Texas Dairy Matters

Higher Education Supporting the Industry

The Impacts of the Reproductive Microbiome on Dairy Cattle Fertility

Dallas Soffa, M.S.
Doctoral Student
Department of Animal Science
The Texas A&M University System

Reproductive failure, which includes failure to become pregnant and pregnancy loss during any point of gestation, financially devastates the dairy industry each year. With over $2,000 in loss per pregnancy failure, understanding how to mitigate reproductive inefficiency is imperative[1]. Recent research has focused on the bacterial communities of the reproductive tract and how they may impact fertility. Certain bacteria have been associated with various internal and external factors such as disease and external contamination, and by understanding these trends, producers will be able to make more informed management decisions to improve reproductive efficiency in their herd. This article will focus on discussing the reproductive microbiome and how different factors change it to impact fertility in dairy cattle.

Reproductive Microbiome

The reproductive microbiome consists of the microbial communities located within the organs of the reproductive tract, i.e. vagina, uterus, etc.[2]. These microbial communities can be made up of bacteria, fungi and archaea; however, most studies focus on the influence of bacteria, as these are the most prevalent throughout the reproductive tract[2].

The abundance, composition and diversity of bacterial populations are the main focus points for determining beneficial versus pathogenic bacteria. Grasping how these communities change based on different factors can help producers understand the benefits and hindrances on fertility in their dairy operation.

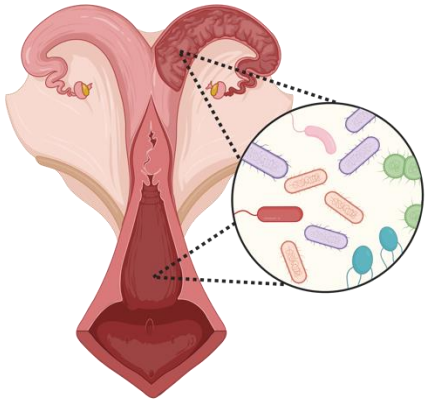

Figure 1. The reproductive microbiome consists of many different types of bacteria within reproductive tract organs including the uterus and vagina.

Internal and External Factors

Many of the same bacteria have been found in the vagina and uterus of both heifers and cows[2,3-6]. However, these bacterial populations appear to

shift in abundance and diversity with the influence of different internal and external factors on the animal.

For instance, bacteria within the reproductive tract are associated with disease status and can inherently impact a female's ability to become pregnant. Postpartum dairy cows known to be more susceptible to uterine diseases have altered bacteria profiles compared to healthy cows[2,7]. Specifically, an increased abundance and lower diversity of pathogenic bacteria is associated with endometritis and metritis infections[2,8-10]. This may be caused by injury to the reproductive tract due to issues in labor, including retained placenta or tissue tearing from passage of the calf. In fact, passage of the calf through the vagina alone can introduce new and potentially pathogenic bacteria, so that multiparous cows with a larger number of calvings have increased bacteria diversity[3,11]. Increases in bad bacteria during the postpartum period can then prevent cows from becoming pregnant and thus increase the number of days open. Therefore, maintaining a herd with healthy reproductive tracts during the postpartum period is important. Producers that are vigilant in assisting cows having calving issues and quickly removing retained placentas and providing antibiotics can help prevent colonization of pathogenic bacteria that lead to disease and eventual reproductive failure.

Contamination of the reproductive tract with bad bacteria can also be caused by external factors including artificial insemination or controlled internal drug release devices[3,12]. Specifically, the vaginal microbiome has been shown to change across multiple artificial insemination services[12]. This may be due to a lack of cleanliness which can come from introduction of dirt or feces from the artificial insemination rod itself as it is inserted through the reproductive tract. Thus, it is important for artificial insemination technicians to clean the rods between cows and remove any feces from the vulva area prior to insemination. The use of controlled internal drug release devices can also be a cause of external contamination where proper cleaning and sanitation techniques will be useful in minimizing the risk of introducing pathogenic bacteria to the cow's reproductive tract. Producers may also implement estrus synchronization protocols that do not require the use of a controlled internal drug release device to avoid this risk.

Additionally, circulating hormone concentrations of estradiol and progesterone have been shown to alter the vaginal microbiome[3,4]. The follicular phase is characterized by greater estradiol concentrations and includes the time when cows are ready to be bred, while the luteal phase is characterized by greater progesterone concentrations[4]. An increase in progesterone, due to the use of controlled internal drug release devices or development of a corpus luteum following an injection of gonadotropin releasing hormone can increase bacteria abundance and diversity in the vagina[3]. In cows with greater estradiol concentrations, an increase in beneficial bacteria has been found which could aid in promoting pregnancy establishment[4]. This implies that circulating hormone concentrations can influence the reproductive microbiome, therefore influencing fertility status of the cow during the breeding season. Thus, estrus synchronization protocols effective in increasing or decreasing estradiol or progesterone concentrations may influence pregnancy success.

In terms of pregnancy status, little data has been established in dairy cattle compared to beef cattle. One study has shown no differences in bacteria abundance between pregnant and open dairy cows. However, there were differences between days, where the diversity of bacteria was lower 18 days post-artificial insemination (Figure 2)[13]. This indicates that factors at the time

of artificial insemination may play a role in bacteria populations later, further emphasizing that minimizing sources of external contamination and ensuring the cow has a healthy reproductive tract at the time of artificial insemination can be important for more beneficial bacteria to populate the reproductive tract and potentially promote pregnancy.

Conclusion

The abundance and diversity of bacteria within the reproductive tract of dairy cattle will shift and differ based on internal and external factors and can impact fertility status. By understanding the implications of the bacterial communities on reproduction in dairy cattle, physiological strategies, such as minimizing external contamination and assisting in difficult calvings, can allow beneficial bacteria to flourish for promotion of pregnancy. Producers could also select estrus synchronization protocols that limit external contamination and increase estradiol concentrations to optimize reproductive success following artificial insemination. It is important for dairy producers to be aware of the implications of the reproductive microbiome and what factors impact its role on fertility to make suitable management decisions for profitability and sustainability moving forward. Further research is needed on determining how to successfully and easily implement a microbiome detection method producers may be able to use in the future for reproductive management as well.

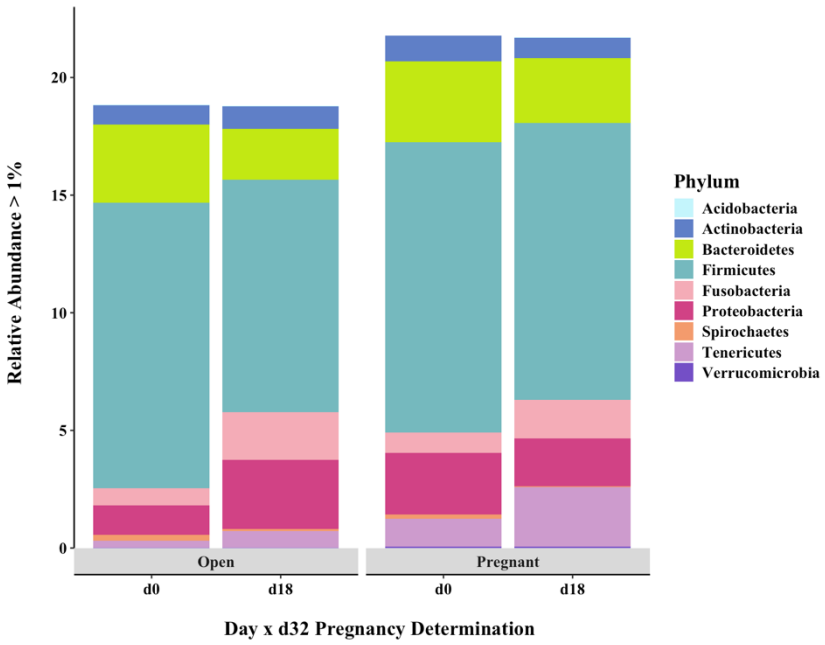

Figure 2. Bacterial phyla, a broad term for classifying different types of bacteria that are greater than 1% relative abundance between days and pregnancy status. There were no differences between pregnancy status; however, bacterial phyla did shift from day of artificial insemination to day 18.[14]

References

[1] Lee, J.-I. and I.-H. Kim. 2007. Pregnancy loss in dairy cows: the contributing factors, the effects on reproductive performance and the economic impact. Journal of veterinary science 8(3):283.

[2] Poole, R. K., D. R. Soffa, B. E. McAnally, M. S. Smith, K. J. Hickman-Brown, and E. L. Stockland. 2023. Reproductive microbiomes in domestic livestock: Insights utilizing 16S rRNA gene amplicon community sequencing. Animals 13(3):485.

[3] Quadros, D. L., R. Zanella, C. Bondan, G. C. Zanella, F. L. Facioli, A. N. da Silva, and E. L. Zanella. 2020. Study of vaginal microbiota of Holstein cows submitted to an estrus synchronization protocol with the use of intravaginal progesterone device. Research in veterinary science 131:1-6.

[4] Quereda, J. J., M. Barba, M. L. Mocé, J. Gomis, E. Jiménez-Trigos, Á. García-Muñoz, Á. Gómez-Martín, P. González-Torres, B. Carbonetto, and E. García-Roselló. 2020. Vaginal microbiota changes during estrous cycle in dairy heifers. Frontiers in veterinary science 7:371.

[5] Moore, S., A. Ericsson, S. Poock, P. Melendez, and M. Lucy. 2017. Hot topic: 16S rRNA gene sequencing reveals the microbiome of the virgin and pregnant bovine uterus. Journal of dairy science 100(6):4953-4960.

[6] Sannat, C., A. Nair, S. Sahu, S. Sahasrabudhe, A. Kumar, A. K. Gupta, and R. Shende. 2015. Effect of species, breed, and age on bacterial load in bovine and bubaline semen. Veterinary world 8(4):461.

[7] Miranda-CasoLuengo, R., J. Lu, E. J. Williams, A. A. Miranda-CasoLuengo, S. D. Carrington, A. C. Evans, and W. G. Meijer. 2019. Delayed differentiation of vaginal and uterine microbiomes in dairy cows developing postpartum endometritis. PloS one 14(1):e0200974.

[8] Kudo, H., T. Sugiura, S. Higashi, K. Oka, M. Takahashi, S. Kamiya, Y. Tamura, and M. Usui. 2021. Characterization of reproductive microbiota of primiparous cows during early postpartum periods in the presence and absence of endometritis. Frontiers in Veterinary Science 8:736996.

[9] Bicalho, M., T. Santin, M. Rodrigues, C. Marques, S. Lima, and R. Bicalho. 2017. Dynamics of the microbiota found in the vaginas of dairy cows during the transition period: Associations with uterine diseases and reproductive outcome. Journal of dairy science 100(4):3043-3058.

[10] Moreno, C. G., A. T. Luque, K. N. Galvão, and M. C. Otero. 2022. Bacterial communities from vagina of dairy healthy heifers and cows with impaired reproductive performance. Research in Veterinary Science 142:15-23.

[11] Bogado Pascottini, O., J. Spricigo, S. Van Schyndel, B. Mion, J. Rousseau, J. Weese, and S. LeBlanc. 2021. Effects of parity, blood progesterone, and non-steroidal anti-

inflammatory treatment on the dynamics of the uterine microbiota of healthy postpartum dairy cows. PLoS One 16(2):e0233943.

[12] Chen, S.-Y., F. Deng, M. Zhang, X. Jia, and S.-J. Lai. 2020. Characterization of vaginal microbiota associated with pregnancy outcomes of artificial insemination in dairy cows. Journal of Microbiology and Biotechnology 30(6):804.

[13] Soffa, D.R., K.J. Hickman, J.W. Cain, J.A. Spencer, and R.K. Poole. Vaginal microbiota and circulating interferon-stimulated genes in lactating dairy cows during maternal recognition of pregnancy. *In Review at Journal of Dairy Science*.