

Comparative Analysis of Gut Microbiomes in Wild Buffalo, Domestic Cows, and Urban Stray Cattle: A Metagenomic Study

Introduction:

The gut microbiome plays a critical role in the health and well-being of animals, influencing aspects such as digestion, metabolism, immunity, and disease resistance. While gut microbiome studies in domesticated animals like cows have been conducted extensively, there is a scarcity of data on the gut microbiomes of wild buffalo and urban stray cattle. This research aims to bridge this gap by conducting a comparative metagenomic analysis of the gut microbiomes of these three distinct bovine populations.

Objectives:

1. Comparative Analysis of Gut Microbiomes in Wild Buffalo and Domestic cattle: Assess the impact of domestication on the gut microbiome composition, diversity, and functional potential by comparing wild buffalo to domestic cattle.
2. Comparative Analysis of Gut Microbiomes in Domestic cattle and Urban Stray Cattle: Investigate the influence of urbanization on the gut microbiome composition, diversity, and potential alterations in microbial functions in urban stray cattle.
3. Decipher the trends in change of gut Microbiome during history: Is domestication and urbanization analogous?
4. Yet to be decided.....

Methods:

Sample Collection

- Collect fecal samples from wild buffalo populations in their natural habitat.
- Obtain fecal samples from domestic cows in controlled farm settings.
- Collect fecal samples from urban stray cattle within urban environments.

DNA Extraction

- Isolate DNA from the fecal samples using standardized metagenomic DNA extraction protocols.

Metagenomic Sequencing (will be outsourced)

- Prepare metagenomic libraries from the extracted DNA for each sample.
- Perform high-throughput sequencing (e.g., Illumina) to generate metagenomic datasets.

Data Analysis

- Process and quality-filter the sequencing data.
- Perform taxonomic classification to identify microbial species and their relative abundances.
- Assess alpha and beta diversity to compare microbial richness and community structure.
- Identify differentially abundant taxa and functions among the three groups.
- Conduct statistical analyses (ANOVA) to correlate microbiome composition with relevant environmental factors.

Discussion:

The comparative analysis of the gut microbiomes of wild buffalo, domestic cows, and urban stray cattle will provide insights into the impact of habitat, diet, and domestication on the composition and functional potential of the gut microbiota in these bovine populations.

Understanding these differences may have implications for animal health, adaptation to urban environments, and conservation efforts.

Significance:

This research contributes to our understanding of how anthropogenic factors, such as urbanization and domestication, influence the gut microbiome of bovine species. The findings may have implications for livestock management, wildlife conservation, and the potential role of gut microbiota in adapting to changing environments.

Timeline:

- Sample collection: Months 1-3 (only winter during winters when national parks are open)
- DNA extraction and library preparation: Months 4-6
- Metagenomic sequencing: Months 7-9
- Data analysis: Months 8-9
- Report and manuscript preparation: Months 16-18

Budget:

The budget will include expenses for sample collection (travel, national park, and ticket may cost estimated 10,000), DNA extraction kits (5000 per kit), sequencing costs (6500 per sample, if we take 5 sample size for each group for 15 sample may cost 97500), computational resources (most packages and tools are free but complications may costs extra 500), and personnel.

Discussion:

Previous studies have shown that the gut microbiome composition can differ between wild and captive animal populations (Gibson et al., 2019). These studies have primarily used targeted amplicon sequencing of the 16S rRNA gene. However, a metagenomic approach provides several advantages, including the ability to capture a broader range of microbial taxa and functional genes (Gibson et al., 2019). Additionally, it is not subject to PCR artifacts, which can affect the accuracy of amplicon sequencing (Gibson et al., 2019).

Diet has been shown to influence the diversity of the gut microbiome in cattle (Lau et al., 2018). A study comparing the gut microbiomes of omnivorous and herbivorous cattle found that the omnivorous group had a more diverse microbiome (Lau et al., 2018). This suggests that microbiota diversity increases as diet variation increases (Lau et al., 2018). Understanding the differences in the gut microbiomes of wild buffalo, domestic cows, and urban stray cattle can provide insights into the impact of diet and domestication on the gut microbiome.

The gut microbiome has also been implicated in the metabolism of environmental toxins and pesticides (Gao et al., 2017). Exposure to organophosphate pesticides has been shown to alter the gut microbiome composition and associated metabolites (Gao et al., 2017). This raises the possibility that perturbation of the gut microbiome contributes to the neurotoxicity of these pesticides (Gao et al., 2017). Investigating the gut microbiomes of wild buffalo, domestic cows, and urban stray cattle can provide insights into the potential effects of environmental factors on the gut microbiome.

Furthermore, the gut microbiome has been linked to host behavior (Cusick et al., 2021). Comparative studies across different species or taxa have highlighted the bidirectional relationship between the gut microbiome and host behavior (Cusick et al., 2021). By examining the gut microbiomes of wild buffalo, domestic cows, and urban stray cattle, we can explore potential associations between the gut microbiome and behavior in these populations.

Conclusion:

This research proposal aims to conduct a comparative analysis of the gut microbiomes in wild buffalo, domestic cows, and urban stray cattle using a metagenomic approach. By examining the differences in the gut microbiomes of these populations, we can gain insights into the impact of domestication, diet, environmental factors, and behavior on the gut microbiome composition and function. This study will contribute to our understanding of the gut microbiome in different populations of cattle and its potential implications for animal health and well-being.

References:

Cusick, J., Wellman, C., & Demas, G. (2021). The call of the wild: using non-model systems to investigate microbiome-behaviour relationships. *Journal of Experimental Biology*, 224(10). <https://doi.org/10.1242/jeb.224485>

Gao, B., Bian, X., Mahbub, R., & Lu, K. (2017). Sex-specific effects of organophosphate diazinon on the gut microbiome and its metabolic functions. *Environmental Health Perspectives*, 125(2), 198-206. <https://doi.org/10.1289/ehp202>

Gibson, K., Nguyen, B., Neumann, L., Miller, M., Buss, P., Daniels, S., ... & Pukazhenthi, B. (2019). Gut microbiome differences between wild and captive black rhinoceros – implications for rhino health. *Scientific Reports*, 9(1). <https://doi.org/10.1038/s41598-019-43875-3>

Lau, S., Teng, J., Chiu, T., Chan, E., Tsang, A., Panagiotou, G., ... & Woo, P. (2018). Differential microbial communities of omnivorous and herbivorous cattle in southern china. *Computational and Structural Biotechnology Journal*, 16, 54-60. <https://doi.org/10.1016/j.csbj.2018.02.004>

Further readings:

- [1] Youngblut et al., "Large-Scale Metagenome Assembly Reveals Novel Animal-Associated Microbial Genomes, Biosynthetic Gene Clusters, and Other Genetic Diversity," *Msystems* (2020). doi:10.1128/msystems.01045-20
- [2] Gao et al., "Sex-Specific Effects of Organophosphate Diazinon on the Gut Microbiome and Its Metabolic Functions," *Environmental health perspectives* (2017). doi:10.1289/ehp202
- [3] Ben-Yacov et al., "Personalized Postprandial Glucose Response–Targeting Diet Versus Mediterranean Diet for Glycemic Control in Prediabetes," *Diabetes care* (2021). doi:10.2337/dc21-0162
- [4] Gibson et al., "Gut microbiome differences between wild and captive black rhinoceros – implications for rhino health," *Scientific reports* (2019). doi:10.1038/s41598-019-43875-3
- [5] Phillips et al., "The Effects of Landscape Urbanization on the Gut Microbiome: An Exploration Into the Gut of Urban and Rural White-Crowned Sparrows," *Frontiers in ecology and evolution* (2018). doi:10.3389/fevo.2018.00148
- [6] Abed et al., "Gut metagenome profile of the Nunavik Inuit youth is distinct from industrial and non-industrial counterparts," *Communications biology* (2022). doi:10.1038/s42003-022-04372-y
- [7] Zhu, "New challenges in the study of the evolution of wild animals and their gut microbiome," *Ecology and evolution* (2022). doi:10.1002/ece3.8904
- [8] Lau et al., "Differential Microbial Communities of Omnivorous and Herbivorous Cattle in Southern China," *Computational and structural biotechnology journal* (2018). doi:10.1016/j.csbj.2018.02.004
- [9] Chong et al., "Looking like the locals - gut microbiome changes post-release in an endangered species," *Animal microbiome* (2019). doi:10.1186/s42523-019-0012-4
- [10] Sun et al., "Analysis of the Gut Microbiome of Wild and Captive Père David's Deer," *Frontiers in microbiology* (2019). doi:10.3389/fmicb.2019.02331