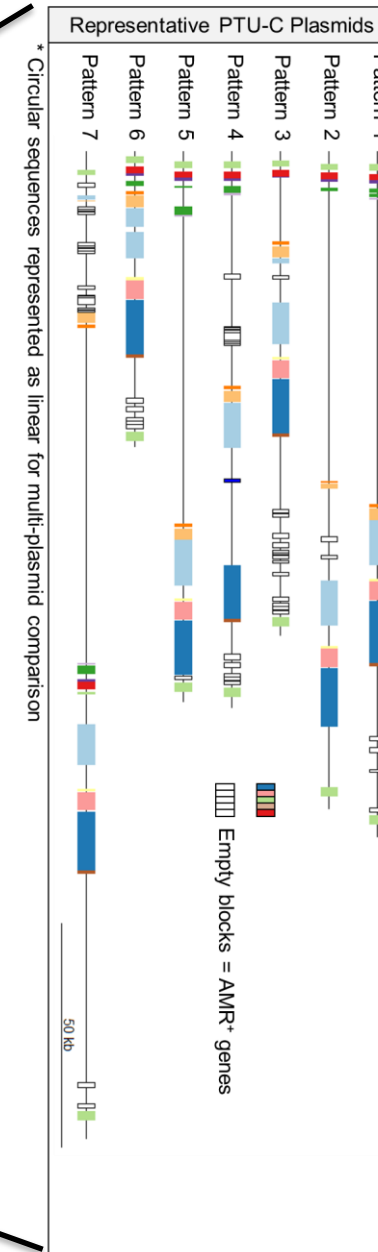


- | | | | | | |
|---|---|---|--|--|--|
| ● <i>Bacillus</i> | ● <i>Escherichia</i> | ● <i>Borrelia</i> | ● MOB _C | ● MOB _H | ● MOB _Q |
| ● <i>Lactobacillus</i> | ● <i>Salmonella</i> | ● <i>Borrelia</i> | ● MOB _F | ● MOB _P | ● MOB _V |
| ● <i>Staphylococcus</i> | ● <i>Klebsiella</i> | ● Others | ● MOB _T | ● MOB _M | ● MOB _B |
| | | | ● Multiple MOB | ● No MOB | |

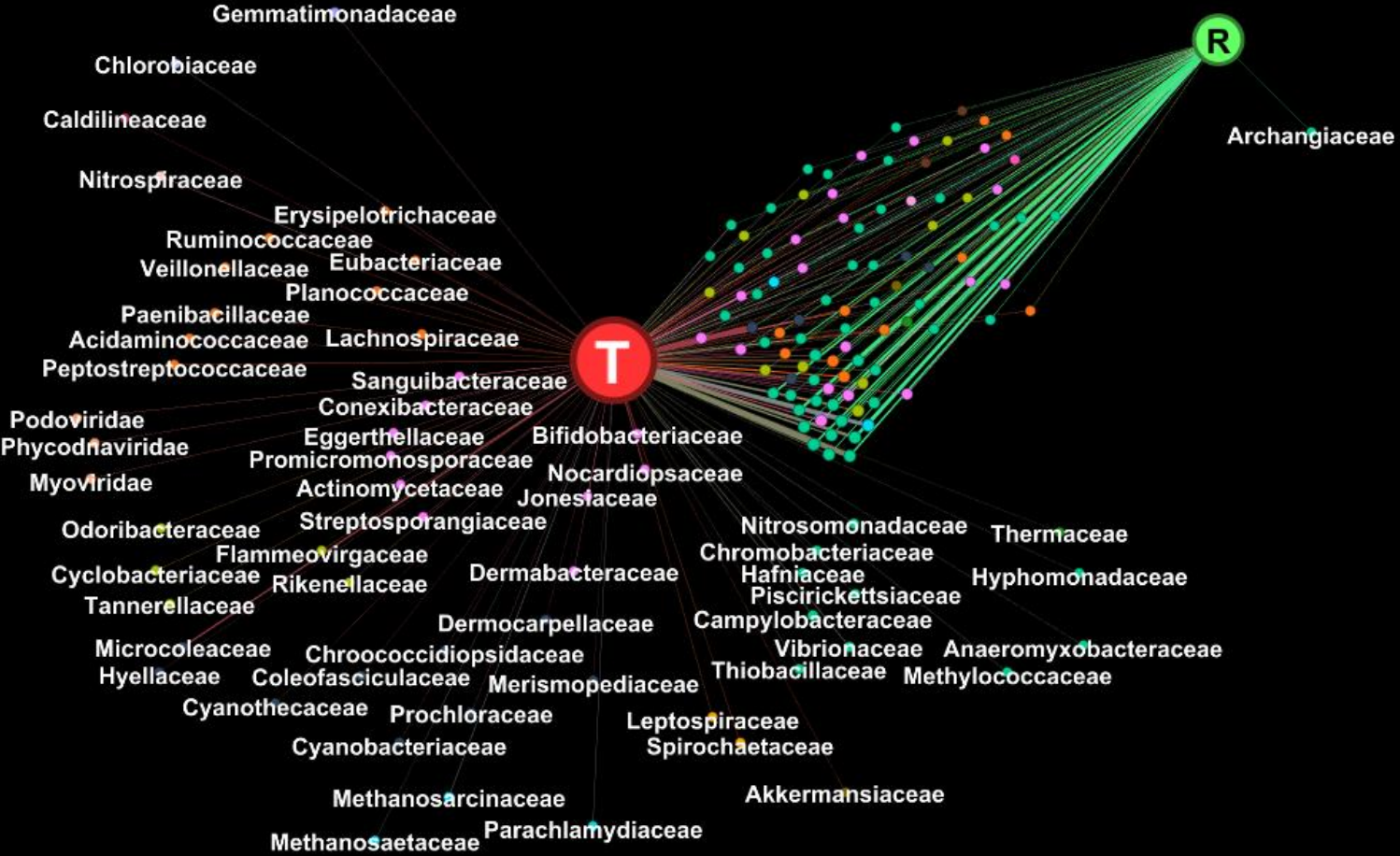
Similarity networks of the RefSeq84 prokaryotic plasmidome obtained using the ANI_{L50} algorithm as described in Methods. Nodes, corresponding to plasmid genomes, are colored according to their cognate host taxonomy (a) or MOB class, as defined by MOBscan (b). Source data are provided as a Source Data file.

Source Data file.

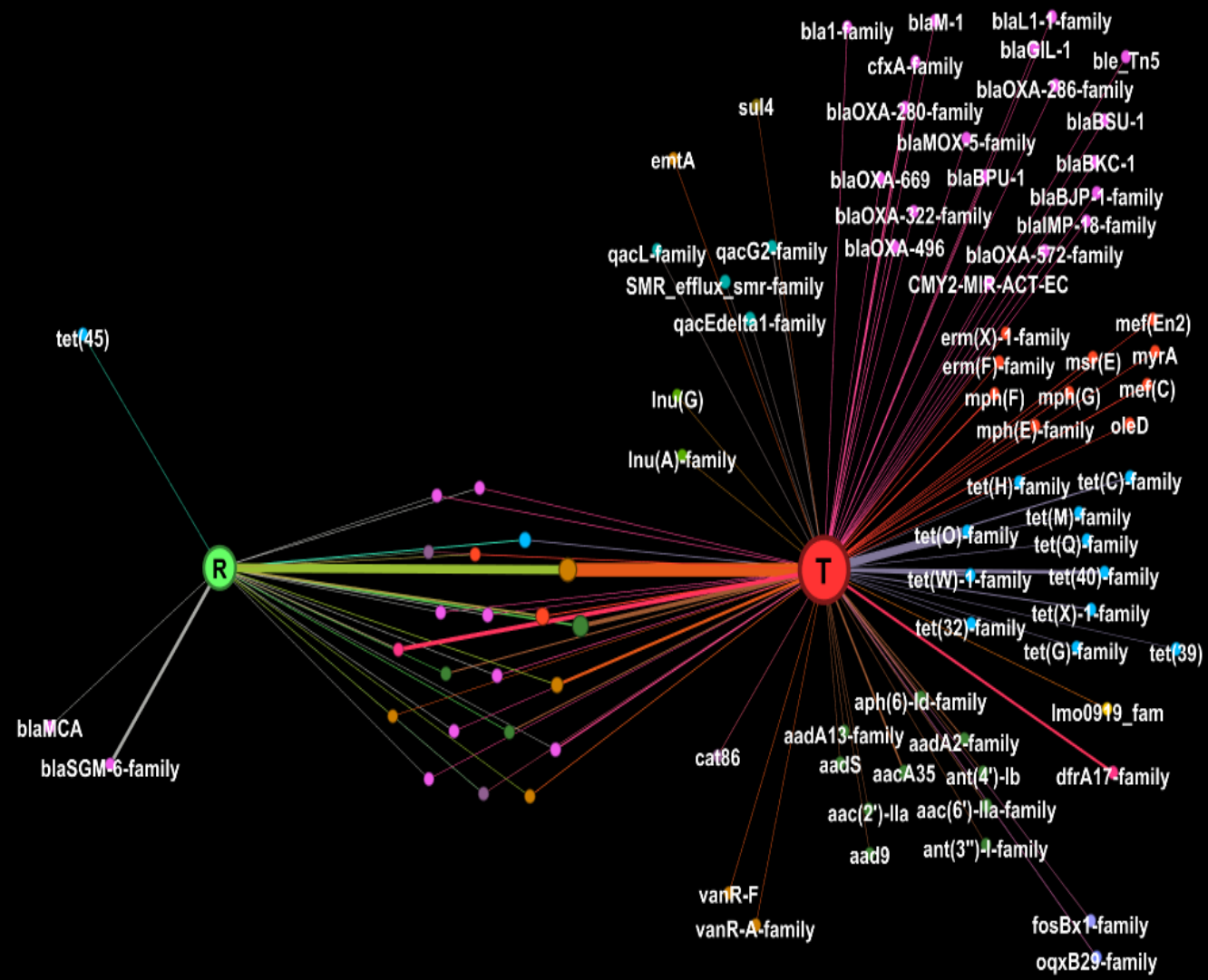
Plasmid Taxonomic Units (PTUs)



Taxonomic Differences between Less (R) and More (T) Impacted Surface Water



The Water Resistome: Comparison of Less (R) and More Impacted (T) Surface Waters



Outlook

- The NARMS strategic direction is towards defining best practices in One Health national antimicrobial resistance monitoring
- Environmental testing has begun with pilot projects to explore surface waters as points of confluence of AMR runoff from built human and agricultural environments.
- The scope of NARMS surveillance is being evaluated with pilot surveys of other food animals raised with antibiotics.
- We are fully exploiting DNA sequencing technologies to get detailed information on resistance and associated biological features and sharing data as soon as possible.
- We are planning a public meeting in September 2022



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