

## **Presence of multi-drug resistant pathogens and antibiotic resistance genes in waterways** and seafood populations of rural Southeastern Louisiana, USA

# Ethan Naquin, J.P. Diagle, and Dr. Raj Boopathy, Biological Sciences, Nicholls State University

## Introduction

Antibiotic resistance in bacteria is a natural phenomenon arising from the selective pressure due to exposure to clinical antibiotics and is also caused by misuse and overuse of antibiotics. This can cause considerable public health problems. Within the past decade alone, the Center for Disease Control has identified various bacteria as posing serious, urgent, and concerning threats to the US healthcare system due to its resistance to antibiotics (CDC, 2013). Improper usage and disposal of antibiotics by consumers, hospitals, industries, and sewage treatment plants has furthered the emergence of antibiotic resistance in the waterways of Southeast Louisiana, namely Bayou Lafourche and Bayou Terrebonne, a main source of drinking water impacting over 300,000 individuals that live along its banks. Furthermore, antibiotic resistant bacteria (ARB) has been found in raw sewage and treated sewage being released into the environment in the bayous. Ultimately, the ARB and antibiotic resistance genes (ARG) in the treatment plants affect wildlife, where the treated water is being released (Naquin et al., 2015). These water sources drain into the Gulf of Mexico, so monitoring antibiotic levels, ARB, and ARG, especially in seafood populations, are critical.

≻In Louisiana, one out of every seventy jobs are related to the seafood industry, and this region exports roughly 1 billion pounds of seafood each year at a value of 2.4 billion USD. Although the implications of an increasing presence of antibiotic resistance in the rural environment is alarming, there are no studies reported on this issue in Southeast Louisiana and the Gulf region.

### **Objectives:**

**1.Isolate and identify if antibiotic resistant bacteria (ARB) and antibiotic resistant genes** (ARG) are present in samples collected from various seafood species. 2. Determine if bacteria isolated in pure culture can thrive in environments with various concentrations of antibiotics.

**3.**Analyze concentrations of antibiotics in our waterways.

## Methods

- 1. Pure Cultures were isolated and identified from various seafood species a. Colonies were isolated as pure cultures in Tryptic Soy Broth (TSB) from quadrant
- streak method on Tryptic Soy Agar (TSA) from Black Drum, Blue Crab, Shrimp, Oyster, Redfish, Speckled Trout, Cobia, Mahi-Mahi, and Amberjack.
- b. BIOLOG identification technique was used to identify bacterial species.
- 2. Antibiotic resistance was observed using Kirby-Bauer Assay:
- a. Pure Cultures were streaked as a bacterial lawn onto Mueller Hinton (MH) Agar and antibiotic discs were stamped onto the agar using an antibiotic disc dispenser. The following eight antibiotics were used: Tetracycline (TE 30), Streptomycin (S 10), Penicillin (P 10), Ampicillin (AM 10), Sulfamethoxazole-Trimethoprim (SXT), Vancomycin (VA 5), Bacitracin (B 10), and Clindamycin (CC 2).
- Plates were incubated at 37°C for 24 hours, and the zones of inhibition were measured. Bacteria were classified as Susceptible (S), Intermediate (I), or Resistant (R).
- 3. Antibiotic resistance genes were identified
- a. Genome sequencing was performed on two isolates
- b. BLAST was used for antibiotic resistance gene identification
- 4. Bacterial Growth Curve was performed
- a. One bacteria resistant to tetracycline was chosen at random from a fish species to perform a growth curve at varying concentration of tetracycline (0 mg/L, 250 mg/L, 500 mg/L, 750 mg/L, and 1000 mg/L) in Basic Mineral Salt Media.
- b. Lactococcus garvieae resistant to TE 30 was chosen from Redfish.
- The bacterial growth was analyzed using HACH DR6000 spectrophotometer:
  - <u>Ammonia</u>: absorbance on Day 0 and Day 10 (initial and final)
  - Optical Density (OD): absorbance on Day 0 through Day 10

## 5. Antibiotic levels in local waterways were analyzed

- One site along Bayou Lafourche and one site along Bayou Terrebonne were sampled for antibiotic pollution.



**Figure 1.** Local Speckled Trout on ice. Samples were taken by swabbing the external extremities of the fish using a sterile cotton swab and sterile DI water.

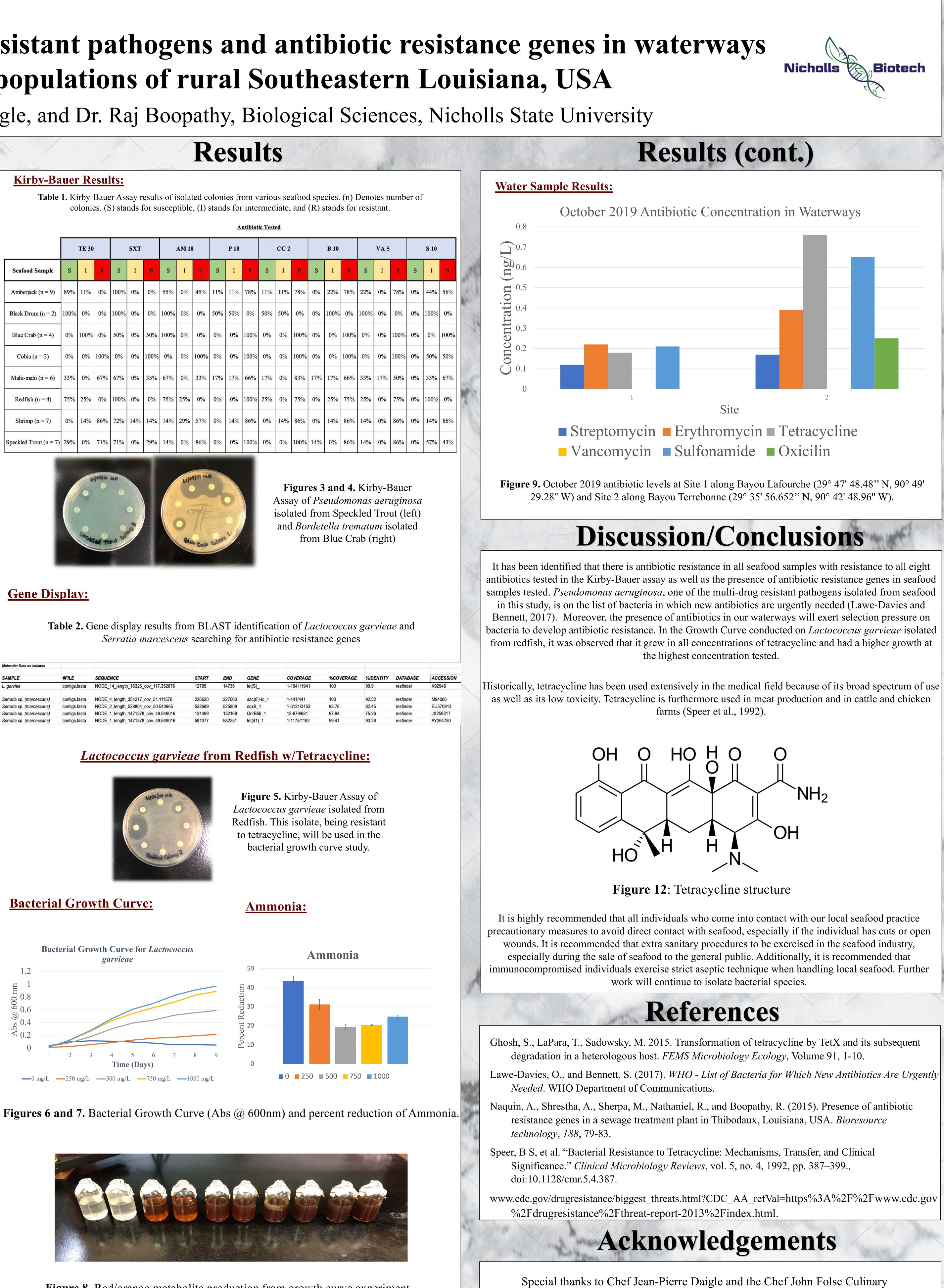
Figure 2. Sites in Southeast Louisiana where water samples were analyzed. (1) Represents the Bayou Lafourche site, (2) represents the Bayou Terrebonne site, and (N) represents Nicholls State University.

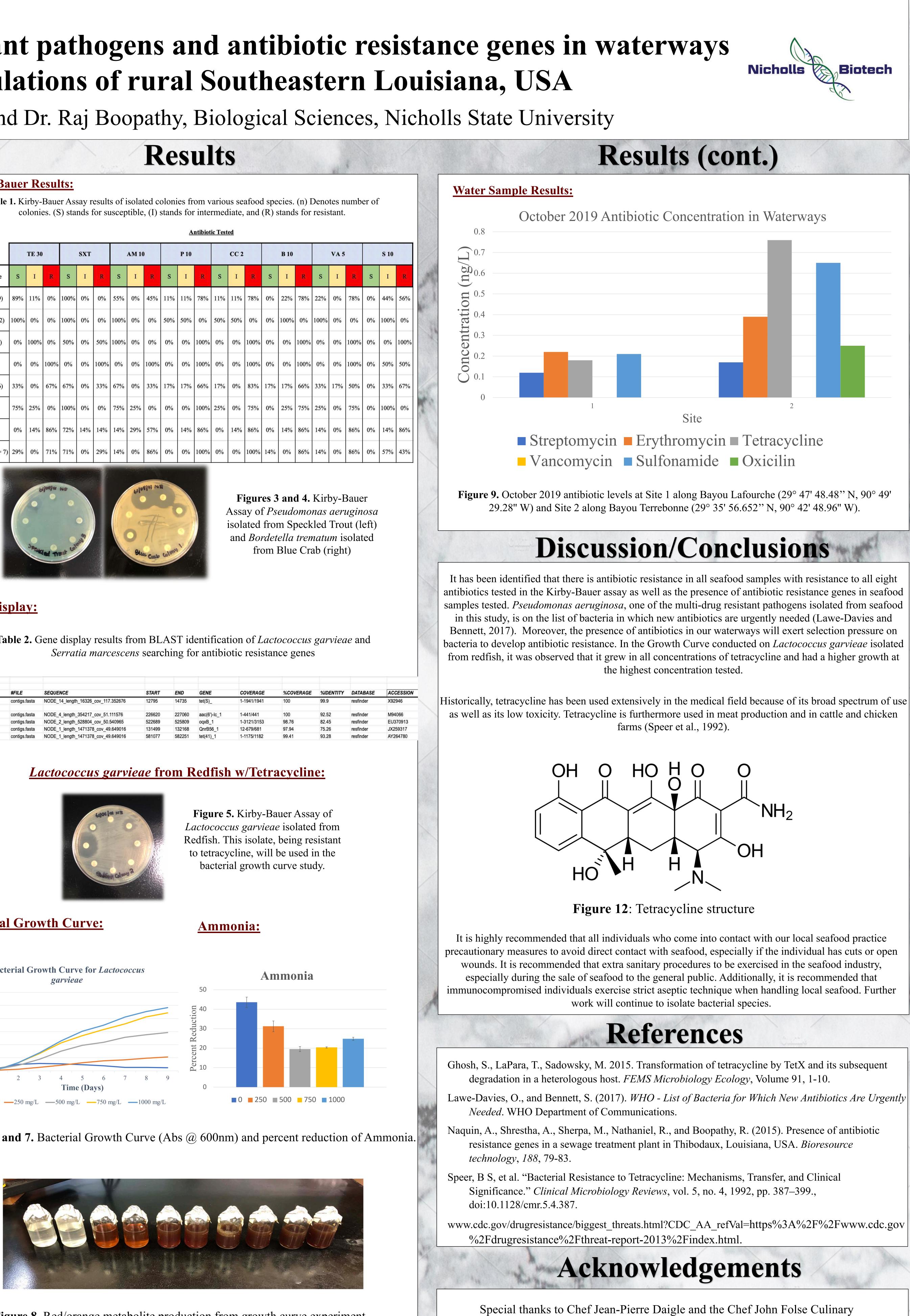
		Antibiotic Tested										ed		
	TE 30			SXT			AM 10			P 10			CC 2	
Seafood Sample	S	I	R	S	Ι	R	S	I	R	S	Ι	R	S	I
Amberjack (n = 9)	89%	11%	0%	100%	0%	0%	55%	0%	45%	11%	11%	78%	11%	11%
Black Drum $(n = 2)$	100%	0%	0%	100%	0%	0%	100%	0%	0%	50%	50%	0%	50%	50%
Blue Crab $(n = 4)$	0%	100%	0%	50%	0%	50%	100%	0%	0%	0%	0%	100%	0%	0%
Cobia (n = 2)	0%	0%	100%	0%	0%	100%	0%	0%	100%	0%	0%	100%	0%	0%
Mahi-mahi (n = 6)	33%	0%	67%	67%	0%	33%	67%	0%	33%	17%	17%	66%	17%	0%
Redfish $(n = 4)$	75%	25%	0%	100%	0%	0%	75%	25%	0%	0%	0%	100%	25%	0%
Shrimp (n = 7)	0%	14%	86%	72%	14%	14%	14%	29%	57%	0%	14%	86%	0%	14%
Speckled Trout $(n = 7)$	29%	0%	71%	71%	0%	29%	14%	0%	86%	0%	0%	100%	0%	0%



	Molecular Data on isolates						
	SAMPLE	#FILE	SEQUENCE	START	END	GENE	co
1	L. garviae	contigs.fasta	NODE_14_length_16326_cov_117.352676	12795	14735	tet(S)_	1-19
1	Serratia sp. (marcescans)	contigs.fasta	NODE_4_length_354217_cov_51.111576	226620	227060	aac(6')-lc_1	1-44
	Serratia sp. (marcescans)	contigs.fasta	NODE_2_length_528804_cov_50.540965	522689	525809	oqxB_1	1-31
	Serratia sp. (marcescans)	contigs.fasta	NODE_1_length_1471378_cov_49.649016	131499	132168	QnrB56_1	12-6
	Serratia sp. (marcescans)	contigs.fasta	NODE_1_length_1471378_cov_49.649016	581077	582251	tet(41)_1	1-11







**Figure 8.** Red/orange metabolite production from growth curve experiment.

Institute at Nicholls State University for providing fish for sampling