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## How Microbiomes Can Feed the World: A Look into Bovine Reproduction

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# **How Microbiomes Can Feed the World: A Look into Bovine Reproduction**

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The University of Tennessee, Knoxville

Chancellor's Honors Program

Department of Animal Science

**Undergraduate Thesis**

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## **Introduction**

As the human population continues to grow, a greater demand is put on the animal agriculture industry to increase both quantity and quality of food animal products. With a world population of approximately one billion cattle that govern a billion dollar market, cattle industries, including both dairy and beef, are of great importance to international agriculture and economy (Laguardia-Nascimento, 2015).

As is the goal of any business, the animal agriculture industry seeks to produce the highest quantity of marketable product in the shortest amount of time to maximize efficiency. However, animal producers have an extra obstacle to tackle when it comes to maximizing productivity. Biological constraints such as the inability to shorten and manipulate gestation periods have a very tight control on our ability to meet a growing consumer demand. These constraints leave a lot of pressure on minimizing the time it takes a female animal to become pregnant again after parturition. In order to minimize the postpartum interval, animal agriculture has focused research and technological innovation on a broad spectrum of reproductive applications.

Although a lot of improvements in reproductive efficiency can be made through human designed procedures such as super ovulation and embryo transfer, the sole productivity of the cattle industry still rests on the cow's ability to achieve and maintain a viable pregnancy. Despite our countless attempts to gather information on outside factors that affect fertility such as nutrition, the natural reproductive environment has been greatly neglected. Although animal scientists are familiar with the presence of gastrointestinal symbionts and their influence on productivity, little information is known about the microorganism composition of the reproductive tract and the roles these organisms may play in fertility status (Durso, 2015).

## **Microbiomes**

In recent years, the study of micro-organisms has moved from an individual in vitro focus to a more ecological perspective by focusing on how these organisms interact intra- and interspecifically in niches called microbiomes (Yeoman, 2011). Although the term microbiome refers to the array of micro-organisms that peacefully inhabit and coincide with a species, disturbances in these natural populations can have detrimental effects on health and normal physiological conditions (Aagard, 2014). With the rising threat of drug resistant microbes, information regarding the way these populations function collectively in their natural environment may provide invaluable answers to the medical field (Foxman, 2015).

In 2007, the National Institutes of Health led the effort to discover and outline all of the commensal bacterial organisms that share the human body through initiating the Human Microbiome Project (Sirota, 2014). Because approximately 80% of human-associated microorganisms cannot be successfully cultivated in a lab setting, this project succeeded at compiling a more accurate species profile through collecting information in the organisms' natural human niche (Green, 2015). This unique project and subsequent research have helped make connections between individual micro-organisms and particular physiological and medical conditions affecting the fertility of their human host. It is now widely accepted that the communities present in the female reproductive tract shape multiple facets of our lives ranging from the vitality of our immune system and our ability to reproduce (Sirota, 2014).

In spite of expanding current information on the existence of microbial populations in the reproductive tract, the Human Microbiome Project brought to light how much information is lacking on specifically how these microbiomes function and affect their environment. Research is still underway to define how these microbiomes are established and why they vary between

individuals. Little of the information established can be applied until further information is collected on how these specialized communities are affected by factors such as an individual's genetics, diet, environment, history, and physiological processes. The more information we discover about each species, the more potential we have to accurately diagnose an abnormal microbiome and utilize individualized medicine to treat disease and infertility effectively. This implication is pertinent to the bovine industry where microbial related diseases often halt reproductive productivity and continue to be one of the top costs to producers (Santos, 2012).

### **Current Human Implications**

Much of our current knowledge of the female reproductive microbiome comes from research investigating human infertility, pregnancy loss, and disease. Most research studies conducted to evaluate the reproductive microbiome in human females focus on assessing problems associated with sexually transmitted diseases (STDs), bacterial vaginosis related infertility, and newborn immunity (Braundmeier, 2015).

With the reproductive tract as no exception, every microbiome has a normal communal population that can fluctuate to an infectious state. When fluctuations in microorganism diversity or abundance reach towards the extremes, infection and inflammation can occur in forms such as bacterial vaginosis (BV). Although bacterial vaginosis commonly affects reproductive-age women, this condition can lead to increased risk for severe infections, STDs, changes in cyclicity, and infertility. Although the causes of these fluctuations are not completely understood, BV has been highly correlated with the use of certain contraceptives. Studies into the effects of certain materials and chemicals on the reproductive microbiome are working towards

developing better contraceptive methods that do not disrupt the microbial composition or leave increased risk for infection (Braundmeier, 2015).

Because STDs are caused by micro-organisms either viral or bacterial, evaluation of the reproductive microbiomes of affected and non-infected individuals has provided pathological insight on these diseases as well as helped define individuals who may be more susceptible versus those who may have better defenses. Several studies have now established that those individuals prone to pelvic inflammatory disease, which involves migration of vaginally-associated bacterial to the upper reproductive tract, are at higher risk of contracting certain sexually transmitted diseases such as HIV and chlamydia. Likewise, individuals who participate in certain physical activities that affect hygiene and microbiome composition may also be at higher risk for bacterial vaginosis and subsequent STD infection (Green, 2015). Research into the causes of microbiome migration may help design new methods for prevention of these diseases.

Microbiome research has also played an important role in shaping the choices of future mothers. It was not until recently that doctors began to accept that babies are not born sterile and that the natural birth process plays a large role in shaping a newborns microbiome. According to several studies conducted on babies born through the natural labor process versus those born through caesarian section, researchers found that babies born through natural birth exhibited a microbiome most similar to that of their mother and had higher immunity levels. With this information, the popularity of choosing a caesarian section out of convenience may sharply decline. Future mothers who are informed that a natural birth may lead to a healthier baby are more than likely to consider a caesarian section as more of an emergency procedure. (Funkhouser, 2013).

The information provided through the Human Microbiome Project has already provided many applications, solutions, and further questions to explore. Much of this information can be readily applied to the reproductive physiology and health of the bovine. Not only do cattle carry similar microbial species, they also share relative reproductive cycles, conditions and diseases with humans.

### **Bovine Implications**

In order to reach maximum production, cattle producers have to meet a goal of one calf per year while working with a gestation period of around 274 days. To accomplish this goal, cows must be able to establish a pregnancy only 80 days after parturition. Even with current technology and medicine, producers continue to fight a losing battle with delayed cyclicity and infertility problems that keep them from reaching the goal of one calf every 365 days. Most of these problems stem primarily from infectious microbial conditions such as endometritis. Hopefully, research into the bovine reproductive microbiome will provide as many possibilities for improvement as the Human Microbiome Project did towards infertility. Although STDs can be avoided in cattle thanks to artificial insemination (AI) technologies, much of the human implications of microbiome research apply to food animal reproduction. Very little research has been done so far towards profiling the bovine reproductive microbiome, but what has been collected has verified many of the observations from human studies.

Through the correlations that human research has drawn between contraceptive materials and microbial disruption, bovine reproductive specialists should draw conclusions that certain materials used in current assisted reproductive technologies may need to be improved in order to

protect fertility rates. The research areas are endless when it comes to assessing how certain hormone or drug administration used to manipulate cyclicity affect microbiome composition and related fertility. On the other hand, a small collection of research suggests that inoculation of tools used in assisted reproductive technologies with certain types of microbial populations, such as *Lactobacillus*, may counteract any microbial disruption and improve pregnancy rates (Franasiak, 2015).

Forefront research characterizing microbes present in the vaginal microbiomes of ewes and cows has established that many of these microbes play a positive role in regulating pH levels to protect the rest of the reproductive environment (Swartz, 2014). Additionally, several studies have suggested that future research may reveal a correlation between placental microbiomes and pregnancy loss as well as the ability to detect certain stages of pregnancy via microbial signatures. Both of these possibilities would be of positive impact to the productivity of the industry with less financial loss and cheaper more convenient methods of pregnancy detection, respectively (Aagard, 2012).

It is easy to see the possibilities for innovation in the field of bovine reproduction as more information is collected through in vivo observation and research. The cattle industry should place a high value on this new realm of information and how it can affect the future of animal agriculture. As can be seen from the variety of human research collected, there are endless implications for the information gained about the reproductive microbiome.



## Conclusion

As of November 24, 2015, only two research projects have been published profiling and characterizing the reproductive microbiome of cattle using samples collected in vivo (Laguardia-Nascimento, 2015). There is a great need for further research because the microbiome may play a large role in the reproductive diseases and infertility that cost producers substantial losses each year. The cattle industry is of pronounced economic importance worldwide and, with a growing consumer population, cattle fertility will need to be at optimum percentages in order for productivity and genetic improvements to meet both quantity and quality demands.

By looking at experiments and models already performed in human research, we can best shape future research efforts to collect more information about the microbiomes of our food animals and how they affect the status of not only healthy and sick individuals, but fertile and infertile individuals as well. The more details we know about the composition and function of each species in the various niches of the reproductive microbiome, the better our capabilities for diagnostic, preventative care, treatment and reproductive success. Using this information to minimize postpartum interval and infertility issues will maximize productivity in both dairy and beef industries to help meet the demand of a hungry world.

As can be seen in the small amount of information already collected in bovine research, the reproductive microbiome plays a large role in maintaining the reproductive tract, developing a successful pregnancy, maintaining a pregnancy, and shaping the immune system and health status of the newborn calf. With the widespread use of assisted reproductive technologies like artificial insemination, monitoring the microbial population will be a convenient task that can be performed on a regular basis and prove no trouble for even the most inexperienced producer. These commensal organisms may also be invaluable as a tool to boost the success of these

technologies. Although micro-organisms tend to have a negative connotation, further knowledge and information on the beneficial roles they play in creating a perfect reproductive environment may help us utilize these organisms to grow the cattle industry and feed our growing world.

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