MYCOPLASMOLOGY

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Summary

Members of the genus *Mycoplasma* and the class *Mollicutes* are highly unusual organisms in that they lack a cell wall, are orders of magnitude smaller than most known bacteria, and have minimalist genomes. This lineage of bacteria has undergone intensive degenerate evolution, and as such, all species are obligate parasites that must live in association with other organisms. Most species are commensals or causes of minor infections, but a small number are major pathogens that contribute to substantial economic losses relating to both human and animal infections. Finally, the reduced genome size of *Mollicutes* made them excellent targets for pioneering work in genome sequencing projects, attempts to define the minimal genome required for life, and the creation of the first known self-replicating synthetic cells. This chapter represents an overview of the cellular biology, clinical diseases, and societal impacts of mycoplasmas.

1. Introduction to Mycoplasmology

1.1. History of Mycoplasmology

The first clinically recognized mycoplasmosis, contagious bovine pleuropneumonia (CBPP), was caused by the first mycoplasma to be grown in culture, *Mycoplasma mycoides* subspecies *mycoides* (formerly termed "variant small colony (SC)"). The genus *Mycoplasma* was given its name in 1956, long after the first recognition of mycoplasmosis. This delay in apt nomenclature is highly atypical and stemmed from an inability to resolve many seemingly paradoxical findings. The causative agent of CBPP could pass through filters typically used to remove bacterial cells and could not be viewed by light microscopy.

Conversely, this entity was able to grow in the absence of eukaryotic cells, yet seemed to require several eukaryotic cell components for viability. *Mycoplasma mycoides* displayed characteristics of both bacteria and viruses, and as such it was the first of a short-lived category of pathogens, the pleuropneumonia-like organisms (PPLOs).

Multiple theories surfaced regarding the identity and origin of mycoplasmas. Kleineberger *et al.* suggested that mycoplasmas were L-forms (L-phase variants) (Klieneberger, 1939), a notion that was later refuted by Razin *et al.* in 1969. The contradictory work demonstrated that PPLOs seemed to have smaller genomes and lower guanine+cytosine (G+C) contents than those of L-forms, which retain the traits of their parent species (Razin, 1969). As evidence mounted that mycoplasmas were a unique and simplistic variety of bacteria, the proposition was made that they were the progenitors of more complex bacteria (Wallace and Morowitz, 1973).

The confusion recurred when the causative agent of human primary atypical pneumoniae (PAP) was cultured in chicken embryos and fulfilled Koch's postulates by producing disease in hamsters and rats (Meiklejohn et al, 1945). As the infectious agent was filterable, could not be visualized by light microscopy, and was resistant to penicillin, the authors concluded that it was an unknown virus, and termed it Eaton's agent. Attempts to culture Eaton's agent in PPLO medium were unsuccessful, adding to the notion that it was a viral agent. Subsequent studies showed sensitivity to other antibacterial compounds (Eaton and Liu, 1957; Eaton et al, 1951), and eventually growth in an alternate cell-free medium. Eaton's agent was reclassified and renamed *Mycoplasma pneumoniae* (Chanock, 1963).

The complex and textured nature of the history of mycoplasmas is easily understood in retrospect. It is now clear why these bacteria displayed certain characteristics normally associated with viruses. Two such characteristics, the observations that the agents of CBPP and PAP could pass through filters and could not be visualized by light microscopy, is due to the currently known size of mycoplasmas. Copious studies using electron microscopy to visualize mycoplasmas demonstrated that they are 200-500 nm; making them more comparable in size to viruses than other bacteria.

The observation by Meiklejohn *et al.* that the agent of PAP could grow in chicken embryos in the presence of penicillin despite being bacterial (Meiklejohn et al, 1945) is

also explainable by subsequent data. The antimicrobial mechanism of penicillin involves breaking down the peptidoglycan layer of the bacterial cell wall (Fisher, 1946). It became clear 15 years after the initial description of Eaton's agent that mycoplasmas lack cell walls, and are enclosed only by a sterol-containing cell membrane. Such organisms would obviously have an intrinsic resistance to penicillin.

The final observations used to conclude that the agent of PAP was caused by a virus were the growth of the agent in chicken embryos and lack of viability of the agent in cell-free culture. Culture media used in an attempt to cultivate Eaton's agent included the medium intended to grow PPLOs (developed for growth of *M. mycoides*), which was considerably more rich than typical bacterial growth media. Eaton's agent required eukaryotic cells, or so it seemed.

The cultivation of Eaton's agent by Chanock *et al.* in 1960 (Chanock et al, 1960) in a cell-free medium (PPLO medium supplemented with horse serum and yeast extract, now known as Hayflick's medium) led to the recognition of this agent as a mycoplasma. Though the newly-named *M. pneumoniae* cells were free-living, self-replicating entities, it was clear that they were heavily reliant on eukaryotic components for growth. It was proposed that mycoplasmas, though bacterial rather than viral pathogens, were prone to parasitism.

1.2. Evolution and Taxonomy

Mycoplasmas fall within the class *Mollicutes* (phylum *Tenericutes*). As there are more than 160 distinct *Mycoplasma* species and 8 distinct *Ureaplasma* speciesaccording the Bergey's Manual of Systematic Bacteriology (Brown et al, 2010), further classification of the *Mycoplasmataceae* was undertaken. *Mycoplasma* species are subdivided into groups, and then into clusters. Phylogenitc analysis based on the 16S rRNA gene clearly indicates that the *Mollicutes* belong to the clade of gram-positive bacteria despite lacking a cell wall.

Mollicutes have undergone extensive reductive evolution enabled by living in associated with eukaryotic hosts, and thus have very small genome sizes. Genetic material is lost through obsolescence as bacteria adapt to living in conjunction with a host, either parasitically or mutualistically. At present, the complete genomes of thirty *Mollicutes* (twenty-seven mycoplasmas) have been sequenced (see Table 1).

An examination of these genomes reveals, among many other things, that mycoplasmas lack biosynthetic capabilities, thus explaining their extreme host dependence. In addition to earlier studies contradicting the notion of mycoplasmas being the progenitors of more complex bacteria (Neimark, 1967; Neimark and Pene, 1965; Woese et al, 1980), the complete genomes clearly indicate that these species have evolved degenerately.

Mollicutes species	Strain	Genome	%G+C	Predicted	Type Stroin ^a	Reference
		(MB)		Reading Frames	Strain	
M. agalactiae	PG2	0.88	29%	742	Yes	Sirand- Pugnet <i>et al</i> , 2010
M. alligatoris	A21JP2	0.97	27%	839	Yes	Brown <i>et al</i> , 2011
M. arthritidis	158L3-1	0.82	30%	631	No	Dybvig <i>et al</i> , 2008
M. bovis ^b	PG45	1.0	29%	868	Yes	Wise <i>et al</i> , 2011
<i>M. capricolum</i> sbsp capricolum ^b	California kid	1.0	23%	812	Yes	Glass <i>et al</i> , 2007
<i>M. capricolum</i> sbsp capripneumoniae	M1601	1.01	23%	875	No	Chu <i>et al</i> , 2011
M. conjunctivae	HRC/581	0.85	28%	727	Yes	Calderon- Copete <i>et al</i> , 2009
M. crocodyli	MP145	0.93	26%	763	Yes	Brown <i>et al</i> , 2011
<i>M. fermentans</i> ^b	JER	0.98	27%	835	No	Shu <i>et al</i> , 2011
M. gallisepticum ^b	R	0.996	31%	726	No	Papazisi <i>et al</i> , 2003
<i>M. genitalium</i> ^b	G37	0.58	31%	475	Yes	Fraser <i>et al</i> , 1995
M. haemofelis ^b	Langford 1	1.15	39%	1545	NA	Barker <i>et al</i> , 2011
M. hominis	PG21	0.67	27.1%	537	Yes	Pereyre <i>et al</i> , 2009
M. hyopneumoniae ^b	J	0.90	28%	657	No	Vasconcelos <i>et al</i> , 2005
M. hyorhinis ^b	HUB-1	0.84	26%	654	No	Liu <i>et al</i> , 2010
M. leachii	PG50	1.01	24%	925	Yes	Wise <i>et al</i> , 2012
M. mobile	163K	0.78	25%	633	Yes	Jaffe <i>et al</i> , 2004
<i>M. mycoides</i> sbsp <i>capri</i>	GM12	1.09	24%	911	Yes	Wise <i>et al</i> 2006
M. mycoides sbsp mycoides ^b	PG1	1.21	24%	1016	Yes	Westberg <i>et</i> <i>al</i> , 2004
M. ovipneumoniae	SC01	1.02	29%	864	No	Yang <i>et al</i> , 2011
M. penetrans	HF-2	1.36	26%	1037	Yes	Sasaki <i>et al</i> , 2002
M. pneumoniae ^b	M129	0.82	40%	689	No	Himmelreich <i>et al</i> , 1996

M. pulmonis	UAB CTIP	0.96	26%	782	No	Chambaud <i>et</i> <i>al</i> , 2001
M. putrefaciens	KS1	0.83	27%	725	Yes	Calcutt and Foecking, 2011
M. suis ^b	Illinois	0.74	31%	783	NA	Messick <i>et al</i> , 2011
M. synoviae	53	0.80	28%	659	No	Vasconcelos et al, 2005
Acholeplasma laidlawii	PG-8A	1.5	31%	1433	Yes	Lazarev <i>et al</i> , 2011
<i>Candidatus</i> Phytoplasma asteris ^b	AYWB	0.71	26%	671	NA	Bai <i>et al</i> , 2009
Mesoplasma florum	L1	0.79	27%	687	Yes	Knight <i>et al</i> , 2004
Ureaplasma parvum ^b	700970	0.75	25%	653	No	Glass <i>et al</i> , 2000
Ureaplasma urealyticum ^b	33699	0.87	26%	695	No	Shrivastava <i>et</i> <i>al</i> , 2012

NOTE: This table is current as of this publication. Additional genome sequencing projects are currently ongoing, and thus this table is by its nature likely to be incomplete

^a NA = not applicable, due to non-culturable status of the species

^b Data for additional strains or serovars have also been reported

Table 1. Characteristics of Sequenced Mollicutes Genomes

1.3. Metabolism and Cell Biology

Mycoplasma cells are highly pleiomorphic due to the lack of a cell wall, and form colonies with "fried egg" morphology when grown on solid agar. A minority of species exhibit polarity due to internal cytoskeletons (Fig. 1, Fig. 2).

These structures seem to have arisen from multiple distinct evolutionary events based on the dissimilarity of the proteins composing and regulating them, and the function of the polar structure. In several species these structure are associated with cell motility, cytadherence, or both (Balish and Krause, 2006). The cellular machinery used for gliding motility differs between species depending on the composition of the cytoskeleton; similarly, the mechanism(s) for cytadherence and the target of cell attachment vary grately by species.

Mycoplasmas have limited capacity for metabolic function, lacking all anabolic and many metabolic and catabolic pathways. The functions that remain are involved in energy generation rather than biomolecule synthesis, as they have evolved mechanisms to rely on their hosts for the latter. Pathways for energy generation are also minimal, as mycoplasmas lack the machinery necessary for the tricarboxylic acid cycle and other mediators of oxidative phosphorylation (Razin et al, 1998). *Mollicutes* have been

demonstrated to catabolize a limited number of sugars, arginine, organic acids, urea, and alcohols for energy generation.



Figure 1. *Mycoplasma* Cellular Morphology. Most *Mycoplasma* cells are highly pleiomorphic due to the lack of a cell wall, and are exemplified here by *Mycoplasma gallinarum* (A). A minority of species exhibit polarity due to internal structures, represented by *Mycoplasma genitalium* (B). Scanning electron microscopy images are presented courtesy of M. F. Balish.



Figure 2. Mycoplasma Colony Morphology. The classical appearance of Mycoplasma colonies on solid agar are said to resemble fried eggs, as exemplified by Mycoplasma anatis (A). Some species have an umbonate (Mycoplasma canis, B) or granular (uncharacterized Mycoplasma species, C) appearance. Colonies images are presented courtesy of D.R. Brown.

Acid-producing mycoplasmas generate much of their energy from glycolysis primarily via glucose utilization, although additional complex glycans can be catabolized by certain species (Abu-Groun et al, 1994; Dahl and Dahl, 1984; Matsuda et al, 1997; Miles et al, 1986). The byproducts of these pathways result in the accumulation of acidic compounds, which results in the characteristic downward pH shift of the culture

medium of these organisms (May et al, 2008). Some mycoplasmas hydrolyze arginine as a means of energy generation.

This occurs through the arginine dihydrolase pathway, which requires only three enzymes. Hydrolysis of arginine results in the accumulation of ammonia, resulting in the characteristic upward pH shift of the culture medium. Some species, such as *M. fermentans*, are capable of utilizing both sugars and arginine as carbon sources (Brown et al, 2010; Brown et al, 2010). Culture medium pH shifts can be used diagnostically as an adjunct to additional techniques (May et al, 2008).

A relatively small number of mycoplasmas have been shown to catabolize organic acids and alcohols as carbon sources. These less common carbon sources include lactic acid, pyruvic acid, and oxobutyric acid, and ethanol, isopropanol, and glycerol (Khan et al, 2005; Razin et al, 1998; Taylor et al, 1994). The catabolism of glycerol leads to the production of hydrogen peroxide, which is now considered to be a component of the virulence of multiple species (Megid et al, 2001; Niang et al, 1998; Pilo et al, 2005).

Certain *Mollicutes* rely on more complex sources of energy as either a primary or secondary source. The hydrolysis of urea for energy has only been observed for species of *Ureaplasma*. Urease inhibitors are toxic to ureaplasmas, indicating that urea may act as a sole a carbon source (Razin, 1978; Romano et al, 1980; Smith et al, 1993). In addition, the potential exists for sialic acid, hyaluronic acid, N-acetylglucosamine, and glucuronic acid to serve as nutritional supplements in the small number of species with genes for catabolism of these glycans (Brown et al, 2004; May and Brown, 2008; Vasconcelos et al, 2005). Experimental confirmation of this utilization remains an ongoing field of study.

The complete lack of anabolic pathways in mycoplasmas is compensated for by an overrepresentation of transport-associated proteins, most commonly ATP-binding cassette transporters (ABC transporters). These integral membrane proteins are highly promiscuous transporters that facilitate the uptake of biomolecules (Saurin and Dassa, 1996). Sugar phosphotransferase transport systems (PTSs) are also found in fermentative *Mycoplasma* species (Razin et al, 1998). It is likely that multiple other transport mechanisms exist to compensate for the limited biosynthetic capabilities of mycoplasmas.

1.4. Molecular Biology of Mycoplasmas

A major hurdle that has yet to be overcome is the limited ability at present to genetically manipulate mycoplasmas. With notable exceptions, mycoplasmas do not appear to harbor naturally occurring self-replicating plasmids, and attempts to transform them with commercial cloning vectors have failed. Success with targeted disruption of genes in order to determine their function has been rare for all species but *Mycoplasma genitalium*. Gene and protein function in mycoplasmas, much like any other species, is most often determined by examining deletion mutants. Mutants are typically obtained by random insertion of transposons such as Tn916 or Tn4001 (Dybvig and Cassell, 1987; Mahairas and Minion, 1989). Several modifications (Table 2) have since been

Transposon	Origin	Resistance Marker	Reporter Gene	Notes/Distinctions
<i>Tn</i> 916	Streptococcus	Tetracycline	None	Large; inefficient; first mycoplasma transpositions
<i>Tn</i> 4001	Staphylococcus	Gentamycin	None	Efficient; more widely used; replaced <i>Tn</i> 916
Tn4001mod	Staphylococcus Tn4001	Gentamycin	None	Multiple cloning site; gene delivery and expression
Tn4001cat	Staphylococcus Tn4001	Chloramphenicol	None	Multiple cloning site; alternative resistance
Mini- Tn4001tet	Staphylococcus Tn4001	Tetracycline	None	Multiple cloning site; alternative resistance; limited mobility
Tn4001lac	Staphylococcus Tn4001	Gentamycin	β- galactosidase	Promoterless <i>lacZ</i> ; assessment of promoter strengths

made to *Tn*4001 (Hahn et al, 1999; Knudtson and Minion, 1993; Pour-El et al, 2002), rendering it one of the most widely used molecular tools in mycoplasmology.

Table 2. Characteristics of Commonly Used Transposons in Mycoplasma spp.

Because mycoplasmas do not successfully carry commercial plasmid vectors, artificial plasmids containing the chromosomal origin of replication have been developed and are termed OriC plasmids (Renaudin and Lartigue, 2005). Distinct vectors must be generated for each species. Successful expression of genes has been described for Spiroplasma citri, Mycoplasma pulmonis, Mycoplasma mycoides subspecies capri, M. mycoides subspecies mycoides, M. capricolum, M. gallisepticum, and M. agalactiae (Chopra-Dewasthaly et al, 2005; Cordova et al, 2002; Renaudin and Lartigue, 2005; Renaudin et al, 1995; Ye et al, 1994). In addition, artificial plasmid vectors have been made based on sequences of integrative conjugal elements (ICE), which are found naturally occurring both intra- and extrachromosomally in certain Mycoplasma species (Brown et al, 2010). A small number of Mollicutes species (Mycoplasma arthritidis, Mycoplasma pulmonis, Mycoplasma fermentans, and multiple Spiroplasma species) are hosts to bacteriophage (Dybvig and Cassell, 1987; Röske et al, 2004; Voelker et al, 1995). None of the bacteriophage infecting mycoplasmas has been successfully used to deliver genes via transduction. Only the virus SpV1, that infects Spiroplasma citri, has been successful (Marais et al, 1993; Stamburski et al, 1991). A factor complicating the cloning and expression of mycoplasmal genes in other bacteria is the usage of the UGA codon to encode tryptophan, making it difficult to express their genes in other bacteria without altering the gene first. Strides have been made in recent years toward expanding the repertoire of molecular tools available for use in mycoplasmas. Commonly used molecular tools are presented in Table 3.

Though the isolation of the first PPLO, much later named *M. mycoides*, occurred fairly early in the discipline of medical microbiology, the implications of the findings were not appreciated until much later. The eventual realization that these pathogens, which blurred the contemporary line between bacteriology and virology, were minimalist bacteria led to the powerful suggestion that they preceded complex life. The observation

that mycoplasmas were parasitic naturally begged the question of how they could possibly have been progenitors. Such queries led to the notion that bacteria can adapt to their niches in a reductive fashion, an important concept in pathogen evolution.

Tool	Description	Uses	Features
Transposons	See Table 2	Gene disruption,	Random insertion, in
		gene expression	trans expression
OriC Plasmids	Commercial	Gene expression,	Direct cassette insertion,
	vector + species	homologous	in cis expression
	origin of	recombination	
	replication		
ICE vectors	Commercial	Gene expression,	Direct cassette insertion,
	vector +	homologous	in cis expression
	mycoplasmal	recombination	Co
	ICE element		
psPuro	Tn4001 mini Tet	Gene disruption,	Random insertion, in
	with pac gene	gene expression	trans expression,
			puromycin selection
Genome	In vitro genesis	Generation of	Specific genome design
Synthesis	of designed	artificial	
	chromosome	chromosome	
Genome	Insertion of	Expression of	Synthetic cell generation,
Transplantation	chromosome	artificial or	species reassignment
	into an existing	heterologous	
	membrane	chromosome	

Table 3. Molecular Tools Used in Mycoplasmology

2. Clinical Manifestations of Mycoplasmosis

Infections with Mycoplasma species exhibit a spectrum of clinical manifestations ranging from asymptomatic states to fulminant inflammatory diseases with high mortality rates. Despite these extremes, the classical manifestation (without clinical intervention) is a chronic inflammatory illness that is not typically fatal, though this is the normal state for a small number of mycoplasma such as *M. alligatoris* and *M.* mycoides subsp. mycoides. Often these infections are compounded by secondary pathogens, resulting in more severe disease with higher rates of morbidity and mortality. The primary sites of most mycoplasmal infections are mucosal surfaces. The establishment of infection is mediated by attachment to the epithelium, where they exist as surface pathogens. Additionally, mounting evidence suggests that multiple species have invasive capabilities and that intracellular phases may be part of the infectious process (Andreev et al, 1995; Dallo and Baseman, 2000; Díaz-García et al, 2006; Jensen et al, 1994; Tarshis et al, 2004; Taylor-Robinson et al, 1991; Winner et al, 2000; Yavlovich et al, 2004). As highly adapted parasites, mycoplasmas tend to exhibit host specificity and tissue tropism, although exceptions to both rules have been extensively documented. The number of distinct Mycoplasma species is large, and as such, detailed clinical descriptions of the disease state of each are not provided. Tables 4-6 describe mycoplasmosis of humans and animals.

2.1. Human Disease

Community-acquired pneumonia and other manifestations of M. pneumoniae

Clinical manifestations of upper respiratory tract infections by *M. pneumoniae* most commonly include pharyngitis and laryngitis, and those of the lower respiratory tract include tracheitis and interstitial pneumonia. The latter is clinically referred to as "community-acquired pneumonia" in addition to PAP, and commonly referred to as "walking pneumonia". Symptoms include low-grade fever, non-productive cough, and chest pain. Community-acquired pneumonia outbreaks are frequently associated with close quarters and stress, and as such are often associated with military barracks or student dormitories. Post-infectious complications following community-acquired pneumonia disease can include the development or exacerbation of asthma and secondary ear infections, and rarely Guillain-Barré syndrome, Stevens-Johnson syndrome, Bell's Palsy, optic neuritis, or demyelinating disorders. Atypical manifestations of *M. pneumoniae* infections are depicted in Figure 3.



Figure 3. Atypical Manifestations of *Mycoplasma pneumoniae* Infection. The primary clinical presentation of *M. pneumoniae* infection is primary atypical pneumonia (community-acquired pneumonia); however, many additional manifestations have been described.

Sexually-acquired mycoplasmosis

Urogenital infection with *M. genitalium*, *M. hominis*, and *Ureaplasma* species can be detected in asymptomatic patients; however, numerous studies have explored the correlation of patient infection with several urogenital lesions. The clinical states

associated with *Ureaplasma* spp. and *M. hominis* appear to be strain- or patient-specific, and can include nongonococcal urethritis (*Ureaplasma* spp.), bacterial vaginosis (*M. hominis*), spontaneous abortion, or preterm labor (both organisms) (Waites and Talkington, 2005). The role of *M. genitalium* in nongonococcal urethritis, pelvic inflammatory disease, spontaneous abortion, and infertility is much less ambiguous, and it is consequently considered an emerging urogenital pathogen (McGowin and Anderson-Smits, 2011). Infection with *M. genitalium* has been associated with increased shedding of human immunodeficiency virus (HIV) particles in one study (Manhart et al, 2008), but did not appear to influence shedding rates in another (Gatski et al, 2011). Because of the enormous public health consequences involved, the notion that *M. genitalium* may facilitate HIV transmission requires further study.

Infection of pregnant women with *Ureaplasma* spp. has been associated with preterm labor and premature rupture of membranes. Disruption of the physical barrier between organisms present in the vagina and a perinatal infant can result in infection of the respiratory tract or central nervous system of the infant. Congenital and neonatal pneumonia is a grave concern of preterm infants, and *Ureaplasma* spp. have been included as causal agents. Chronic lung conditions can persist in these infants following the resolution of infection. *Ureaplasma* and *M. hominis* have also been implicating in neonatal meningitis following premature rupture of the membranes (Washburn et al, 1980).

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Synthetic Genomics' web site describes some of the potential benefits to designed, synthetically created organisms including biofuel production].

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Biographical Sketches

Meghan Anne May was born in 1979. In 2001 she graduated from the University of New Hampshire's Department of Microbiology and went on to earn Master of Science (2004) and Doctor of Philosophy (2006) degrees from the University of Connecticut's Department of Pathobiology and Veterinary Science for her work on avian mycoplasmosis. She then completed postdoctoral work at the University of Florida College of Veterinary Medicine's Department of Infectious Diseases and Pathology focusing on wildlife and agricultural mycoplasmosis. In 2010 Meghan May was appointed to the faculty of the Department of Biological Sciences at Towson University as the expert in Microbiology and Animal Diseases, and currently hold the Fisher Endowed Chair of Biological Sciences. Also in 2010, she was elected to the International Committee for the Systematics of Prokaryotes subcommittee for the taxonomy of *Mollicutes*. Effective July 2012, she will be the chair of the Molecular Genetics Team of the International Research Programme for Comparative Mycoplasmology. She is the author of several peer-reviewed articles and a growing number of textbook chapters, most notably in Bergey's Manual of Systematic Bacteriology. Her scientific interests include the evolution of virulence as modeled by mycoplasmas and novel approaches to treatment and control of livestock mycoplasmosis as a means to combating poverty and malnutrition.

Amanda Victoria Arjoon, Jessica Ann Canter, Dylan William Dunne, and Brittney Terrell are currently enrolled students in the Fisher College of Science and Mathematics and/or the College of Health Professions at Towson University. These early-career scientists are the authors of five presentations at national and international meetings to date.