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FACULDADE DE CIÊNCIAS AGRÁRIAS E VETERINÁRIAS

CAMPUS JABOTICABAL

**GENOTYPE-BY-ENVIRONMENT INTERACTION AND GENOMIC
ARCHITECTURE OF SEXUAL PRECOCITY IN NELLORE CATTLE**

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Animal Scientist

2026

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**GENOTYPE-BY-ENVIRONMENT INTERACTION AND GENOMIC
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POTENTIAL IMPACT OF THIS RESEARCH

First study: This study contributes to understanding genotype-by-environment interactions affecting sexual precocity indicator traits in Nellore cattle. It demonstrates that genetic expression and animal ranking change across environments. Identifying environmental sensitivity in reproductive traits underscores the importance of including genotype-by-environment interactions in genetic evaluations, especially in tropical beef production systems with substantial environmental variation. These results may help develop more accurate breeding strategies. They also enable the identification of animals with greater adaptability, robustness, and stable performance across different environments, supporting improved reproductive efficiency and the long-term sustainability of tropical beef production systems.

Second study: This study expands current knowledge of the genomic architecture underlying environmental sensitivity and sexual precocity in Nellore cattle by integrating genomic reaction norm models and genome-wide association analyses. The identification of genomic regions and candidate genes associated with both average performance and environmental responsiveness provides a foundation for future studies investigating the biological mechanisms involved in adaptation and reproductive performance under tropical conditions. In addition, the results may help refine genomic selection by supporting the incorporation of genomic information on environmental adaptability into breeding programs.

CERTIFICADO DE APROVAÇÃO

TÍTULO DA DISSERTAÇÃO: GENOTYPE-BY-ENVIRONMENT INTERACTION AND GENOMIC ARCHITECTURE OF SEXUAL PRECOCITY IN NELLORE CATTLE

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AUTHOR'S CURRICULAR DATA

Eduarda da Silva Oliveira was born in Sertãozinho, São Paulo, Brazil, on December 8, 1999. In August 2018, she began her undergraduate studies in Animal Science at the Federal University of Uberlândia (UFU). During her undergraduate studies, she was awarded an undergraduate research scholarship from the National Council for Scientific and Technological Development (CNPq). She participated in study groups focused on ruminant nutrition and swine production and gained practical experience through internships in beef cattle, sheep, goat, and swine production systems. In addition, she served twice as a teaching assistant for the Experimental Techniques Applied to Animal Science course, contributing to activities related to experimental animal analysis and statistics. In 2024, she started her Master's degree in Animal Science at São Paulo State University (UNESP). During her graduate studies, she initially received a scholarship from the Coordination for the Improvement of Higher Education Personnel (CAPES) and was later awarded a scholarship from the São Paulo Research Foundation (FAPESP), under the supervision of Professor Dr. Fernando Baldi and co-supervision of Dr. Lúcio Mota. She also completed a research internship abroad funded by FAPESP at Purdue University (West Lafayette, IN, USA), under the supervision of Professor Dr. Hinayah Rojas. During her Master's studies, she had the opportunity to complete a teaching internship in the Animal Breeding course and to develop and collaborate on research projects involving different areas of Animal Science, with emphasis on animal breeding and genetics.

*I dedicate this achievement to my
grandmother, Maria Aparecida, the best heart I
have ever know. I miss you grandma.*

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GENOTYPE-BY-ENVIRONMENT INTERACTION AND GENOMIC ARCHITECTURE OF SEXUAL PRECOCITY IN NELLORE CATTLE

Abstract: Reproductive efficiency is a major challenge in beef cattle production systems, particularly in tropical environments characterized by significant heterogeneity in management, nutrition, and climatic conditions. In Nellore cattle, reproductive and sexual precocity traits are economically relevant because they directly influence productive longevity, herd profitability, and biological efficiency. In this context, the present dissertation aimed to investigate the environmental sensitivity and genomic architecture of sexual precocity indicator traits in Nellore cattle by integrating genomic reaction norm models and genome-wide association analyses (GWAS). The first study evaluated genotype-by-environment interaction (GxE) for scrotal circumference at 365 days (SC365), age at male puberty (APM), age at first calving (AFC), and heifer early calving probability at 30 months (HC30). Genetic parameters, heritability estimates, and genetic correlations were estimated across an environmental gradient derived from production conditions. The results revealed environmental sensitivity for all evaluated traits, characterized by changes in genetic variances and genotype re-ranking across environments, particularly under contrasting production conditions. Female reproductive traits were more environmentally sensitive than male traits. Additionally, the identification of robust and plastic animals demonstrated variability in adaptive responses among individuals. The second study integrated genomic reaction norm models with GWAS to identify genomic regions associated with both average performance (intercept) and environmental sensitivity (slope) for sexual precocity traits. Several candidate genes and biological pathways related to reproductive development, endocrine regulation, metabolism, immune response, and cellular growth were identified. Taken together, the findings of this dissertation demonstrate that the genetic expression of sexual precocity traits in Nellore cattle is strongly influenced by environmental conditions and reinforce the importance of incorporating GxE into genomic evaluations. and provide relevant information to develop more accurate breeding strategies.

Keywords: genomic reaction norms, environmental sensitivity, genome-wide association study, reproductive traits.

INTERAÇÃO GENÓTIPO-AMBIENTE E ARQUITETURA GENÔMICA DA PRECOCIDADE SEXUAL EM BOVINOS NELLORE

Resumo: A eficiência reprodutiva é um grande desafio nos sistemas de produção de bovinos de corte, particularmente em ambientes tropicais caracterizados por significativa heterogeneidade no manejo, nutrição e condições climáticas. Em bovinos Nelore, características reprodutivas e de precocidade sexual são economicamente relevantes, pois influenciam diretamente a longevidade produtiva, a rentabilidade do rebanho e a eficiência biológica. Nesse contexto, a presente dissertação teve como objetivo investigar a sensibilidade ambiental e a arquitetura genômica de características indicadoras de precocidade sexual em bovinos Nelore, integrando modelos de norma de reação genômica e análises de associação genômica ampla (GWAS). O primeiro estudo avaliou a interação genótipo-ambiente (GxE) para circunferência escrotal aos 365 dias (CE365), idade da puberdade masculina (IPM), idade ao primeiro parto (IPP) e probabilidade de parto precoce em novilhas aos 30 meses (PP30). Parâmetros genéticos, estimativas de herdabilidade e correlações genéticas foram estimados ao longo de um gradiente ambiental derivado das condições de produção. Os resultados revelaram sensibilidade ambiental para todas as características avaliadas, caracterizada por mudanças nas variâncias genéticas e reclassificação de genótipos em diferentes ambientes, particularmente sob condições de produção contrastantes. As características reprodutivas femininas mostraram-se mais sensíveis ao ambiente do que as masculinas. Além disso, a identificação de animais robustos e plásticos demonstrou variabilidade nas respostas adaptativas entre os indivíduos. O segundo estudo integrou modelos de norma de reação genômica com GWAS para identificar regiões genômicas associadas tanto ao desempenho médio (intercepto) quanto à sensibilidade ambiental (inclinação) para características de precocidade sexual. Vários genes candidatos e vias biológicas relacionadas ao desenvolvimento reprodutivo, regulação endócrina, metabolismo, resposta imune e crescimento celular foram identificados. Em conjunto, as descobertas desta dissertação demonstram que a expressão genética de características de precocidade sexual em bovinos Nelore é fortemente influenciada pelas condições ambientais e reforçam a importância da incorporação da interação genótipo x ambiente (GxE) em avaliações genômicas, fornecendo informações relevantes para o desenvolvimento de estratégias de melhoramento genético mais precisas.

Palavras-chave: normas de reação genômica, sensibilidade ambiental, estudo de associação genômica ampla, características reprodutivas

CHAPTER 1: GENERAL CONSIDERATIONS

1.1. Introduction

Improving the reproductive performance of Nellore cattle can positively impact production systems in economic and sustainable terms (Brumatti et al., 2011). Therefore, including these traits in genetic evaluations represents an important strategy to promote genetic gain through reproductive traits (Portes et al., 2021). Female traits, such as age at first calving (AFC) and heifer calving at 30 months (HC30), and male traits, such as scrotal circumference at 365 days (SC365) and age at puberty in males (APM), have been the focus of studies because they are associated with sexual precocity in animals, potentially resulting in more efficient males and females for the herd (Mota et al., 2020; Silva Neto et al., 2020; Mota et al., 2024; Oliveira et al., 2026).

However, it is known that these traits are influenced by several factors that need to be controlled, such as environmental factors. Some studies in the literature have reported that traits related to sexual precocity generally present low to moderate heritability estimates (Chiaia et al., 2015; Silva Neto et al., 2020; Kluska et al., 2018; Brunes et al., 2023). Studies evaluating the environmental interference on these traits have observed changes in the reproductive performance of animals across different environments (Chiaia et al., 2015; Mota et al., 2020; Fernandes Júnior et al., 2022), highlighting the importance of considering environmental effects, including climate, management, altitude, and housing structure, in genetic evaluations. Thus, considering these factors may provide a more accurate selection of superior animals for sexual precocity, since environmental changes and different producer objectives may alter selection strategies (Silva Neto et al., 2024).

When genotype expression is altered in response to environmental changes, genotype-by-environment interaction (GxE) occurs (Falconer & Mackay, 1996). Particularly in Brazil, a tropical country with a high diversity of production systems, considering GxE is extremely important. Furthermore, it is known that selection environments, such as nucleus herds, for example, differ from commercial production environments, which may lead to producer dissatisfaction, since they may acquire a genetically superior animal that will not fully express its genetic potential on their property (Menezes et al., 2022; Silva Neto et al., 2024).

These sexual precocity traits are considered complex because they are difficult to measure, are recorded in only one sex, and are often measured later in life, in addition to

presenting difficulties in model adjustment for their genetic evaluation (Eler, 2010; Mamede et al., 2023). Therefore, there is a scarcity of studies involving GxE for these traits. It is well established that the inclusion of genomics in GxE studies has increased the accuracy of results (Silva et al., 2014; Mota et al., 2020; Oliveira et al., 2026), which are commonly conducted using the reaction norm approach, which describes the continuous change in the phenotypic expression of animals according to environmental variations (Mota et al., 2019; Silva Neto et al., 2024).

Hence, the objectives of this Master's thesis were to: (i) investigate GxE for sexual precocity traits in Nellore cattle using genomic reaction norm (RN) models, aiming to estimate genetic parameters and genetic associations for HC30, AFC, SC365, and APM across the environmental gradient, evaluate genotype reranking under contrasting production conditions, and identify animals with greater environmental robustness or plasticity; and (ii) integrate RN models with genome-wide association analyses (GWAS) to identify environmentally sensitive SNPs associated with sexual precocity traits, as well as to detect candidate genes, biological processes, and metabolic pathways potentially involved in the regulation of sexual precocity under heterogeneous tropical environments.

3.7. Conclusions

This study provides new understandings into the genetic architecture of sexual precocity traits in Nellore cattle by integrating RN models with GWAS. For HC30, genes associated with the intercept were linked to folliculogenesis and ovarian development, while those associated with the slope reflected metabolic regulation, immune responses, and cellular stress resilience. SC365 revealed a contrasting pattern, with most significant genes shared between intercept and slope, suggesting that the same genomic determinants contribute to both baseline testis development and limited environmental sensitivity. APM presented only intercept-associated candidate genes related to DNA repair, endoplasmic reticulum stress, and immune response, with no slope-exclusive protein-coding genes or enriched biological processes detected. Together, these findings underscore the importance of environmentally sensitive loci and pathways in influencing reproductive function, providing a more comprehensive understanding of how baseline genetic potential and environmental sensitivity contribute to sexual precocity in Nellore cattle.

3.8. Supplementary files

Supplementary material is available at the permanent link:
<https://doi.org/10.1186/s12864-026-12547-8>

3.9. Declarations

3.9.1. Ethics approval and consent to participate

Not applicable

3.9.2. Consent for publication

Not applicable

3.9.3. Availability of data and materials

The phenotypic and genotypic information is available for academic use from the authors upon reasonable request (contacting the National Association of Breeders and Researchers (ANCP, Ribeirão Preto, SP, Brazil; email: transf.tecnologia@ancp.org.br).

3.9.4. Competing interests

The authors declare that they have no competing interests.

3.9.5. Funding

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3.9.7. Authors' contributions

FB conceived and coordinated the study. ESO, LFMM, FB and HRO performed the study

design. LFMM, HRO and HAM contributed to the statistical analysis and manuscript preparation. ESO drafted the manuscript. FB, HRO, MAFC, JBSN, HAM and LFMM contributed to interpreting results and critically revised the manuscript. All authors read, revised, and approved the final manuscript.

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