

UNIVERSIDADE FEDERAL DO PARANÁ

RAFAELA MARTINS

MACRO E MICRO SENSIBILIDADE AMBIENTAL PARA CARACTERÍSTICAS
PRODUTIVAS E REPRODUTIVAS EM BOVINOS DA RAÇA HOLANDESA NO
PARANÁ

CURITIBA

2025

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MACRO E MICRO SENSIBILIDADE AMBIENTAL PARA CARACTERÍSTICAS
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PARANÁ

Tese apresentada ao Programa de Pós-Graduação em Zootecnia, Setor de Ciências Agrárias da Universidade Federal do Paraná, como requisito parcial à obtenção de título de Doutora em Zootecnia.

Orientadora: Profa. Dra. Laila Talarico Dias

Coorientadora: Profa. Dra. Lucia Galvão de Albuquerque

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PROGRAMA DE PÓS-GRADUAÇÃO ZOOTECNIA -
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**ATA DE SESSÃO PÚBLICA DE DEFESA DE DOUTORADO PARA A OBTENÇÃO DO
GRAU DE DOUTORA EM ZOOTECNIA**

No dia vinte e cinco de março de dois mil e vinte e cinco às 08:30 horas, na sala ME-01, Bloco Marcos Enrietti, Setor de Ciências Agrárias da UFPR, foram instaladas as atividades pertinentes ao rito de defesa de tese da doutoranda **RAFAELA MARTINS**, intitulada: **Macro e micro sensibilidade ambiental para características produtivas e reprodutivas em bovinos da raça Holandesa no Paraná**, sob orientação da Profa. Dra. LAILA TALARICO DIAS. A Banca Examinadora, designada pelo Colegiado do Programa de Pós-Graduação ZOOTECNIA da Universidade Federal do Paraná, foi constituída pelos seguintes Membros: LAILA TALARICO DIAS (UNIVERSIDADE FEDERAL DO PARANÁ), RODRIGO DE ALMEIDA (UNIVERSIDADE FEDERAL DO PARANÁ), MARCOS VINICIUS GUALBERTO BARBOSA DA SILVA (EMBRAPA), LENIRA EL FARO ZADRA (INSTITUTO DE ZOOTECNIA IZ/APTA-SAA/SP). A presidência iniciou os ritos definidos pelo Colegiado do Programa e, após exarados os pareceres dos membros do comitê examinador e da respectiva contra argumentação, ocorreu a leitura do parecer final da banca examinadora, que decidiu pela APROVAÇÃO. Este resultado deverá ser homologado pelo Colegiado do programa, mediante o atendimento de todas as indicações e correções solicitadas pela banca dentro dos prazos regimentais definidos pelo programa. A outorga de título de doutora está condicionada ao atendimento de todos os requisitos e prazos determinados no regimento do Programa de Pós-Graduação. Nada mais havendo a tratar a presidência deu por encerrada a sessão, da qual eu, LAILA TALARICO DIAS, lavrei a presente ata, que vai assinada por mim e pelos demais membros da Comissão Examinadora.

CURITIBA, 25 de Março de 2025.

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Presidente da Banca Examinadora

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TERMO DE APROVAÇÃO

Os membros da Banca Examinadora designada pelo Colegiado do Programa de Pós-Graduação ZOOTECNIA da Universidade Federal do Paraná foram convocados para realizar a arguição da tese de Doutorado de **RAFAELA MARTINS**, intitulada: **Macro e micro sensibilidade ambiental para características produtivas e reprodutivas em bovinos da raça Holandesa no Paraná**, sob orientação da Profa. Dra. LAILA TALARICO DIAS, que após terem inquirido a aluna e realizada a avaliação do trabalho, são de parecer pela sua APROVAÇÃO no rito de defesa.

A outorga do título de doutora está sujeita à homologação pelo colegiado, ao atendimento de todas as indicações e correções solicitadas pela banca e ao pleno atendimento das demandas regimentais do Programa de Pós-Graduação.

CURITIBA, 25 de Março de 2025.

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LENIRA EL FARO ZADRA
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Em especial aos meus pais, à minha mãe Sandra, que sempre acreditou em mim, e mesmo hoje estando no céu, me abençoa todos os dias. Espero ter me tornado a pessoa e filha que você gostaria. Ao meu pai George, pelo apoio e por acreditar em meus sonhos e lutá-los comigo.

Ser filha de vocês é o maior privilégio que Deus poderia ter me dado.

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E tudo o que pedirem em oração, se crerem, vocês receberão.

Mateus 21:22

RESUMO

Os objetivos desta tese de doutorado foram avaliar a macrosensibilidade ambiental, representada pela interação genótipo ambiente (IGA), em bovinos da raça Holandesa, com foco em características produtivas e reprodutivas e identificar a microsensibilidade ambiental, entendida como resiliência, por meio da análise de indicadores de resiliência baseados nos desvios da produção de leite e das correlações entre os indicadores de resiliência e as características produtivas, de saúde e reprodutivas. A tese está estruturada em cinco capítulos: **Capítulo I – Revisão de Literatura. Capítulo II - Mapeamento Bibliométrico da Interação Genótipo × Ambiente em Animais de Produção.** Neste capítulo foram analisadas publicações de 1952 até julho de 2023 sobre os efeitos da IGA na pecuária, destacando tendências, países líderes e avanços científicos na área. Os dados foram coletados na base Web of Science (WOS) e processados no software VOSviewer. Os resultados mostraram que o Brasil e os Estados Unidos lideram as pesquisas sobre IGA, enquanto Índia, China e Uruguai despontam como países emergentes. Dentre os periódicos mais citados estão Journal of Animal Science, Journal of Dairy Science e Revista Brasileira de Zootecnia. No Brasil, destacam-se os grupos de pesquisa da UNESP (Jaboticabal) e FZEA/USP (Pirassununga), ambas instituições do Estado de São Paulo. Provavelmente, as mudanças climáticas têm impulsionado o interesse por estudos sobre IGA, além disso, a análise identificou um crescimento de integração de dados genômicos às pesquisas, o que pode aprofundar o entendimento sobre como os animais respondem às variações ambientais. Desse modo, o estudo reforçou a relevância de países como o Brasil nos avanços sobre o tema e revelou algumas tendências, como a utilização da genômica como ferramenta para identificar animais robustos a diferentes desafios ambientais. **Capítulo III - Influência de Diferentes Desafios Ambientais na Expressão das Características Produtivas em Bovinos Holandeses na Região Sul do Brasil.** O objetivo neste capítulo foi avaliar os efeitos da interação genótipo x ambiente sobre as produções de leite (PL305), produção de gordura no leite (PG305) e produção de proteína no leite (PP305), ajustadas aos 305 dias de lactação, em vacas Holandesas no Paraná. Foram utilizados 378.000 registros de vacas de primeira a terceira lactação, provenientes de 513 rebanhos, coletados nos anos de 2012 a 2022. O gradiente ambiental foi estabelecido com base nas soluções dos grupos contemporâneos, em que utilizou a produção de leite corrigida para 305 dias (PL305) como variável dependente. Utilizou-se o modelo de norma de reação (MNR) e correlações genéticas para avaliar a presença ou ausência do efeito da IGA. A herdabilidade da PL305 foi moderada (0,28) em gradientes menos desafiadores e baixa (0,18) nos mais desafiadores. Para a PG305, a herdabilidade variou de baixa (0,09) em ambientes menos desafiadores a moderada (0,28) em ambientes mais desafiadores, enquanto a PP305 manteve herdabilidade baixa, independentemente do ambiente. Não foram identificados efeitos de IGA sobre a PG305, em nenhuma das ordens de lactação. Não houve efeito da IGA sobre PL305 ou PP305 na primeira e segunda lactação. Contudo, na terceira lactação, a IGA afetou, significativamente, a PL305 e a PP305, especialmente sob gradientes ambientais extremos. Assim sendo, concluiu-se que a seleção para PL305, PP305 e PG305 durante a primeira lactação pode ser a estratégia mais eficaz, em função da menor influência da IGA nessa fase. **Capítulo IV – Influência de diferentes desafios ambientais na expressão de características reprodutivas em gado Holandês no Sul do Brasil.** Neste estudo o objetivo foi avaliar o impacto da interação genótipo x ambiente (IGA) sobre as características: idade ao primeiro parto (AFC), idade ao primeiro serviço (AFS) e intervalo entre partos (CI) em bovinos da raça Holandesa no estado do Paraná. Foram analisados dados de 179.492 animais de primeira, segunda e terceira lactação, coletados entre 2012 e 2022, provenientes de 513 rebanhos em 72 municípios do Paraná. O gradiente ambiental foi determinado com base nas soluções dos grupos contemporâneos, em que utilizou a produção de leite corrigida para 305 dias (PL305) como variável dependente. Para avaliar os efeitos da IGA foi utilizado um modelo de regressão aleatória. Foram estimadas as

herdabilidades e as correlações genéticas entre as características estudadas. Nas condições ambientais mais favoráveis, o coeficiente de herdabilidade foi moderado (0,23) para AFC e baixo para as demais características. O impacto da IGA sobre o CI foi pequeno, mas para AFC e AFS foi relevante em todos os gradientes ambientais. A alteração na classificação dos genótipos sob condições ambientais extremas sugere que o genótipo de melhor desempenho em um ambiente pode não ser o mais eficiente em outro. Conclui-se que a IGA influenciou o desempenho dos animais para as características avaliadas, especialmente em condições ambientais extremas, o que reforça a importância de considerar o efeito da IGA em programas de seleção para o melhoramento genético animal. **Capítulo V - Análise genética da resiliência de vacas primíparas da raça Holandesa.** Os objetivos deste estudo foram estimar o coeficiente de herdabilidade para a característica resiliência usando-se três diferentes indicadores baseados nos desvios da produção de leite: 1) logaritmo natural da variância (LnVar), 2) autocorrelação (Auto) e 3) assimetria (Assim), e as correlações genéticas entre a resiliência e as características produtivas, de saúde e fertilidade em vacas primíparas da raça Holandesa. Embora o coeficiente de herdabilidade para resiliência tenha sido de baixa magnitude, independente do indicador de resiliência utilizado, foi possível identificar variabilidade genética, sendo que, o LnVar foi o que se destacou. Logo, espera-se que a seleção para essa característica seja possível. No entanto, a seleção para maior produção de leite poderá reduzir a resiliência das vacas Holandesas. Ainda assim, o LnVar mostrou-se uma ferramenta viável para avaliar e identificar a resiliência e auxiliar no melhoramento genético de bovinos leiteiros.

Palavras-chave: Adaptação ambiental. Desvios da curva de lactação. Genótipo robusto. Normas de reação. Plasticidade fenotípica.

ABSTRACT

The objectives of this doctoral thesis were to evaluate macro-environmental sensitivity, represented by genotype-environment interaction (GEI), in Holstein cattle, focusing on productive and reproductive traits, and to identify micro-environmental sensitivity, understood as resilience, through the analysis of resilience indicators based on milk production deviations and the correlations between resilience indicators and productive, health, and reproductive traits. The thesis is structured into five chapters: **Chapter I – Literature Review. Chapter II – Bibliometric Mapping of Genotype × Environment Interaction in Production Animals.** This chapter analyzed publications from 1952 to July 2023 on the effects of GEI in livestock, highlighting trends, leading countries, and scientific advances in the field. Data were collected from the Web of Science (WOS) database and processed using the VOSviewer software. The results showed that Brazil and the United States lead GEI research, while India, China, and Uruguay are emerging countries in the field. Among the most cited journals are the *Journal of Animal Science*, *Journal of Dairy Science*, and *Revista Brasileira de Zootecnia*. In Brazil, research groups from UNESP (Jaboticabal) and FZEA/USP (Pirassununga), both institutions in the state of São Paulo, stand out. Climate change has likely driven interest in GEI studies, and the analysis identified a growing integration of genomic data into research, which may deepen the understanding of how animals respond to environmental variations. Thus, the study reinforced the relevance of countries like Brazil in advancements on the subject and revealed some trends, such as the use of genomics as a tool to identify animals robust to different environmental challenges. **Chapter III – Influence of Different Environmental Challenges on the Expression of Productive Traits in Holstein Cattle in Southern Brazil.** The objective of this chapter was to evaluate the effects of genotype × environment interaction on milk production (PL305), milk fat production (PG305), and milk protein production (PP305), adjusted to 305 days of lactation, in Holstein cows in Paraná. A total of 378,000 records from first to third lactation cows from 513 herds, collected from 2012 to 2022, were used. The environmental gradient was established based on the solutions of contemporary groups, using milk production corrected to 305 days (PL305) as the dependent variable. The reaction norm model (RNM) and genetic correlations were used to assess the presence or absence of GEI effects. The heritability of PL305 was moderate (0.28) in less challenging gradients and low (0.18) in more challenging ones. For PG305, heritability ranged from low (0.09) in less challenging environments to moderate (0.28) in more challenging ones, while PP305 maintained low heritability regardless of the environment. No GEI effects were identified for PG305 in any lactation order. No GEI effect was observed for PL305 or PP305 in the first and

second lactations. However, in the third lactation, GEI significantly affected PL305 and PP305, especially under extreme environmental gradients. Therefore, it was concluded that selecting for PL305, PP305, and PG305 during the first lactation may be the most effective strategy, given the lower influence of GEI at this stage. **Chapter IV – Influence of Different Environmental Challenges on the Expression of Reproductive Traits in Holstein Cattle in Southern Brazil.** This study aimed to evaluate the impact of genotype $\times$ environment interaction (GEI) on the traits: age at first calving (AFC), age at first service (AFS), and calving interval (CI) in Holstein cattle in Paraná. Data from 179,492 animals in their first, second, and third lactation, collected between 2012 and 2022 from 513 herds in 72 municipalities in Paraná, were analyzed. The environmental gradient was determined based on the solutions of contemporary groups, using milk production corrected to 305 days (PL305) as the dependent variable. A random regression model was used to assess GEI effects. Heritabilities and genetic correlations between the studied traits were estimated. Under more favorable environmental conditions, the heritability coefficient was moderate (0.23) for AFC and low for the other traits. The impact of GEI on CI was small, but for AFC and AFS, it was relevant across all environmental gradients. Changes in genotype rankings under extreme environmental conditions suggest that the best-performing genotype in one environment may not be the most efficient in another. It was concluded that GEI influenced animal performance for the evaluated traits, especially under extreme environmental conditions, reinforcing the importance of considering GEI effects in selection programs for genetic improvement in dairy cattle. **Chapter V – Genetic Analysis of Resilience in Primiparous Holstein Cows.** The objectives of this study were to estimate the heritability coefficient for the resilience trait using three different indicators based on milk production deviations: 1) natural logarithm of variance (LnVar), 2) autocorrelation (Auto), and 3) skewness (Assim), and to estimate the genetic correlations between resilience and productive, health, and fertility traits in primiparous Holstein cows. Although the heritability coefficient for resilience was of low magnitude, regardless of the resilience indicator used, genetic variability was identified, with LnVar standing out. Thus, selection for this trait is expected to be possible. However, selecting for higher milk production may reduce the resilience of Holstein cows. Nevertheless, LnVar proved to be a viable tool for evaluating and identifying resilience and aiding in the genetic improvement of dairy cattle.

Keywords: Environmental adaptation. Lactation curve deviations. Robust genotype. Reaction norms. Phenotypic plasticity.

LISTA DE FIGURAS

CAPÍTULO I - REVISÃO DE LITERATURA

Figura 1 Classificações da interação genótipo x ambiente.....	23
--	----

CAPÍTULO II - BIBLIOMETRIC MAPPING OF GENOTYPE X ENVIRONMENT INTERACTION IN PRODUCTION ANIMALS

Figure 1 Heat map by country of papers focusing upon genotype $\times$ environment interaction in farm animals	38
---	----

Figure 2 Animal species used in genotype $\times$ environment interaction studies (A) and number of documents	39
--	----

Figure 3 Type of document (A), area of knowledge (B), top institutions (C), and financing agencies (D) in genotype	40
---	----

Figure 4 Publication parameters for co-authorship in publications on genotype $\times$ environment interaction in farm animals.....	41
--	----

Figure 5 Publication parameters for co-authorship in publications on genotype $\times$ environment interaction in farm animals.....	44
--	----

Figure 6 Bibliographic coupling analysis for publications on genotype $\times$ environment interaction in farm animals.....	46
--	----

Figure 7 Co-citation analysis for publications on genotype $\times$ environment interaction in farm animals.....	48
---	----

CAPÍTULO III INFLUENCE OF DIFFERENT ENVIRONMENTAL CHALLENGES ON THE EXPRESSION OF PRODUCTIVE TRAITS IN HOLSTEIN CATTLE IN THE SOUTHERN REGION OF BRAZIL

Figure 1 Additive genetic and environmental variances for 305-day corrected milk yield in the first (a, d), second (b, e), and third (c, f) lactations in Holstein cattle in the state of Paraná ...	69
---	----

Figure 2 Heritability estimates for milk yield in the first (a), second (b), and third (c) lactations in Holstein cattle in the state of Paraná across environmental gradients.....	70
--	----

Figure 3 Additive genetic and environmental variances for 305-day corrected milk fat yield in the first (a, d), second (b, e), and third (c, f) lactations in Holstein cattle in the state of Paraná	72
---	----

Figure 4 Heritability estimates for milk fat yield in the first (a), second (b), and third (c) lactations in Holstein cattle in the state of Paraná across environmental gradients	73
---	----

Figure 5 Additive genetic and environmental variances for 305-day corrected milk protein yield in the first (a, d), second (b, e), and third (c, f) lactations in Holstein cattle in the state of Paraná	74
---	----

Figure 6 Heritability estimates for milk protein yield in the first (a), second (b), and third (c) lactations in Holstein cattle in the state of Paraná across environmental gradients	75
---	----

Figure 7 Reaction norms of estimated breeding values for 305-day corrected milk yield in Holstein cattle as a function of environmental gradients	77
--	----

Figure 8 Reaction norms of estimated breeding values for 305-day corrected milk fat yield in Holstein cattle as a function of environmental gradients	78
--	----

Figure 9 Reaction norms of estimated breeding values for 305-day corrected milk protein yield in Holstein cattle as a function of environmental gradients	79
--	----

CAPÍTULO IV - INFLUENCE OF DIFFERENT ENVIRONMENTAL CHALLENGES ON THE EXPRESSION OF REPRODUCTIVE TRAITS IN HOLSTEIN CATTLE IN SOUTHERN BRAZIL

Figure 1 Additive genetic and environmental variances for age at first service (orange), age at first calving (blue), and calving interval (purple) of Holstein cattle across environmental gradients in the state of Paraná, Brazil	99
---	----

Figure 2 Heritability for reproductive traits: (a) age at first service (orange), (b) age at first calving (blue), and (c) calving interval (purple) of Holstein cattle across environmental gradients in the state of Parana, Brazil	100
--	-----

Figure 3 Reaction norms of estimated breeding values for reproductive traits: age at first service (orange), age at first calving (blue), and calving interval (purple)	102
--	-----

CAPITULO V - ANÁLISE GENÉTICA DE INDICADORES DE RESILIÊNCIA PARA VACAS PRIMÍPARAS DA RAÇA HOLANDESA

Figura 1 Exemplos dos métodos de ajuste de curva de lactação para uma vaca exemplo. As linhas pretas mostram a produção de leite observada, e as linhas roxas mostram a produção de leite prevista; (A) média móvel, (B) mediana móvel, (C) curva de Wilmink, (D) regressão quantílica	114
---	-----

LISTA DE TABELAS

CAPÍTULO I - REVISÃO DE LITERATURA

Tabela 1 Estimativa de herdabilidades e correlações genéticas para idade ao primeiro parto (IPP), idade ao primeiro serviço (IPS) intervalo entre partos (IEP), produção de leite (PL), produção de gordura (PG) e produção de proteína (PP) em populações de Bovinos da raça Holandesa em diferentes regiões	25
--	----

CAPÍTULO II - BIBLIOMETRIC MAPPING OF GENOTYPE X ENVIRONMENT INTERACTION IN PRODUCTION ANIMALS

Table 1 Bibliometric parameters for publications on genotype environment interaction in farm animals.....	36
Table 2 Top 20 authors for publications on genotype × environment interaction in farm animals.....	42
Table 3 Top cited papers of publications on genotype × environment interaction in farm animals	43
Table 4 Top 10 papers in bibliographic coupling for publications on genotype × environment interaction in farm animals	45
Table 5 Top co-cited documents for publications on genotype × environment interaction in farm animals	47

CAPÍTULO III INFLUENCE OF DIFFERENT ENVIRONMENTAL CHALLENGES ON THE EXPRESSION OF PRODUCTIVE TRAITS IN HOLSTEIN CATTLE IN THE SOUTHERN REGION OF BRAZIL

Table 1 Descriptive statistics for 305-day corrected milk yield (MY305), fat yield (FY305), and protein yield (PY305) in Holstein cattle in the state of Paraná	67
Table 2 Mean values 305-day corrected milk yield (MY305), fat yield (FY305), and protein yield (PY305) in Holstein cattle in the state of Paraná as a function of environmental Gradients.....	68
Table 3 Heritability estimates for 305-day corrected milk yield (MY305), fat yield (FY305), and protein yield (PY305) in Holstein cattle in the state of Paraná, for the environmental gradients with the lowest and greatest challenge.....	71
Table 4 Spearman correlation between the breeding values of 305-day corrected milk yield (MY305), fat yield (FY305), and protein yield (PY305) in Holstein cattle in the state of Parana, as a function of environmental gradients (EG).....	76

CAPÍTULO IV - INFLUENCE OF DIFFERENT ENVIRONMENTAL CHALLENGES ON THE EXPRESSION OF REPRODUCTIVE TRAITS IN HOLSTEIN CATTLE IN SOUTHERN BRAZIL

Table 1 Descriptive statistics for age at first service (AFS), age at first calving (AFC) and calving interval (CI) of Holstein cattle in the state of Paraná, Brazil.....	98
Table 2 Mean values for age at first service (AFS), age at first calving (AFC) and calving interval (CI) of Holstein cattle as a function of the environmental gradients (EG)	98
Table 3 Heritability estimates for age at first service (AFS), age at first calving (AFC) and calving interval (CI) in days of Holstein cattle in the environmental gradients (EG) with lowest and greatest challenge in the state of Paraná, Brazil	101
Table 4 Correlation between the rankings of breeding values for age at first service (AFS), age at first calving (AFC) and calving interval (CI) of Holstein cattle across environmental gradients (EG) in the state of Paraná, Brazil	101

CAPÍTULO V - ANÁLISE GENÉTICA DE INDICADORES DE RESILIÊNCIA PARA VACAS PRIMÍPARAS DA RAÇA HOLANDESA

Tabela 1 Estatísticas descritivas dos indicadores de resiliência com base em diferentes métodos de ajuste de curva de lactação.....	118
Tabela 2 Componentes de variância e herdabilidades dos indicadores de resiliência com base em diferentes métodos de ajustes de curva de lactação	118
Tabela 3 Correlações genéticas entre o indicador de resiliência LnVar e as características produtivas, saúde e de fertilidade de bovinos da raça Holandesa.	119
Tabela Suplementar 1 Números de registros e de vacas após cada etapa de edição de dados	128
Tabela Suplementar 2 Correlações genéticas entre os indicadores de resiliência (Autocorrelação e Assimetria) e as características produtivas, de saúde e de fertilidade em vacas primíparas da raça Holandesa.....	129

SUMÁRIO

1. INTRODUÇÃO GERAL	20
2. CAPÍTULO I - REVISÃO DE LITERATURA.....	22
2.1 MACROSSENSIBILIDADE AMBIENTAL	22
2.2 MICROSSENSIBILIDADE AMBIENTAL.....	27
REFERÊNCIAS	29
3. CAPÍTULO II - BIBLIOMETRIC MAPPING OF GENOTYPE X ENVIRONMENT INTERACTION IN PRODUCTION ANIMALS.....	34
ABSTRACT	34
3.1 INTRODUCTION	35
3.2 MATERIAL AND METHODS	36
3.3 RESULTS.....	37
3.4 DISCUSSION.....	49
3.5 CONCLUSION	52
REFERENCES	53
4 CAPÍTULO III INFLUENCE OF DIFFERENT ENVIRONMENTAL CHALLENGES ON THE EXPRESSION OF PRODUCTIVE TRAITS IN HOLSTEIN CATTLE IN THE SOUTHERN REGION OF BRAZIL.....	61
ABSTRACT	61
4.1 INTRODUCTION	62
4.2 MATERIALS AND METHODS.....	64
4.2.1 DATA.....	64
4.2.2 DETERMINATION OF THE ENVIRONMENTAL GRADIENT (EG).....	64
4.2.3 REACTION NORMS MODEL (RNM)	65
4.2.4 CORRELATION BETWEEN ESTIMATES OF BREEDING VALUES (EBV) ...	66
4.3 RESULTS.....	67
4.4 DISCUSSION.....	79
4.5 CONCLUSION	79
REFERENCES	86
5 CAPÍTULO IV - INFLUENCE OF DIFFERENT ENVIRONMENTAL CHALLENGES ON THE EXPRESSION OF REPRODUCTIVE TRAITS IN HOLSTEIN CATTLE IN SOUTHERN BRAZIL.....	92
ABSTRACT	92

5.1 INTRODUCTION	93
5.2 MATERIALS AND METHODS.....	94
5.2.1 DATA.....	95
5.2.2 DETERMINATION OF THE ENVIRONMENTAL GRADIENT	95
5.2.3 REACTION NORM MODEL (RNM).....	96
5.3 RESULTS.....	98
5.3.1 HERITABILITY	100
5.3.2 RANK CORRELATION BETWEEN EBVS ACROSS ENVIRONMENTAL GRADIENTS	101
5.4 DISCUSSION.....	102
REFERENCES	105
6 CAPÍTULO V – ANÁLISE GENÉTICA DA RESILIÊNCIA DE VACAS PRIMÍPARAS DA RAÇA HOLANDESA.....	109
RESUMO.....	109
6.1 INTRODUÇÃO	110
6.2 MATERIAL E MÉTODOS	111
6.2.1 DADOS	111
6.2.2 AJUSTE CURVAS DE LACTAÇÃO INDIVIDUAIS.....	112
6.2.3 AJUSTE NÃO PARAMÉTRICO (MÉDIA MÓVEL E MEDIANA MÓVEL)	112
6.2.4 AJUSTE BASEADO NO MÉTODO DA CURVA DE LACTAÇÃO DE WILMINK.....	113
6.2.5 AJUSTE BASEADO NO METÓDO DE REGRESSÃO POLINOMIAL DE QUARTA ORDEM	113
6.2.6 DEFINIÇÃO E INTERPRETAÇÃO DOS INDICADORES DE RESILIÊNCIA COM BASE EM DESVIOS DAS CURVAS DE LACTAÇÃO.....	115
6.2.7 EDIÇÃO DOS DADOS.....	115
6.2.8 PARÂMETROS GENÉTICOS.....	116
6.3 RESULTADOS	117
6.4 DISCUSSÃO	120
6.4.1 COEFICIENTE DE HERDABILIDADE PARA A CARACTERÍSTICA RESILIÊNCIA AVALIADA POR MEIO DE DIFERENTES INDICADORES.....	120
6.4.2 CORRELAÇÃO DOS INDICADORES DE RESILIÊNCIA COM.....	121
CARACTERÍSTICAS PRODUTIVAS, REPRODUTIVAS E DE SAÚDE	121

6.4.3 QUAL MÉTODO DE AJUSTE DE CURVA FOI MAIS ADEQUADO?.....	123
6.4.4 SELEÇÃO DE ANIMAIS RESILIENTES COM BASE NA PRODUÇÃO DE LEITE	123
6.5 CONCLUSÕES.....	124
REFERÊNCIAS	125
7. CONSIDERAÇÕES FINAIS.....	130
8. ANEXOS	132

1. INTRODUÇÃO GERAL

A sensibilidade ambiental ou plasticidade fenotípica é a capacidade que um genótipo tem de produzir diferentes fenótipos, dependendo das condições ambientais (ALFORD et al., 2006). Indivíduos que apresentam genótipos plásticos são aqueles que têm maior sensibilidade, já os de genótipos robusto são aqueles com menor sensibilidade ambiental.

A sensibilidade ambiental pode ser classificada como: macroambiental e micro ambiental (WU, 1997), sendo a macro referente às mudanças na média do desempenho do animal em diferentes ambientes e a micro expressa pelas diferenças na variância residual, no mesmo ambiente ao qual é submetido (IUNG et al., 2018; SANCRISTOBAL- GAUDY et al., 1998).

Os fatores macroambientais são geralmente conhecidos, como por exemplo, clima: tropical, subtropical ou temperado. A influência dos fatores macroambientais pode ser avaliada por meio de modelos de norma de reação, visto que, alguns genótipos exibem diferentes respostas fenotípicas de acordo com o ambiente em que foi exposto (MULDER, 2016, LU et al., 2013). As normas de reação são frequentemente representadas em gráficos, em que a elevada plasticidade em uma característica resulta em uma norma de reação com acentuada inclinação, entretanto, as características não plásticas resultam em uma norma de reação substancialmente plana (GAUTIER; NAVES, 2011), o que pode ser observado em análises de interação genótipo ambiente (IGA).

Assim sendo, a IGA ocorre quando diferenças fenotípicas entre genótipos variam de ambiente para ambiente (HAMMAMI et al., 2009). Desse modo, ao selecionar um touro, em um determinado ambiente, é provável que suas filhas tenham desempenhos distintos quando expostas a ambientes diferentes. Segundo Hayes et al. (2013), quando a IGA é significativa, o desempenho poderá ser diferente do esperado e, por consequência, poderá ocorrer a reclassificação dos genótipos ao longo dos gradientes ambientais.

Em contraste, os fatores microambientais são esporádicos, episódicos, condicionais ou específicos do indivíduo, tais como: flutuações diárias de temperatura e umidade do ambiente, estados socioafetivos e condições de saúde (CHEN et al., 2023). Neste contexto, o termo resiliência foi proposto para medir as respostas individuais às perturbações microambientais conhecidas e desconhecidas.

Todavia, a característica resiliência é de difícil mensuração de forma direta, desse modo, Scheffer et al. (2018) desenvolveram métodos para medir a resiliência em vacas utilizando

dados rotineiramente coletados nas fazendas. Esses métodos partem da premissa de que as vacas estão continuamente sujeitas a perturbações desconhecidas, o que resultará em flutuações nas características frequentemente observadas. Vacas que apresentam flutuações mínimas no seu desempenho são menos impactadas por perturbações do que aquelas com flutuações mais acentuadas (POPPE et al., 2020), assim, espera-se que o padrão de flutuação forneça informações relevantes sobre a resiliência.

Diversos indicadores de resiliência que descrevem flutuações em características frequentemente medidas foram sugeridos, entre os quais a variância da característica (indica a variabilidade da medida), a autocorrelação da característica (indica a associação entre os desempenhos tomados em um mesmo animal ao longo de um determinado período de tempo) e a assimetria (indica discrepância ou diferença entre as mensurações da característica) (SCHEFFER et al., 2018; BERGHOF et al., 2019). Até o momento, a validação desses indicadores de resiliência tem sido desafiadora devido à falta de frequência nas avaliações dos dados sobre perturbações. Além disso, a análise genética pode ser empregada para aprofundar a compreensão da biologia da característica e contribuir para o desenvolvimento de novos indicadores de resiliência, de maneira semelhante à validação de características avaliadas subjetivamente, como o escore de condição corporal (VEERKAMP et al., 2002).

OBJETIVOS

GERAIS

- Identificar a macro e microsensibilidade ambiental para características produtivas, como produção de leite (PL), produção de gordura (PG), produção de proteína (PP), características reprodutivas, como idade ao primeiro parto (IPP), idade ao primeiro serviço (IPS) e intervalo entre partos (CI) e características de saúde como contagem de células somáticas (CCS) em bovinos da raça Holandesa.

ESPECÍFICOS

- Identificar a ocorrência de interação genótipo x ambiente (IGA) para as características produtivas (produção de leite (PL), produção de gordura (PG), produção de proteína (PP)) e para as características reprodutivas: idade ao primeiro parto (IPP), idade ao primeiro serviço (IPS) e intervalo entre partos (CI) em bovinos da raça Holandesa.

- Analisar os genótipos quanto à plasticidade e robustez, e verificar se há reclassificação dos genótipos (plasticidade) dos touros em diferentes ambientes de produção para as características produtivas e reprodutivas.

- Estimar parâmetros genéticos para resiliência (por meio de três indicadores: logaritmo natural da variância, autocorrelação e assimetria dos desvios de produção de leite de uma curva esperada e uma curva observada), a partir de informações de lactação completa em bovinos da raça Holandesa.

- Identificar qual indicador de resiliência é mais eficiente e está mais forte, favorável e geneticamente correlacionado com características produtivas, reprodutivas e de saúde em bovinos da raça Holandesa.

2. CAPÍTULO I - REVISÃO DE LITERATURA

Quando um touro é selecionado em um determinado ambiente, existe a possibilidade de que seus filhos apresentem desempenhos distintos quando expostos a ambientes diferentes. Essa diferença pode ser explicada pela ocorrência de interação genótipo ambiente (IGA), ou seja, os animais podem apresentar resposta diferenciada frente as variações ambientais as quais são expostos, além da possibilidade de ocorrência de mudança no ranqueamento dos reprodutores (FALCONER & MACKAY, 1996). Na prática, desconsiderar os efeitos da IGA pode levar a uma seleção inadequada de animais geneticamente superiores, pois as diferenças nas respostas aos ambientes podem influenciar nessa escolha. Assim, identificar genótipos robustos torna-se uma estratégia eficaz para minimizar os impactos da IGA, garantindo uma maior consistência no desempenho dos animais em diferentes condições ambientais.

2.1 MACROSSENSIBILIDADE AMBIENTAL

Um animal é considerado robusto quando seu desempenho permanece constante ao longo dos gradientes ambientais. Em contrapartida, os animais plásticos são aqueles cujo desempenho é alterado conforme a mudança desses gradientes (FALCONER, 1990). A macrosensibilidade ambiental pode ser avaliada por meio de modelos estatísticos que consideram que os indivíduos não variam sua fisiologia em diferentes ambientes.

Um modelo amplamente utilizado para estudar a macrosensibilidade ambiental é o de normas de reação, que permite avaliar quão plástico ou robusto é um fenótipo quando submetido a ambientes diferentes (MULDER et al., 2013).

A sensibilidade à variação ambiental é avaliada por meio da ocorrência da IGA, porque a sensibilidade acontece quando o genótipo apresenta desempenhos diferentes ao ser exposto a ambientes distintos, de maneira que, em dois ambientes diferentes uma mesma característica pode ser expressa de diferentes formas (FREITAS, 2012). Assim, a plasticidade ou robustez de um genótipo em gradientes ambientais distintos pode ser ocasionada pela ocorrência de IGA (KNAP, 2005; TIEZZI et al., 2017).

Segundo PANI et al., (1971) as interações genótipo ambiente podem ser classificadas de quatro formas diferentes, conforme apresentado na Figura 1.

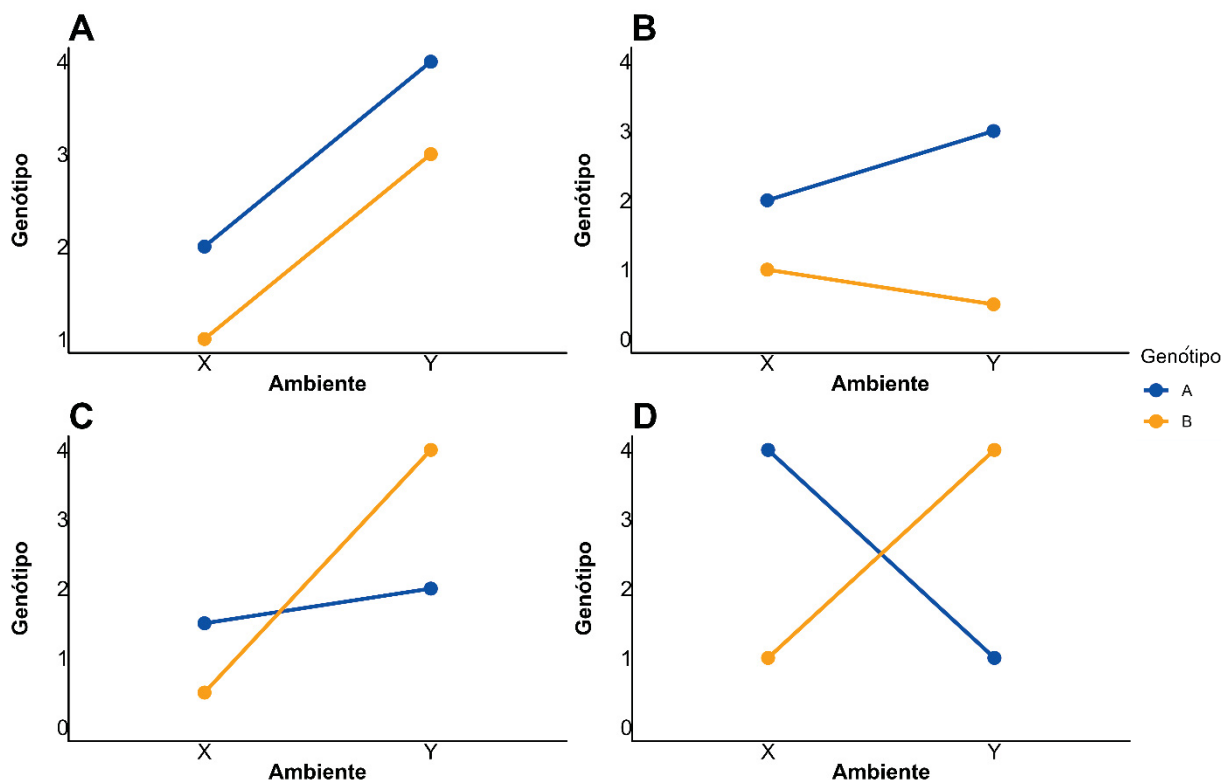


Figura 1 Classificações da interação genótipo x ambiente.

Fonte: Adaptado de Pani et al. (1971).

A: apesar de haver diferenças entre os ambientes, o comportamento dos genótipos é similar, sendo assim, não há IGA.

B: não houve inversão na ordem de classificação dos genótipos, embora o desempenho desses genótipos apresente diferenças nos ambientes diversos, sendo considerada uma interação significativa (devido as alterações nas variâncias), porém, sem reclassificação.

C: houve inversão na ordem de classificação dos genótipos nos ambientes diferentes, uma vez que neste caso há IGA.

D: observa-se importante inversão na ordem de classificação dos genótipos nos ambientes diferentes e a interação é considerada significativa.

A IGA tem grande importância na avaliação do desempenho dos animais candidatos a reprodutores, principalmente, no Brasil onde há grande variação de ambientes para criação de bovinos. Essa diversidade ambiental dificulta a seleção de um único genótipo para todos os tipos de ambiente, o que só seria possível se o ambiente de criação fosse o mesmo da seleção (HAMMAMI et al., 2009).

Para realizar as análises de IGA, usando o modelo de normas de reação (NR), é necessário classificar os ambientes de acordo com os gradientes ambientais (KNAP, 2005). Desse modo, as normas de reação (NR) podem ser utilizadas para evidenciar o melhor desempenho em cada ambiente para a característica selecionada. Dentre as razões que justificam o uso das NR para estudos de IGA em rebanhos leiteiros está a possibilidade de avaliar vários descendentes de um mesmo touro em uma grande diversidade de ambientes (RAUW; GOMEZ-RAYA, 2015). Assim, é possível avaliar a ocorrência na mudança do ranqueamento dos reprodutores para cada ambiente de produção. Dessa forma, é viável realizar escolha de reprodutores mais adequados ao ambiente ou ao sistema de criação, ou seja, onde o mesmo expresse o potencial genético máximo (BIGNARDI et al., 2015).

Santana et al. (2017), ao investigarem taxas de retorno após a inseminação artificial (IA) em animais da raça Holandesa no Brasil, observaram a ocorrência de IGA e reclassificação de alguns touros em diferentes gradientes de temperatura. Shi et al. (2021) identificaram IGA ao analisarem dois ambientes distintos na China para as características de idade ao primeiro parto (IPP), idade ao primeiro serviço (IPS) para vacas da raça Holandesa. Em ambos os trabalhos, os autores mostraram as mudanças na classificação dos touros, em função dos seus valores genéticos, de acordo com o ambiente, evidenciando assim a sensibilidade dos genótipos à variação ambiental, o que resulta na plasticidade fenotípica.

Para características que apresentam sensibilidade fenotípica (plasticidade fenotípica) a variação da herdabilidade em diferentes ambientes precisa ser compreendida (THOMPSON, 1991), pois se a herdabilidade da característica varia entre ambientes, isso indica que a

influência genética também depende do ambiente, o que pode comprometer a eficiência da seleção genética em diferentes condições.

Na Tabela 1 estão apresentados os coeficientes de herdabilidade e correlação genética para as características reprodutivas e produtivas em populações de bovinos da raça Holandesa em diferentes estudos sobre Interação Genótipo x Ambiente.

Tabela 1: Estimativas de herdabilidade e correlação genética para características reprodutivas e produtivas em Bovinos da raça Holandesa sob diferentes condições ambientais.

Autor (es)	Característica	Herdabilidade ± erro padrão	Regiões/Países	Número de animais	Correlações Genéticas ± erro padrão
Muasya et al. (2014)	IPP	$0,25 \pm 0,02$ $0,32 \pm 0,01$	2 ambientes (seleção x produção) no Kenya	9,035*	$0,44 \pm 0,08$
	IEP	$0,02 \pm 0,02$ a $0,04 \pm 0,02$			$0,79 \pm 0,11$
Neser et al. (2014)	IPP	$0,055 \pm 0,009$ a $0,063 \pm 0,005$	2 gradientes ambientais na África do Sul	277	$0,28 \pm 0,12$
Montaldo; Pelcastre-Cruz (2017)	IPP	$0,06 \pm 0,01$	México x Canadá	1,149	$0,45 \pm 0,07$ a $0,48 \pm 0,16$
			México x Canadá		$0,48 \pm 0,07$ a $0,68 \pm 0,16$
	IEP	$0,03 \pm 0,006$	México x EUA	997	$0,64 \pm 0,07$ a $0,73 \pm 0,16$
			EUA x Canadá		$0,93 \pm 0,05$ a $0,97 \pm 0,02$
	IPS	$0,03 \pm 0,01$	México x Canadá	997	$0,87 \pm 0,04$ a $0,89 \pm 0,04$
Liu et al. (2019)	IEP	$0,005 \pm 0,002$ a $0,008 \pm 0,003$	Sistema de criação (Convencional x Orgânico) na Dinamarca	1,636	$0,929 \pm 0,181$
Atrian-Afiani et al. (2020)	IPP	$0,171 \pm 0,008$ a $0,218 \pm 0,011$	3 zonas climáticas no Irã	7,301	$0,858 \pm 0,030$ a $0,0909 \pm 0,018$
	IEP	$0,042 \pm 0,004$ a $0,048 \pm 0,005$			$0,890 \pm 0,043$ a $0,942 \pm 0,021$

continua.

continuação

Autor	Característica	Herdabilidade ± erro padrão	Regiões	Número de animais	Correlação Genética ± erro padrão
Santos et al. (2020)	IPP	0,04 a 0,28	24 gradientes ambientais no Brasil	18,822	-0,99 a 0,99
Wahinya et al. (2020)	IPP	0,05 ± 0,03 a 0,26 ± 0,05	3 sistemas de produção no Kenya	2,554	0,08 ± 0,07 a 0,27 ± 0,09
Chuma-Alvarez et al. (2021)	IPP	0,06 ± 0,005 a 0,09 ± 0,013	4 regiões no Chile	5,268	0,26 ± 0,19 a 0,75 ± 0,09
	IEP	0,02 ± 0,006 a 0,04 ± 0,011		4,481	0,36 ± 0,24 ± 0,98 ± 0,20
Shi et al. (2021)	IPP	0,16 ± 0,011	2 Gradientes ambientais na China	6,556	-0,46 ± 0,01 a -0,90 ± 0,03
	IEP	0,06 ± 0,007			-0,46 ± 0,02 a -0,94 ± 0,03
Muuttoranta et al. (2019)	IPS	0,03 ± 0,01 a 0,07 ± 0,02	Dinamarca, Finlândia, Suécia	44,294	0,45 ± 0,14 a 0,91 ± 0,15
Mulim et al. (2020)	PL	0,18 ± 0,009 a 0,23 ± 0,002	Brasil 17°C a 19,5°C	67,360	0,87 a 1,00
Mulim et al. (2021)	PG	0,21 ± 0,015 a 0,27 ± 0,014	Brasil 17°C a 19,5°C	67,360	0,90 a 1,00
	PP	0,14 ± 0,014 a 0,20 ± 0,013			0,90 a 1,00
Paula et al. (2009)	PL	0,23 a 0,39	Brasil (7 Bacias leiteiras do estado do Paraná)	49,676	0,09 a 0,57

Pela Tabela 1 é possível observar que as herdabilidades para as características reprodutivas são geralmente de baixa magnitude (0 a 0,20). Características que apresentam baixa herdabilidade, normalmente, sofrem maior influência ambiental, bem como, da

sensibilidade ambiental na expressão fenotípica. De acordo com Muuttoranta et al. (2019), embora a influência ambiental seja maior em características relacionadas à reprodução é possível obter progresso genético ao selecionar animais mais adaptados ao ambiente de criação.

Entretanto, não é apenas a macrosensibilidade ambiental que pode resultar em perdas significativas no desempenho dos animais. A microsensibilidade ambiental, imposta diariamente, como por exemplo: a formação hierárquica de grupos de animais, escassez de alimentos em épocas de seca, má gestão no manejo da fazenda pode refletir diretamente no desempenho dos animais. De tal modo que, avaliar a microsensibilidade ambiental poderá ajudar a minimizar os prejuízos do produtor ao adequar o ambiente de produção.

2.2 MICROSSENSIBILIDADE AMBIENTAL

Para bovinos leiteiros, os índices de seleção foram propostos de forma a atribuir ponderações distintas para cada critério de seleção. Mas, geralmente, o peso para a característica produção de leite é maior do que para as demais características que o índice contempla. Porém, sabe-se que a seleção intensa para aumentar a produção de leite influenciou negativamente algumas características de saúde, fertilidade e adaptabilidade (PRITCHARD et al., 2013). De acordo com Wu (1997), os fatores microambientais são classificados como desconhecidos, pois há inúmeros fatores que podem influenciar o desempenho dos animais no dia a dia da fazenda.

É possível que existam variações genéticas para essa sensibilidade, o que indica que os animais são geneticamente diferentes em suas respostas frente às interferências ambientais (MULDER et al., 2013). Alguns animais, mesmo quando há variação ambiental, conseguem manter seus níveis de produção e reprodução, pois são capazes de responder rapidamente ao impacto causado pelo ambiente e, por essa razão, são considerados como resilientes. Dessa forma, animais resilientes são definidos como aqueles que retornam rapidamente ao seu nível normal de desempenho, ou que seu desempenho não é prejudicado quando expostos à variações no ambiente de criação (BERGHOF et al., 2019). Segundo Poppe et al. (2020), uma vaca (genótipo) pode ser considerada resiliente quando mesmo sendo exposta a variações ambientais diversas, tais como: patógenos, ondas de calor, diferença na alimentação, ainda assim, mantém a sua produção.

Um animal com baixa resiliência às condições desafiadoras, pode vir a gerar descarte involuntário, devido a possibilidade de aumento de problemas de fertilidade, saúde do úbere, problemas uterinos, redução da longevidade e perdas devido a menor produção de leite ou leite

sendo descartado (MANOJ et al., 2017). Além disso, a manutenção de animais pouco resilientes e/ou inférteis nas propriedades podem resultar em aumento dos custos com tratamentos veterinários, manejo reprodutivo e sanitário, abate involuntário e, consequentemente, na redução da produtividade do rebanho, além de afetar diretamente os custos de produção (GONZÁLEZ-RECIO et al., 2004).

Dessa forma, selecionar animais resilientes à microsensibilidade ambiental pode resultar na redução dos custos, além de aumentar o progresso genético do rebanho. De acordo com Elgersma et al. (2018), espera-se que vacas resilientes apresentem produções de leite diárias minimamente afetadas por adversidades patogênicas e ambientais e, caso afetadas, retornem rapidamente à produção anterior. Assim, a identificação de famílias e/ou animais resilientes permitiria maior otimização das decisões, por meio da seleção de vacas que se desenvolvam melhor no ambiente de criação (ADRIAENS et al., 2020).

Entretanto, a resiliência é uma característica complexa, que não pode ser diretamente mensurada. Para que seja possível avaliar a resiliência de um animal frente à adversidade ambiental, algumas características podem ser utilizadas como indicadoras. Segundo Scheffer et al. (2018), a resiliência pode ser avaliada por meio de características que oscilam ao longo do tempo. Para a atividade leiteira, uma das principais características que apresentam oscilações é a produção de leite diária que já foi utilizada como indicadora de resiliência para caprinos e bovinos leiteiros (POPPE et al., 2021; POPPE et al., 2020; ELGERSMA et al., 2018 e FRIGGENS et al., 2016).

Ahmed et al. (2019), ao analisarem a produção de leite como ferramenta para medir as perturbações, observaram que, de acordo com as perturbações (tempo, intensidade, colapso e recuperação), seria possível melhorar o gerenciamento da fazenda, para que a produção de leite fosse minimamente afetada. Essas perturbações causadas pelo manejo podem ser classificadas como sensibilidade microambiental, visto que, muitas vezes são desconhecidas no ambiente de produção, mas afetam o desempenho dos animais. De acordo com Ben Abdelkrim et al. (2021), incluir em programas de melhoramento, ou mesmo dentro do próprio gerenciamento da propriedade, a característica resiliência pode ser importante para obter soluções mais eficazes e aplicáveis para a produção leiteira.

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3. CAPÍTULO II - BIBLIOMETRIC MAPPING OF GENOTYPE X ENVIRONMENT INTERACTION IN PRODUCTION ANIMALS

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ABSTRACT

The objective was to explore publications on the effects of genotype $\times$ environment interaction (GEI) in livestock farming. The dataset used for this analysis came from the Web of Science (WOS) database, and the search was carried out from the first article identified in the WOS database until the search date (August 17, 2023). A set of minimum parameters was defined, and then the data was processed using the VOSviewer® software. To generate visual representations in VOSviewer, fractional counting was used, in which the contribution of each article is divided proportionally based on the number of co-authors. Consequently, if an article has three authors, the weight of each author is calculated as 1/3. Brazil and the United States lead research on GEI, while India, China, and Uruguay are emerging countries on the subject. The most cited journals on GEI include the Journal of Animal Science, Journal of Dairy Science, Animal, Livestock Science, Journal of Animal Breeding and Genetics, and Revista Brasileira de Zootecnia. In Brazil, the research groups are at the forefront of publications related to GEI. Ongoing climate changes over the years have likely led to further investigations into this matter. In the Brazilian context, research groups from the São Paulo State University (UNESP), College of Agricultural and Veterinary Sciences - Jaboticabal, and the Faculty of Veterinary Medicine and Animal Science at the University of São Paulo (FZEA/USP, Campus Pirassununga) have played a prominent role in advancing this area of study. Furthermore, our

bibliometric analysis revealed future trends in GEI publications, including an increasing integration of genomic information into research.

Keywords: beef cattle, climate challenges, cluster analysis, dairy cattle, timeline.

3.1 INTRODUCTION

The majority of economically significant traits are under the influence of genetic and environmental factors, as well as the interaction between the two (Hay and Roberts, 2018). Genotype $\times$ environment interaction (GEI) constitutes a complex system that presents challenges for advancing genetics in livestock animals (Araújo et al., 2022). However, despite the potential influence of GEI on animal performance, most selection programs in Brazil do not incorporate this factor into their evaluations (de Paula Freitas et al., 2021). Neglecting GEI in selection makes it challenging to select animals that exhibit plasticity in the face of differing climatic challenges (Tiezzi et al., 2017).

Bibliometric analysis is a statistical methodology that permits the quantitative examination of studies within a specific domain (Chen et al., 2014). It enables the establishment of connections between research articles and topics (McManus et al., 2023a), provides information on the evolution and changes in a field of study (Yu et al., 2020), and aids in determining the origins of key concepts (Fellnhöfer, 2019). As such, this analysis facilitates the understanding of the diverse areas of research including GEI and the identification of the main research groups and publications within the field. VOSviewer®, a tool for conducting bibliometric analysis, allows users to create and explore network-based maps. It facilitates the examination of co-authorship, co-occurrence, citation, bibliographic coupling, and co-citation links (Westby, 2021). In the literature, several studies have employed literature mapping to investigate the areas of animal genetic resources and their response to climate change (Vieira and McManus, 2023), as well as heat tolerance in production animals (McManus et al., 2023a). However, there is a noticeable gap in research addressing GEI in livestock animals. Given the significance of accounting for GEI effect on animal performance and its impact on the proper selection of breeding stock, this study identified the principal countries and research groups focused on the subject. Additionally, it highlighted novel methodologies employed in GEI research. Therefore, the objectives were to unveil research trends through publications addressing GEI in production animals and to elucidate the strengths and weaknesses of research conducted in this area.

3.2 MATERIAL AND METHODS

In examining the global literature concerning GEI in production animals (cattle, sheep, goats, pigs, and poultry), we utilized the Web of Science database, renowned for its extensive publication coverage (Singh et al., 2020). The search on Web of Science incorporated criteria such as year of publication, language, journal, title, author, affiliation, keywords, document type, abstract, and citations. These data were exported in comma-separated values (CSV) format to Microsoft Excel, with information retrieval completed on August 17, 2023. A set of minimum parameters was defined (Table 1). Following this, the data underwent processing via VOSviewer® software (version 1.6.15) (Van Eck and Waltman, 2020) to generate the figures and tables featured in this study.

Table 1 - Bibliometric parameters for publications on genotype environment interaction in farm animals

	Total	Minimum number of Papers or citations	After Minimum applied¹	Linked²	Number of Clusters³
Co-Authors	1.326	2	283	136	7
Countries	50	3	28	83	6
Keywords	715	3	103	388	12
	715	5	52	201	6
Citation - Documents	415	10	189	443	13
Sources	76	3	27	131	7
Authors	1.382	3	112	1.197	9
Countries	50	3	28	218	5
Bibliometric Coupling	415	15	142	1.967	11
Sources	76	3	27	320	6
Authors	1.382	3	112	3.364	14
Countries	50	3	28	378	6
Co-citation - References	9.106	20	23	219	4
Sources	2.738	20	76	2.296	7
Authors	5.421	20	77	71	4

¹Number of authors, countries, Keywords etc, after applying for the minimum number from the previous column;

²the number of authors, countries, and Keywords with linkages to others in the analysis; ³total number of clusters formed per the criteria defined in the analysis.

The choice of VOSviewer was justified by its user-friendly interface, high-quality graphics, and seamless integration with the Web of Science database (Westby, 2021). In generating the visual representations in VOSviewer, fractional counting was employed, wherein the contribution of each article is divided proportionally based on the number of co-

authors (Martínez López et al., 2020). Consequently, if an article has three authors, each author's weight is calculated as 1/3 (Perianes-Rodriguez et al., 2016). This methodology results in the creation of networks illustrating co-authorship, keyword co-occurrence, citation relationships, bibliographic coupling, and co-citation (Van Eck and Waltman, 2020).

Co-authorship analysis took into account the number of co-authors in articles found on Web of Science, their countries, affiliations, and the link between them (McManus et al., 2023b). This approach visualizes outcomes as a collaborative network image, highlighting the academic frequencies of authors and countries (Shah et al., 2020), with cluster size representing the relevance of the author of the article and its countries of origin. Keyword co-occurrence analysis, as specified by the authors, is represented as nodes, and each instance of co-occurrence is depicted as a link (Radhakrishnan et al., 2017).

Citation analysis was conducted based on documents (articles), sources (journals), authorship, and the countries of origin of articles. This analysis discerns the link between variables, in which one entity cites the other (McManus et al., 2023b). A higher frequency of citation of information (documents, sources, authors, and countries of origin) signifies its greater importance for science (Small, 2003).

Bibliographic coupling identifies documents (articles), sources (journals), references, and countries addressing the subject matter, gauging the similarity between two documents based on the number of shared references or the extent to which two documents are interconnected via their bibliographies or reference lists (Maseda et al., 2022). Co-citation analysis, in turn, ascertains the extent to which two or more documents are frequently cited together in other scientific articles. This method allows for the identification of influential articles and researchers in a given research area (Mas-Tur et al., 2021).

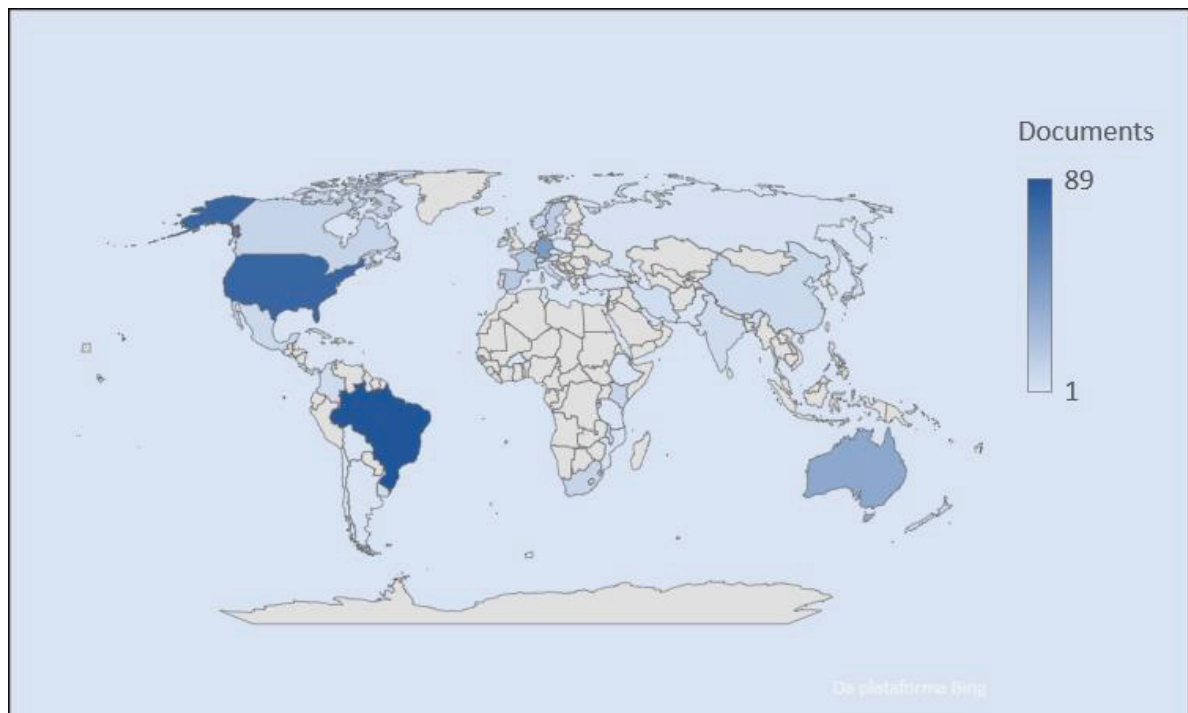
Larger clusters indicate a greater contribution of information (author, country of origin of the article, source [journal], keywords, document [article], and reference). Additionally, if the color of the connection between words is more vibrant, it means that the information appears more frequently in various documents. If the connection is small, the color will be less vibrant (Bilad, 2022). Furthermore, we can identify the evolution of information over the years and its future trends (Ding and Yang, 2022).

3.3 RESULTS

The countries with over 20 documents were Brazil (89 articles), the United States (79 articles), Germany (45 articles), Australia (38 articles), The Netherlands (28 articles), and

Scotland (23 articles) (Figure 1). Most of the published documents on GEI demonstrate a concentration in the bovine species (Figure 2A). The earliest recorded published article in the database dates back to 1952 (Figure 2B). There was a significant increase in publications from 2000 to 2022. The year with the highest number of publications in the field was 2020, with 26 documents, followed by 2021 with 24 publications.

The majority of documents (Figure 3A) consists of scientific articles published in journals (88.94%), followed by review articles (4.94%), simple and expanded abstracts published in conference proceedings (3.29%), conference papers (2.35%), and books (0.47%). The three primary areas of knowledge (Figure 3B) that we identified are Agriculture (67.86%), Veterinary Science (13.57%), and Food Science and Technology (9.64%).



Color darkness for a country indicates progressively larger numbers of publications in Web of Science.

Figure 1 Heat map by country of papers focusing upon genotype $\times$ environment interaction in farm animals.

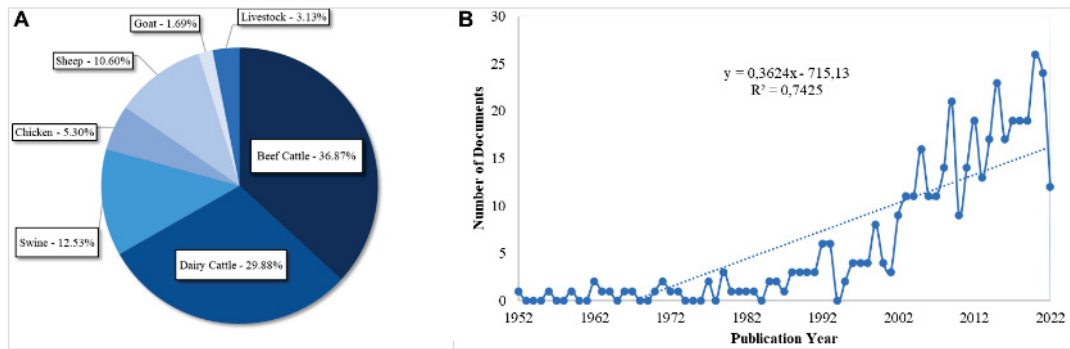


Figure 2 Animal species used in genotype × environment interaction studies (A) and number of documents.

The three most prominent institutions (Figure 3C) in this field are Brazilian, including the Brazilian Agricultural Research Corporation (EMBRAPA), Wageningen University Research, and São Paulo State University (UNESP). The leading Brazilian funding bodies (Figure 3D) include the National Council for Scientific and Technological Development (CNPq), linked to the Ministry of Science and Technology; the Coordination for the Improvement of Higher Education Personnel (CAPES), linked to the Ministry of Education; and the São Paulo Research Foundation (FAPESP).

According to the parameters we retrieved from the article in Web of Science (Table 1), 1,326 authors were identified. Of these, approximately 283 authors had at least two published documents in this area. Among the 50 countries with publications, only 28 had at least three publications. Of the 715 keywords, 103 were repeated at least three times, and 52 were repeated at least five times in publications. The most frequently used keywords include “genotype-environment interaction” (101 repetitions), “beef cattle” (47 repetitions), “dairy cattle” (47 repetitions), and “reaction norm model” or “reaction norms” (38 repetitions).

However, based on the timeline (Figure 4), as of 2020 (yellow cluster), words such as “environmental gradients”, “heat stress”, “thermoregulation”, “Genome-Wide Association Studies” (GWAS), and “SNP” (Single Nucleotide Polymorphism) gain increased prominence.

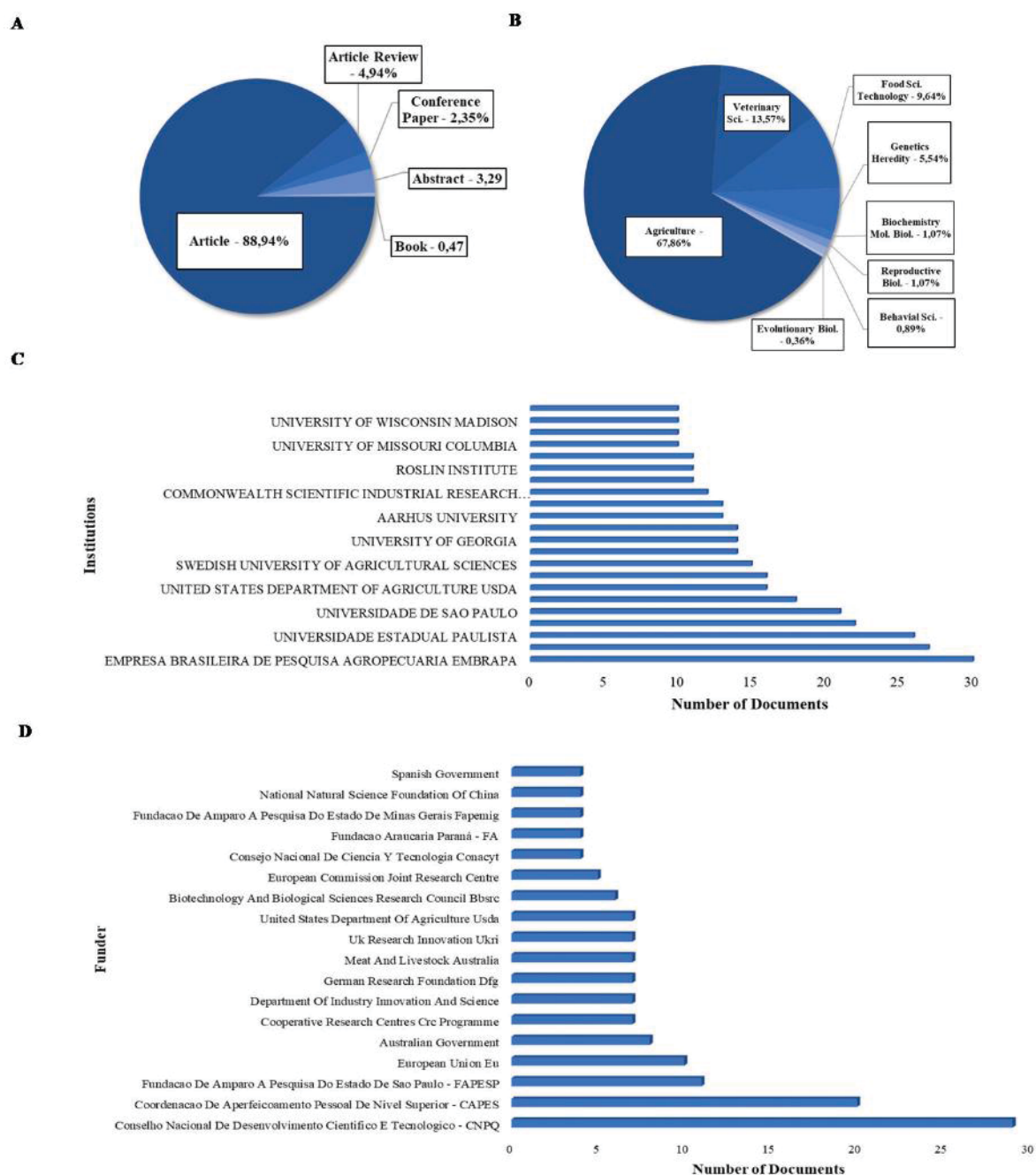


Figure 3 Type of document (A), area of knowledge (B), top institutions (C), and financing agencies (D) in genotype.

In co-authorship analysis (Figure 4), we identified the formation of clusters for authors (seven clusters), countries (six clusters), and keywords (12 clusters). Different cluster sizes correspond to the relevance of the information. Furthermore, the timeline provides information on the average year of publications, with darker colors indicating older publications and lighter colors representing more recent publications. In the list of the main authors and their countries

of origin (Figure 4 and Table 2), we observed a predominance of authors from Brazil, the USA, and the Netherlands, with 12, five, and three authors, respectively.

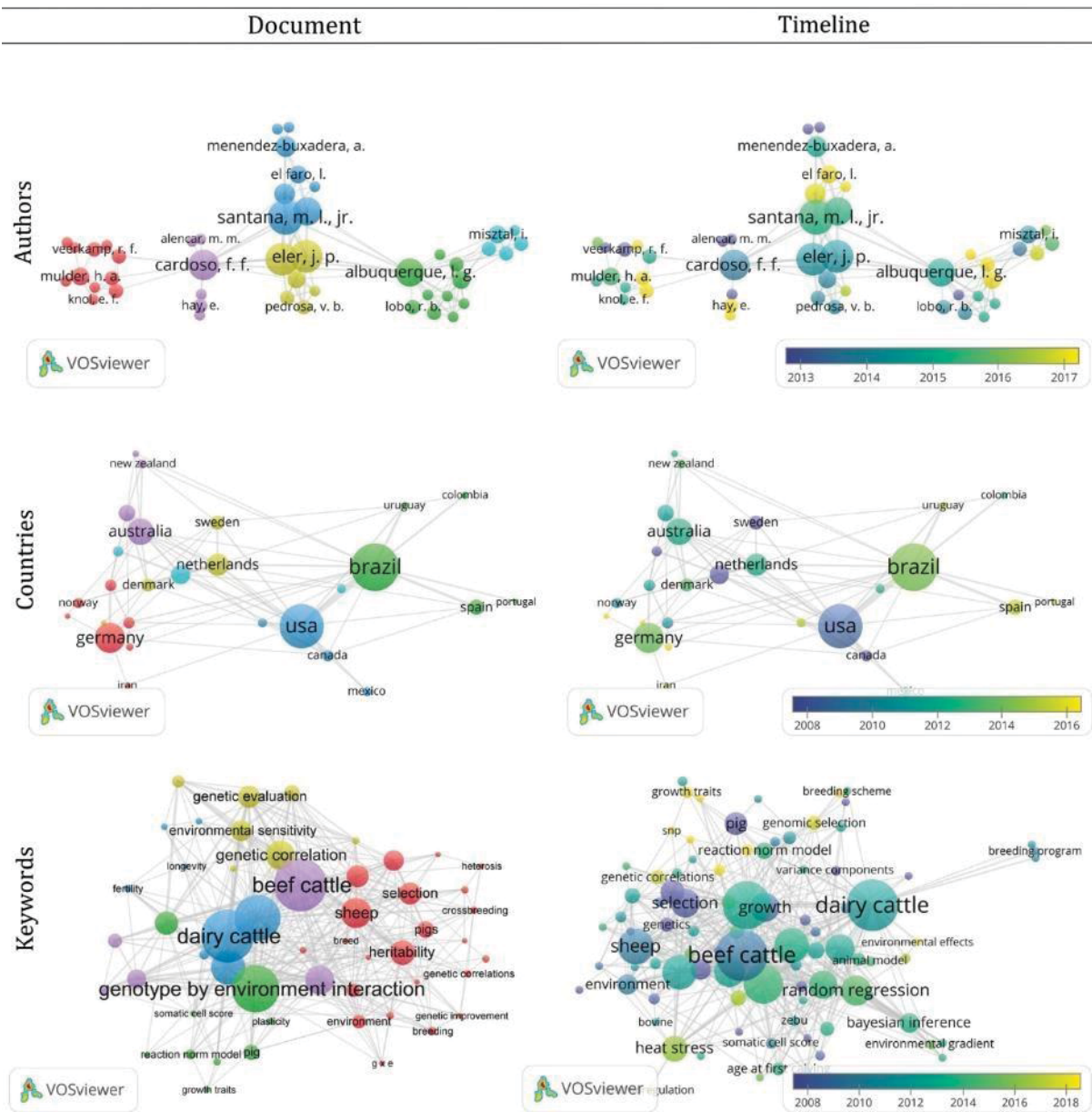


Figure 4 Publication parameters for co-authorship in publications on genotype $\times$ environment interaction in farm animals.

Table 2 - Top 20 authors for publications on genotype $\times$ environment interaction in farm animals

Author	Country	Cluster	Links	Total link strength	Docs	Cites	Normalized citations	Publication year	Avg. citations	Avg. normalized citations
Cardoso, F. F.	Brazil (1)	4	14	8	9	194	11.63	2013	21.56	1.29
Albuquerque, L. G.	Brazil (02)	2	19	8	8	130	10.93	2014	16.25	1.37
Santana Jr, M. L.	Brazil (03)	6	10	11	11	139	10.13	2015	12.64	0.92
Misztal, I.	USA (01)	5	7	4	4	101	9.26	2014	25.25	2.32
Mulder, H. A.	Netherlands (01)	1	7	4	4	68	8.16	2015	17.00	2.04
Lopes, P. S.	Brazil (04)	1	6	3	3	54	7.72	2017	18.00	2.58
Silva, F. F.	Brazil (05)	1	6	3	3	54	7.72	2017	18.00	2.58
Knol, E. F.	Netherlands (02)	1	4	2	2	54	7.33	2015	27.00	3.67
Mathur, P. K.	Netherlands (03)	1	4	2	2	54	7.33	2015	27.00	3.67
Tsuruta, S.	USA (02)	5	7	3	3	78	7.26	2013	26.00	2.42
Bignardi, A. B.	Brazil (06)	6	9	8	8	102	7.19	2015	12.75	0.90
Lourenço, D. A. L.	USA (03)	5	7	3	3	59	6.72	2016	19.67	2.24
Baldi, F.	Brazil (07)	2	11	4	4	64	6.63	2017	16.00	1.66
Eler, J. P.	Brazil (08)	3	10	10	10	86	6.59	2014	8.60	0.66
Ferraz, J. B. S.	Brazil (09)	3	10	10	10	86	6.59	2014	8.60	0.66
Carvalho, R.	Brazil (10)	2	11	3	3	54	6.08	2017	18.00	2.03
Tempelman, R. J.	USA (04)	1	5	3	3	105	5.99	2015	35.00	2.00
Pereira, R. J.	Brazil (11)	6	10	5	5	66	4.70	2016	13.20	0.94
El Faro, L.	Brazil (12)	6	5	4	4	67	4.58	2017	16.75	1.15
De Los Campos, G.	USA (05)	1	2	1	2	60	4.47	2017	30.00	2.24

Despite the prolific production of works in Brazil on this topic, the works of Brazilian researchers are not among the most cited (Figure 5). The paper with the highest number of citations is by Warner et al. (2010) from Australia (Figure 5 and Table 3), a review work in which the researcher gathered articles that analyzed and identified the effects of GEI on meat quality traits in beef cattle. Several factors can influence the citation of an article, including its age (more than 20 years since first publication), the species studied (dairy cows), and, most importantly, the methodology used for the analyses.

The top six journals with the highest number of citations on the effects of GEI are: the Journal of Animal Science (81 documents with 1,190 citations), Journal of Dairy Science (50 documents with 1,814 citations), Livestock Science (25 documents with 234 citations), Journal of Animal Breeding and Genetics (16 documents with 167 citations), and Revista Brasileira de Zootecnia (15 documents with 168 citations) (Figure 5).

Table 3 - Top cited papers of publications on genotype $\times$ environment interaction in farm animals.

Reference	DOI	Cluster	Link	Citation	Normalized citation
Warner et al. (2010)	https://doi.org/10.1016/j.meatsci.2010.04.042	7	2	187	5.29
Kolmodin et al. (2002)	https://doi.org/10.1080/09064700252806380	5	37	184	3.81
Finocchiaro et al. (2005)	https://doi.org/10.3168/jds.s0022-0302(05)72860-5	1	3	117	3.14
Knap (2005)	https://doi.org/10.1071/ea05041	1	10	114	3.06
Mulder et al. (2006)	https://doi.org/10.3168/jds.s0022-0302(06)72242-1	11	16	94	1.45
Windig et al. (2006)	https://doi.org/10.3168/jds.s0022-0302(06)72245-7	10	12	89	1.37
Hammami et al. (2015)	https://doi.org/10.3168/jds.2014-9148	1	5	87	4.76
Calus et al. (2002)	https://doi.org/10.3168/jds.s0022-0302(02)74399-3	8	18	79	1.83
Cardoso and Tempelman (2012)	https://doi.org/10.2527/jas.2011-4333	2	31	66	2.88
Johnston et al. (2003)	https://doi.org/10.1071/ar02087	7	4	66	1.95

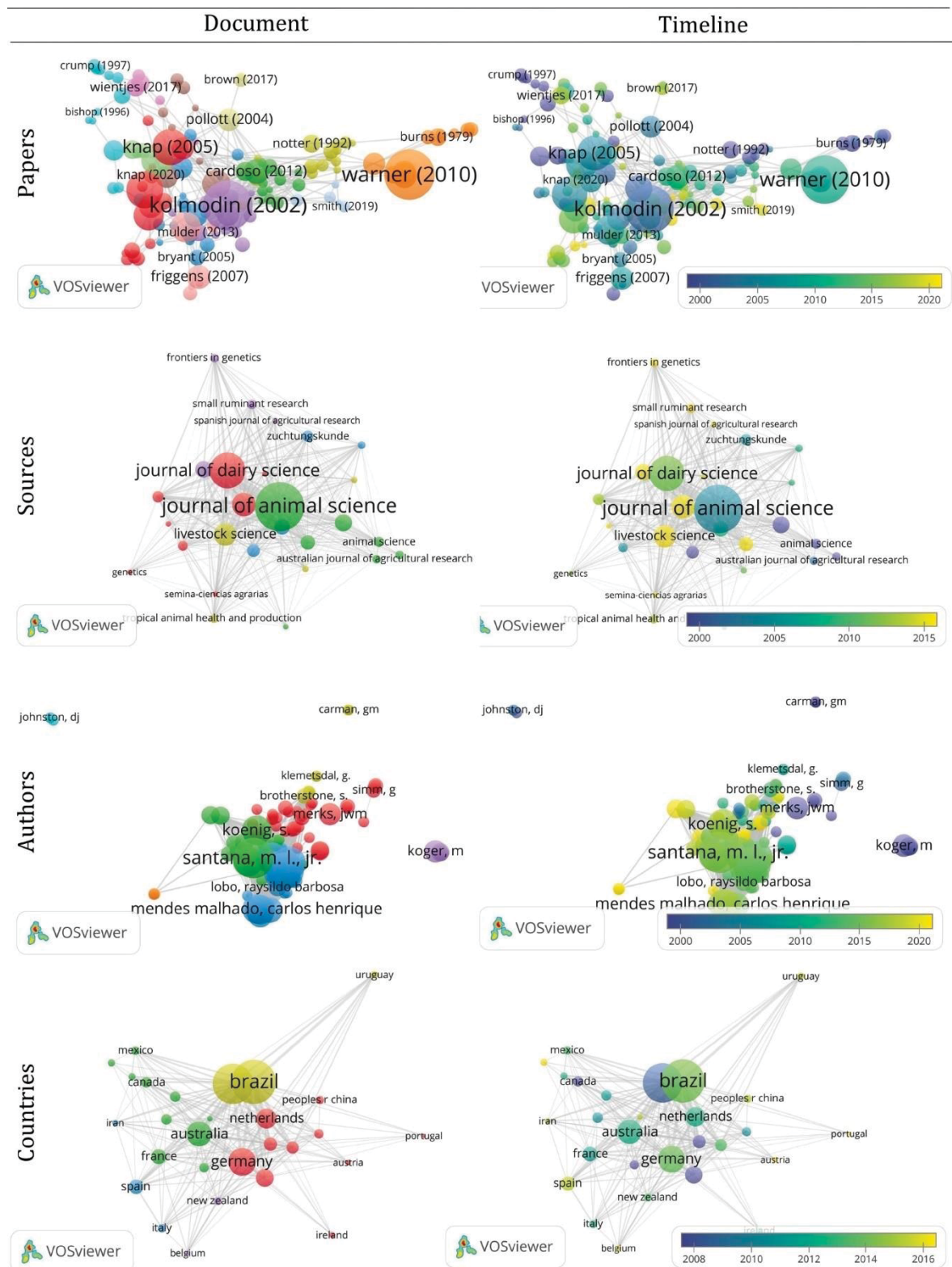


Figure 5 Publication parameters for co-authorship in publications on genotype $\times$ environment interaction in farm animals.

In bibliographic coupling (Table 4 and Figure 6), the article with the highest total link strength is by Cardoso and Tempelman (2012), followed by Streit et al. (2012). In the article by Cardoso and Tempelman (2012) the authors evaluated alternative reaction norm models for the genetic evaluation of Angus cattle in Brazil. This article was published in the Journal of Animal Science, which has an impact factor of 3.338. The article by Streit et al. (2012), published in the Journal of Animal Breeding and Genetics with an impact factor of 2.6, addressed random reaction norm regression models to identify the occurrence of GEI on productive traits (milk, protein, and fat production) and health traits (somatic cell score) in Holstein cattle in Germany. However, the Journal of Dairy Science was the most cited source in this area. The coupling of countries (Figure 5) is generally defined by the researcher's country, with Brazil and the USA being the most prominent. Nevertheless, as indicated by the timeline, Uruguay, Portugal, China, Belgium, India, and Spain are becoming increasingly significant with recent publications in this field.

Table 4 - Top 10 papers in bibliographic coupling for publications on genotype $\times$ environment interaction in farm animals

Document	DOI	Cluster	Link	Total link strength	Citation	Normalized citation
Cardoso and Tempelman (2012)	https://doi.org/10.2527/jas.2011-4333	1	84	38	66	2.89
Streit et al. (2012)	https://doi.org/10.1111/j.1439-0388.2012.00999.x	1	62	38	15	1.13
Bryant et al. (2005)	https://doi.org/10.1016/j.agry.2004.09.004	1	49	33	34	0.91
Santana Jr et al. (2013)	https://doi.org/10.1017/s175173112001711	1	57	29	35	2.65
Carvalho et al. (2019)	https://doi.org/10.1186/s12711-019-0470-x	4	50	27	25	3.02
Mulder et al. (2006)	https://doi.org/10.3168/jds.s0022-0302(06)72242-1	2	57	26	94	2.74
Mattar et al. (2011)	https://doi.org/10.2527/jas.2010-3770	1	44	26	46	1.46
Mulder and Bijma (2006)	https://doi.org/10.3168/jds.s0022-0302(06)72241-x	2	45	26	30	0.46
Kolmodin et al. (2002)	https://doi.org/10.1080/09064700252806380	2	52	25	184	3.82
Tiezzi et al. (2017)	https://doi.org/10.3168/jds.2016-11543	4	61	25	37	2.76

article by Cardoso and Tempelman (2012) the authors evaluated alternative reaction norm models for the genetic evaluation of Angus cattle in Brazil. This article was published in the Journal of Animal Science, which has an impact factor of 3.338. The article by Streit et al. (2012), published in the Journal of Animal Breeding and Genetics with an impact factor of 2.6, addressed random reaction norm regression models to identify the occurrence of GEI on productive traits (milk, protein, and fat production) and health traits (somatic cell score) in Holstein cattle in Germany. However, the Journal of Dairy Science was the most cited source in this area. The coupling of countries (Figure 5) is generally defined by the researcher's country, with Brazil and the USA being the most prominent. Nevertheless, as indicated by the timeline, Uruguay, Portugal, China, Belgium, India, and Spain are becoming increasingly significant with recent publications in this field.

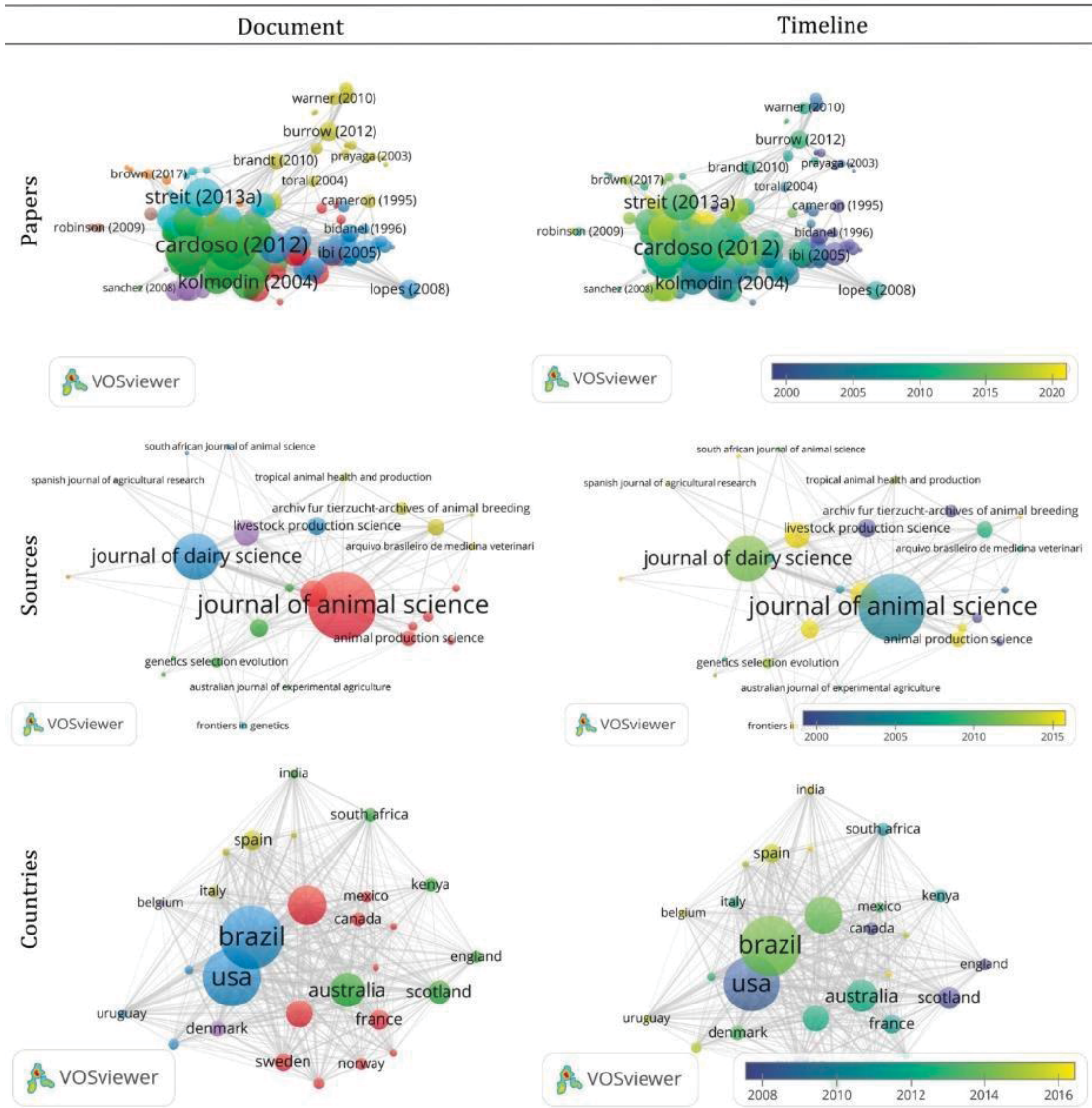


Figure 6 Bibliographic coupling analysis for publications on genotype $\times$ environment interaction in farm animals.

Among the 10 most cited references (Table 5), classified by the strength of the link based on the number of co-citations, the oldest is authored by Robertson (1959), and the most recent is by Cardoso and Tempelman (2012). The article by Robertson (1959) deals with the genetic correlation coefficient to determine the presence of GEI. Cardoso and Tempelman (2012), on the other hand, evaluated alternative reaction norm models to investigate GEI. The most cited source, forming the largest cluster, is from the Journal of Dairy Science, and the most prominent author is Falconer (Figure 7).

Table 5 - Top co-cited documents for publications on genotype $\times$ environment interaction in farm animals.

Label	DOI	Cluster	Links	Total link strength	Citations
Robertson (1959)	https://doi.org/10.2307/2527750	3	22	70	90
Kolmodin et al. (2002)	https://doi.org/10.1080/09064700252806380	1	21	69	73
Falconer and Mackay (1996)	Book	3	21	44	51
Falconer (1952)	https://doi.org/10.1086/281736	3	21	42	50
Su et al. (2006)	https://doi.org/10.2527/jas.2005-517	1	19	37	38
De Jong and Bijma (2002)	https://doi.org/10.1016/S0301-6226(02)00096-9	1	21	34	36
Cardoso and Tempelman (2012)	https://doi.org/10.2527/jas.2011-4333	1	22	35	36
Mattar et al. (2011)	https://doi.org/10.2527/jas.2010-3770	1	21	33	34
Calus and Veerkamp (2003)	https://doi.org/10.3168/jds.S0022-0302(03)73982-4	1	20	34	34
Calus et al. (2002)	https://doi.org/10.3168/jds.S0022-0302(02)74399-3	1	20	27	29

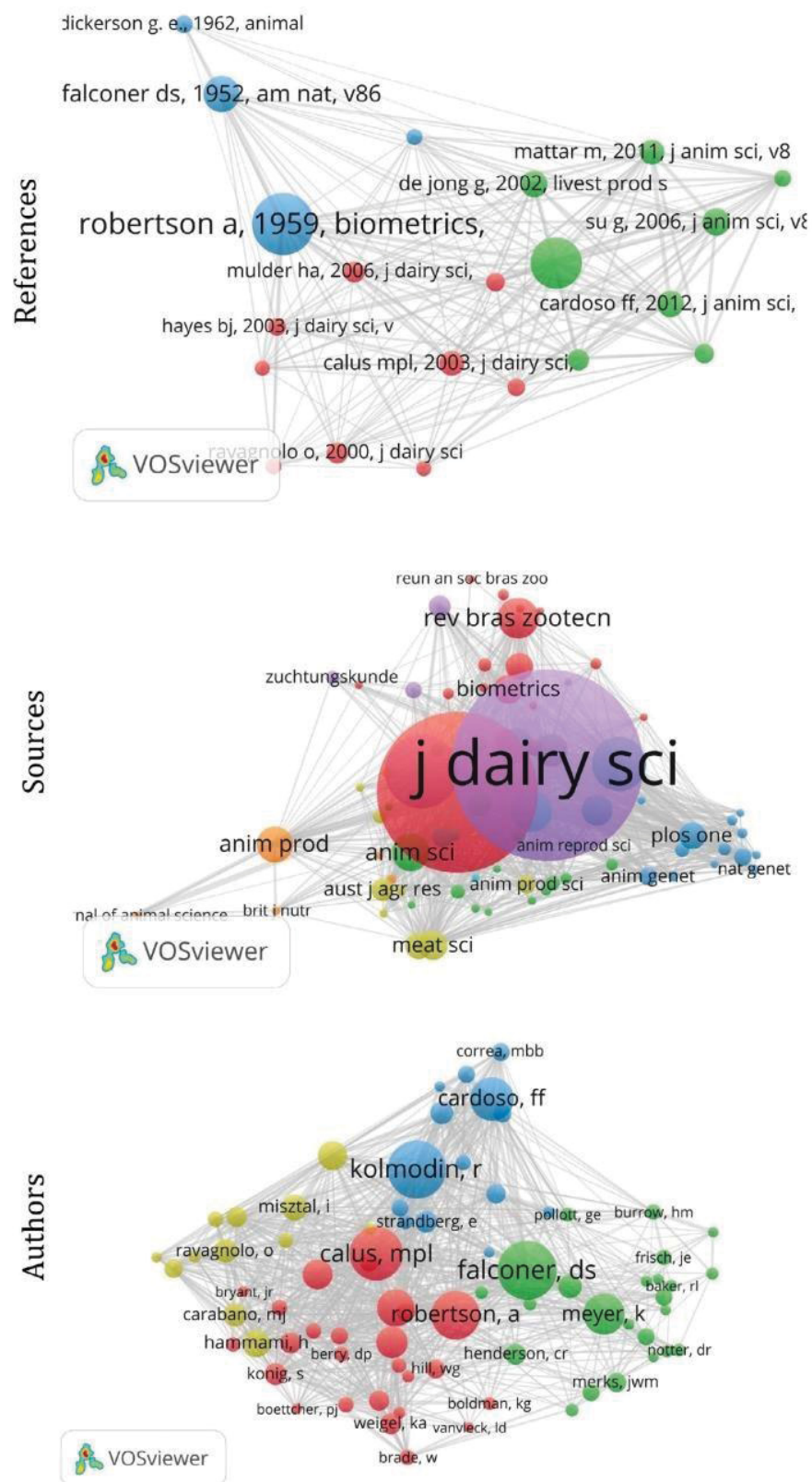


Figure 7 Co-citation analysis for publications on genotype $\times$ environment interaction in farm animals.

3.4 DISCUSSION

Brazil showed most studies on GEI (Figure 1). This is likely due to the country's diverse biomes, climates, and production systems (Mota et al., 2020). Moreover, Brazil is a significant importer of genetic material for production animals (Santos et al., 2020), emphasizing the importance of evaluating the performance of these selected genotypes in contrasting environments compared with those found in the country.

Additionally, among the 20 main authors engaged in GEI studies, 12 are of Brazilian origin (Table 2), underscoring the significance of the topic for the country. Moreover, most of the clusters formed (Figure 4) consist of Brazilian authors, including Albuquerque, L. G., Santana Jr, M. L., Cardoso, F. F. and Eler, J. P., who are prominent researchers in the field of animal genetic improvement. Their primary focus is on working with beef cattle, mainly Angus and Nellore breeds, widely used throughout the country, both as purebreds and crossbreds.

Institutions in Brazil are the leaders in the number of documents on this subject (Figure 3C), and the primary funding sources are organizations that promote research in the country (Figure 3D). These findings reaffirm the importance of GEI studies in Brazil, with Brazilian researchers actively contributing to the publication of documents/articles on the subject.

Most of these documents are published as scientific articles (over 88%) (Figure 3A), serving as the primary means for disseminating knowledge, ensuring accessibility to researchers globally (Canessa and Zennaro, 2008). However, various factors, such as limited access and high publication fees, especially in high-impact journals, can hinder publication or access behind paywalls. For instance, the publication fee for the Journal of Animal Science (JAS) averages US\$340 per page, that is, a 10- page article would cost a total of US\$3,400. Given the scarcity of resources for research and article publication in developing countries like Brazil, where the exchange rate is around five Brazilian Reals per US dollar, publishing in high-impact journals becomes a costly endeavor, leading many researchers to opt for local journals. Consequently, the dissemination of their content through citations is limited (McManus et al., 2020).

As regards the most repeated keywords (Figure 4), “genotype-environment interaction” takes the lead, followed by “beef cattle”, “dairy cattle”, and “reaction norm models”. In the case of cattle, concerns about the effects of GEI are more pronounced in animals raised in uncontrolled environments (Phocas et al., 2016), as controlled environments exhibit less pronounced GEI effects. Reaction norm models describe the trajectory of animal performance

along environmental gradients (Falconer and Mackay, 1996), and although this knowledge is well known, the need for increased computational power to carry out these analyses limited its use until more recently.

Recent publications indicate a shift in keyword usage (Figure 4 – timeline), with increased emphasis on terms like “thermal stress”, “thermoregulation”, “environmental gradients”, and “genomics-related methodologies”. In reaction norm models, the environment is modeled as a continuous variable scale, often incorporating factors such as the temperature-humidity index and disease occurrence (Hayes et al., 2016). Novel approaches to describe the environmental gradient have emerged, including the use of previously estimated solutions from contemporary groups (Carvalho Filho et al., 2022; Nascimento et al., 2022).

Furthermore, there has been a noticeable increase in publications utilizing reaction norm models to assess GEI over the years. This applies to studies involving beef cattle (Bignardi et al., 2015; Fonseca et al., 2015; Ambrosini et al., 2016; Fennewald et al., 2017; MacNeil et al., 2017; Nascimento et al., 2022), dairy cattle (Bohlouli and Alijani, 2012; Montaldo et al., 2017; Zhang et al., 2019; Cheruiyot et al., 2020; Mulim et al., 2020, 2021; Santos et al., 2020), pigs (Camerlink et al., 2015; Hong et al., 2021), poultry (Santos et al., 2008; Felipe et al., 2012), and sheep (Wilkes et al., 2012; Hopkins and Mortimer, 2014). Notably, some more recent studies are already incorporating genomic information into reaction norm models to identify GEI (Tiezzi et al., 2017; Mota et al., 2020; Chen et al., 2021; Nascimento et al., 2022; Toro-Ospina et al., 2023).

The heterogeneity of Brazilian production systems, coupled with climate diversity and varied nutritional practices across farms, and even discrepancies between states, significantly affect the productive and reproductive performance of animals (Santos et al., 2020). Another noteworthy aspect is the widespread utilization of genetic material from US companies, breeders’ associations, and breeding programs by Brazilian breeders. Consequently, there is a pressing need to comprehend the arrangement of genotypes challenged by diverse environmental conditions to attain more efficient genetic advancement, thereby optimizing investments. Although the United States and Brazil lead in citations (Figure 5), Uruguay, Portugal, China, Belgium, India, and Spain have recently emerged with increased contributions in published papers on the topic. This underscores the growing concern about genotype behavior in the face of recurrent global climate changes, which can be attributed to the effects of global warming (Sammad et al., 2020).

The journals receiving the highest number of citations (Figure 5) in the context of GEI studies are the Journal of Animal Science and Journal of Dairy Science. Most research

published in these journals is centered on studies involving cattle as the biological model, highlighting the significance of the topic for this species and its publication focus on these journals. Notably, recent citations have increasingly favored the journal *Livestock Science*, which has an impact factor of 1.8 and offers hybrid-access publication, making it an attractive choice for countries with limited research resources (McManus et al., 2020).

Analyzing the bibliographic coupling of countries (Figure 6), Brazil and the United States take the lead, likely owing to their vast geographical expanse and the climatic diversity they present (Beck et al., 2018). This reinforces the importance of GEI studies given the divergent environmental conditions and production systems these countries exhibit. However, in recent years, the United States has decreased its publications on the subject, while other countries, such as Germany, Spain, China, Portugal, and India, have entered this arena. Despite their smaller territorial extent, these countries still exhibit climatic diversity according to the Köppen classification (Beck et al., 2018) and are undergoing the effects of climate change. Furthermore, these countries mainly rely on genetic materials produced in the USA and Canada for dairy cattle production. In terms of bibliographic coupling, the *Journal of Animal Science* stands out as the most relevant journal (Figure 6) due to its long-standing adoption within the academic community and its current impact factor of 3.3.

Among the co-cited articles, high-impact journals such as *Biometrics*, *Animal Science*, *Journal of Dairy Science*, *Journal of Animal Science*, and *Livestock Production Science* stand out (Table 5 and Figure 7). Furthermore, the most frequently co-cited authors are Falconer and Mackay (1996) and Robertson (1959) (Table 5 and Figure 7), both affiliated with the Edinburgh quantitative genetics group (Hill and Mackay, 2004). These authors are frequently cited together in publications related to GEI. Falconer, in his two publications [Falconer and Mackay, 1996 (book) and Falconer, 1952 (article)], proposed an approach to identifying GEI by assessing the performance of a sire's daughters under different environments, effectively treating it as if they were distinct traits. This methodology allows the investigation of behavior fluctuations under changing environmental conditions. Robertson (1959) suggested that genetic correlations exceeding 0.80 indicate similarity in genotype behavior under different environments, signifying the absence of GEI. Conversely, if the genetic correlation between the performances of offspring from the same breeder, when exposed to different environments, falls below 0.80, it indicates the presence of GEI.

Lastly, it is important to acknowledge certain limitations of bibliometric mapping. Publication bias may emerge due to the reliance on published articles, potentially excluding unpublished or non-indexed studies and thus affecting the representativeness of the results

(McManus et al., 2023a). Subjectivity in the study selection process, even with well-defined criteria, can introduce bias into the review. Additionally, relying on specific databases or limited sources may result in gaps in the coverage of relevant studies, as well as differences in the availability of articles in various languages.

3.5 CONCLUSION

Brazil and the United States are at the forefront of research on genotype $\times$ environment interaction. However, more recently, India, China, Uruguay, Portugal, and other nations have made scientific contributions to this topic. The ongoing climate changes over the years have likely driven new investigations into this subject. In the Brazilian context, research groups at São Paulo State University (UNESP), School of Agricultural and Veterinary Sciences - Jaboticabal, and the Faculty of Veterinary Medicine and Animal Science of the University of São Paulo (FZEA/USP, Pirassununga Campus) have played prominent roles in advancing this area of study. Moreover, our bibliometric analysis has revealed forthcoming trends in genotype $\times$ environment interaction publications, including a growing integration of genomic information into research endeavors.

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4 CAPÍTULO III INFLUENCE OF DIFFERENT ENVIRONMENTAL CHALLENGES ON THE EXPRESSION OF PRODUCTIVE TRAITS IN HOLSTEIN CATTLE IN THE SOUTHERN REGION OF BRAZIL

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ABSTRACT

The genotype-environment interaction (GEI) can lead to variations in gene expression related to traits, affecting the breeding value of animals. Assess the effects of GEI on milk, fat, and protein yields at 305 days in milk in first-, second-, and third-parity cows, employing the reaction norms model for Holstein cattle in Paraná state. The study utilized data from the milk testing service provided by the Paraná Association of Holstein Cattle Breeders (APCBRH) in Curitiba, PR, Brazil. This encompassed records from 378,000 across one to three lactations from 2012 to 2022, originating from 513 herds in 72 cities within the state of Paraná. The environmental gradient was established by standardizing the contemporary group solutions derived from the animal model, disregarding GEI. Reaction norms were then calculated using a Random Regression Model, and genotype classification correlations were determined through Spearman's correlation, comparing the breeding values estimated for the analyzed traits in each environmental gradient. Heritability for milk yield (MY) during the first lactation was moderate (0.28) in the least challenging environmental gradient, but of low magnitude (0.18) in the most

challenging one. Fat yield (FY) heritability estimates varied from low (0.09) to moderate (0.28) across environmental gradients, whereas protein yield (PY) heritability remained low regardless of lactation number and environmental challenge. The study did not identify the occurrence of GEI effects on fat yield, irrespective of parity. No GEI effect was observed on MY or PY in the first and second lactations. However, in the third lactation, GEI significantly affected MY and PY in Holstein cattle in the state of Paraná, particularly under extreme environmental gradients. The selection for MY, PY, and FY during the first lactation may be the best strategy, given the minimal effect of GEI at this stage.

Keywords: dairy cattle, environmental gradient, estimated breeding values, genotype by environment interaction, reaction norms, genotype plasticity.

4.1 INTRODUCTION

Genotype-environment interaction (GEI) involves the differential expression of genotypes when exposed to various environmental conditions, affecting phenotype classification and genetic parameters and thus altering the breeding value estimates of individuals (Streit et al., 2012; Montaldo et al., 2017). These alterations pose a considerable challenge to animal genetic improvement programs, such as a decrease in the accuracy of genetic value estimates (EBVs), the need for evaluations in different environments, phenotypic differences between the selection and rearing environments, increased costs, and greater complexity in structuring these programs (de Araújo et al., 2022; Silva-Neto et al., 2024).

Consequently, selection could be more effective if the imported genetic material originated from bulls evaluated in similar environments (Salvian et al., 2023). Nonetheless, the genetic advancement of dairy cattle in Brazil frequently relies on imported semen (Santos et al., 2020), potentially exacerbating GEI effects.

Given the importance of GEI on key economic traits, various methodologies for its assessment exist, including heritability comparisons, variance component analyses, and genetic correlation investigations across diverse environments (Montaldo et al., 2017; Yao et al., 2017; Bengtsson et al., 2022). An additional approach to evaluate GEI are reaction norms models (RMNs), which provide a means to ascertain genotype responses in different environmental conditions (Tiezzi et al., 2017; Mota et al., 2020; Schmid et al., 2021; Toro-Ospina et al., 2023). This is a widely adopted methodology in dairy farming, as daughters from a single sire are reared in distinct environment settings (Rauw et al., 2015).

The RNM model has been used to estimate the effects of GEI interactions, as it highlights a genotype's responses to environmental changes and identifies its phenotypic variability under different conditions (Ribeiro et al., 2015). RNMs allow for the accommodation of various environmental levels with few parameters, facilitating the visualization of genetic behavior along an environmental gradient (Su et al., 2006), and are particularly suitable when descriptors are continuous (Windig et al., 2011). Another important advantage is the possibility of reclassifying animals according to environmental variations, which facilitates the selection of breeders adapted to specific environments, resulting in better-adapted offspring (Bignardi et al., 2015). This model has also been widely applied in dairy herds, allowing for the evaluation of sire genotypes in different environments and the monitoring of bulls' genetic performance (Tiezzi et al., 2017). Additionally, RNMs enable the assessment of environmental factors that interfere with productivity, such as management, production level, and temperature, in the genetic expression of animals. However, RNMs also has some disadvantages. The main limitation is the computational and statistical complexity of higher-order models, which can hinder their application, especially when dealing with high-order polynomial models. Moreover, the need for large volumes of data to adequately capture environmental variations and describe environmental gradients poses a challenge, particularly in systems with limited monitoring (Schaeffer, 2004).

In countries like Brazil, because of the vast environmental variability demand to consider GEI effect on the genetic evaluation (Nascimento et al., 2022). Environmental factors pose challenges such as thermal stress in summer, low pasture availability in winter, high humidity favoring parasitic and respiratory diseases, as well as variations in the nutritional quality of feed, all of which impact herd productivity and health. Even within smaller geographical confines, such as a single state (southern region of Brazil), environmental discrepancies can be pronounced, yet studies in these contexts remain scarce (de Paula et al., 2009). Hence, implementing local breeding programs that include genetic evaluations and progeny testing within the nation could be advantageous (Wahinya et al., 2022).

Therefore, this study proposes to assess the influence of GEI on milk, fat, and protein yields at 305 days in milk for cows in their first to third parity, employing a reaction norms model for Holstein cattle in Paraná state.

4.2 MATERIALS AND METHODS

No approval from the Animal Ethics and Use Committee (CEUA) was necessary for this study, as all data was sourced from an existing database.

4.2.1 DATA

The study utilized data from the milk testing service provided by the Paraná Association of Holstein Cattle Breeders (APCBRH) in Curitiba, PR, Brazil. The dataset included records from 378,000 Holstein cows across their first, second, or third lactations, collected from 2012 to 2022. These cows were part of 513 herds located in 72 different cities throughout the state of Paraná.

Data curation was conducted using R statistical software (R Core Team 2023), employing the 'dplyr' package (Wickham et al., 2019). The data were refined by removing records that did not meet specific criteria: animals less than 60 or more than 500 days in milk, milk yields below 5 kg/day or above 75 kg/day, fat yields during lactation less than 60 kg or exceeding 800 kg, and protein yields below 60 kg or over 600 kg. The exclusion was carried out by visually inspecting the values that appeared as outliers in the graph. Additionally, contemporary groups (CG) defined by herd, year, and calving season containing fewer than 10 animals were excluded, or less than 10 genetic links among them, verified by the AMC software (Roso and Schenkel, 2006). Following these adjustments, the refined dataset comprised 143,826 animals, with 75,146 in their first lactation, 38,680 in their second, and 30,000 in their third lactation.

4.2.2 DETERMINATION OF THE ENVIRONMENTAL GRADIENT (EG)

The environmental gradient (EG) for each lactation was established using the CG solutions for milk yield specific to each lactation, derived from the best linear unbiased predictor (BLUP) analysis conducted with the BLUPF90+ software suite (Misztal et al., 2018), utilizing the AIREMLF90 program. In the model, the CG effect was treated as a fixed factor, the linear and quadratic effects of cow age were included as covariates, and the direct additive genetic effect was modeled as a random factor. Following the acquisition of the CG solutions, the EGs were standardized according to the equation:

$$EG = \frac{CG_{sol} - CG_{mean}}{CG_{sd}}$$

where: EG = environmental gradient; CG_{sol} = solution for each CG derived from the animal model; CG_{mean} = mean of CG solutions; and CG_{sd} = standard deviation of CG solutions.

As milk yield was the basis for EG estimation, it is anticipated that higher EG values (+4) would indicate less challenging environments conducive to higher milk production. Conversely, lower EG values (-4) would signify more challenging conditions, under which cows are expected to yield less milk.

4.2.3 REACTION NORMS MODEL (RNM)

The second step involved determining the RNM via a random regression model. As outlined by Chiaia et al. (2015), the model is represented as follows:

$$Y_{ij} = F_{ij} + \sum_{m=0}^{kb-1} \beta_m \varphi_m(t_{ij}) + \sum_{m=0}^{ka-1} \alpha_{im} \varphi_m(t_{ij}) + e_{ij}$$

where Y_{ij} = observation of the traits adjusted to animal i in t environment j ; F_{ij} = fixed effects (CG); β_m = average trajectory of the population; t_{ij} = levels of standardized environments (EG); φ_m = Legendre's linear polynomial; α_{im} = individual random regression coefficient of the direct genetic effect; k_b and k_a = order of the corresponding polynomials; and e_{ij} = random residual effect.

Following this, variance components for the traits milk yield (MY), fat yield (FY), and protein yield (PY) across the first three lactations were estimated using BLUPF90+ software, as described by Misztal *et al.* (2018). The additive genetic variance was determined using the equation:

$$(Var(a)|EG) = Var(a_i + b_i \cdot EG) = \alpha^2 + \alpha^2 \cdot EG^2 + 2 \cdot EG \cdot \alpha_{a,b}$$

where $(Var(a)|EG)$ = additive genetic variance per EG; a_i and b_i = intercept and slope of the RNM, respectively, α^2 = additive genetic variance for the intercept; α^2 = additive genetic

variance for the slope, EG = environmental gradient, as defined previously; $\alpha_{a,b}$ = covariance between the intercept (a) and the slope (b).

Because environmental variance was considered heterogeneous in this analysis, it was determined using the equation:

$$(Var(e)|EG) = \exp(z_0 + z_1 \cdot EG)$$

where $(Var(e)|EG)$ = residual variance per EG; exp = exponential function to transform the values of the residual coefficients, derived by the logarithmic function; z_0 = intercept of the residual function for the traits; z_1 = slope of the residual function for the traits in the RNM, under the assumption of heterogeneous residual variance.

Heritability coefficients (h^2) for each trait were estimated using the equation:

$$(h^2|EG) = \frac{(Var(a)|EG)}{(Var(a)|EG) + (Var(e)|EG)}$$

where $(h^2|EG)$ = heritability per EG; $(Var(a)|EG)$ = additive genetic variance per EG; and $(Var(e)|EG)$ = residual variance per EG.

Breeding values for each animal within each EG were subsequently estimated as:

$$EBVi|EG = b_{0i} + b_{1i} \cdot EG$$

where $EBVi|EG$ are the estimated breeding values for each animal per EG; b_{0i} is the intercept of the reaction norm for animal i; b_{1i} is the slope of the reaction norm for animal i; and EG is the environmental gradient. Finally, the *ggplot2* package (Wickham, 2011) in R software was employed for the visualization of heritability and EBV across EGs.

4.2.4 CORRELATION BETWEEN ESTIMATES OF BREEDING VALUES (EBV)

The Spearman correlation among the EBVs of traits across the highest, intermediate, and lowest EGs was computed using the 'corrplot' function (Wei et al., 2017) in R software (R Core Team 2023). This was followed by a significance analysis ($P < 0.001$) of these correlations. Estimates of heritability and correlations were interpreted according to the magnitudes established by Bourdon (2013).

4.3 RESULTS

The descriptive statistics for milk yield (MY), fat yield (FY), and protein yield (PY) in Holstein cattle within the state of Paraná are summarized in Table 1. The data indicate that cows in their first lactation exhibited lower mean values for these traits, whereas the highest means were recorded in the third lactation.

Table 1 - Descriptive statistics for 305-day corrected milk yield (MY305), fat yield (FY305), and protein yield (PY305) in Holstein cattle in the state of Paraná.

Trait	Lactation number	N ^A	Mean $\pm$ standard deviation	Minimum	Maximum
MY305 (kg)	1	75,146	9,586.97 $\pm$ 2,078.40	1,506.06	20,635.61
	2	38,680	11,127.77 $\pm$ 402.87	2,402.87	21,069.32
	3	30,000	11,251.83 $\pm$ 706.83	1,702.14	24,593.11
FY305 (kg)	1	75,146	341.64 $\pm$ 84.53	60.01	882.04
	2	38,680	393.75 $\pm$ 109.95	61.26	799.76
	3	30,000	393.53 $\pm$ 109.17	60.06	799.06
PY305 (kg)	1	75,146	304.21 $\pm$ 65.87	60.06	696.51
	2	38,680	354.28 $\pm$ 88.00	60.82	599.19
	3	30,000	353.88 $\pm$ 85.32	60.03	698.88

N^A: number of animals

Table 2 presents the mean values of MY, FY, and PY across different environmental gradients.

Table 2 - Mean values 305-day corrected milk yield (MY305), fat yield (FY305), and protein yield (PY305) in Holstein cattle in the state of Paraná as a function of environmental gradients.

Trait	Lactation number	Environmental gradient		
		Lowest challenge	Intermediate challenge	Greatest challenge
MY305 (kg)	1	9,987.11	8,848.56	8,332.98
	2	10,267.33	10,075.23	8,792.04
	3	14,438.95	10,437.54	12,142.21
FY305 (kg)	1	352.97	343.78	327.44
	2	371.27	366.75	351.67
	3	392.09	384.22	320.92
PY305 (kg)	1	277.22	270.70	263.42
	2	302.57	293.46	271.59
	3	381.69	322.34	354.17

The analysis revealed that the mean values for all traits were lower under the most challenging environmental conditions, whereas higher mean values were observed in the least challenging environments.

Figures 1a and 1b illustrate an increase in additive genetic variance for the first and second lactations as environmental conditions improve, with the highest variance noted in the least challenging environments. However, this trend was not observed in third-lactation animals (Fig. 1c).

Environmental variance (Fig. 1d, 1e, and 1f) exhibited a pattern similar to that of the additive genetic variance across all lactation numbers, with the lowest variances occurring in the least challenging environmental gradient.

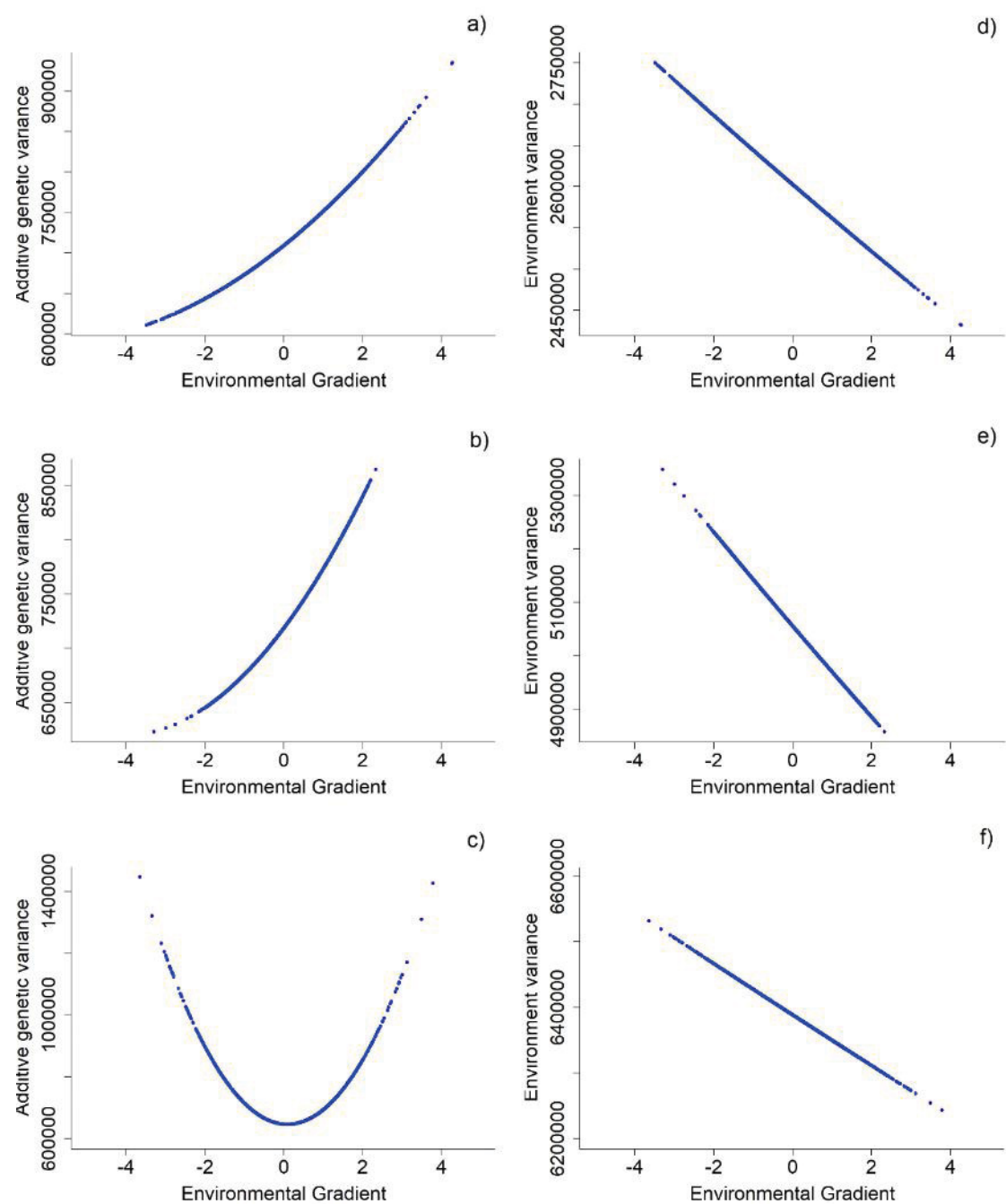


Figure 1 Additive genetic and environmental variances for 305-day corrected milk yield in the first (a, d), second (b, e), and third (c, f) lactations in Holstein cattle in the state of Paraná.

The heritability of MY in the first (Fig. 2a), second (Fig. 2b) and thirist (Fig. 2c) lactations was higher in the environmental gradient with less challenge.

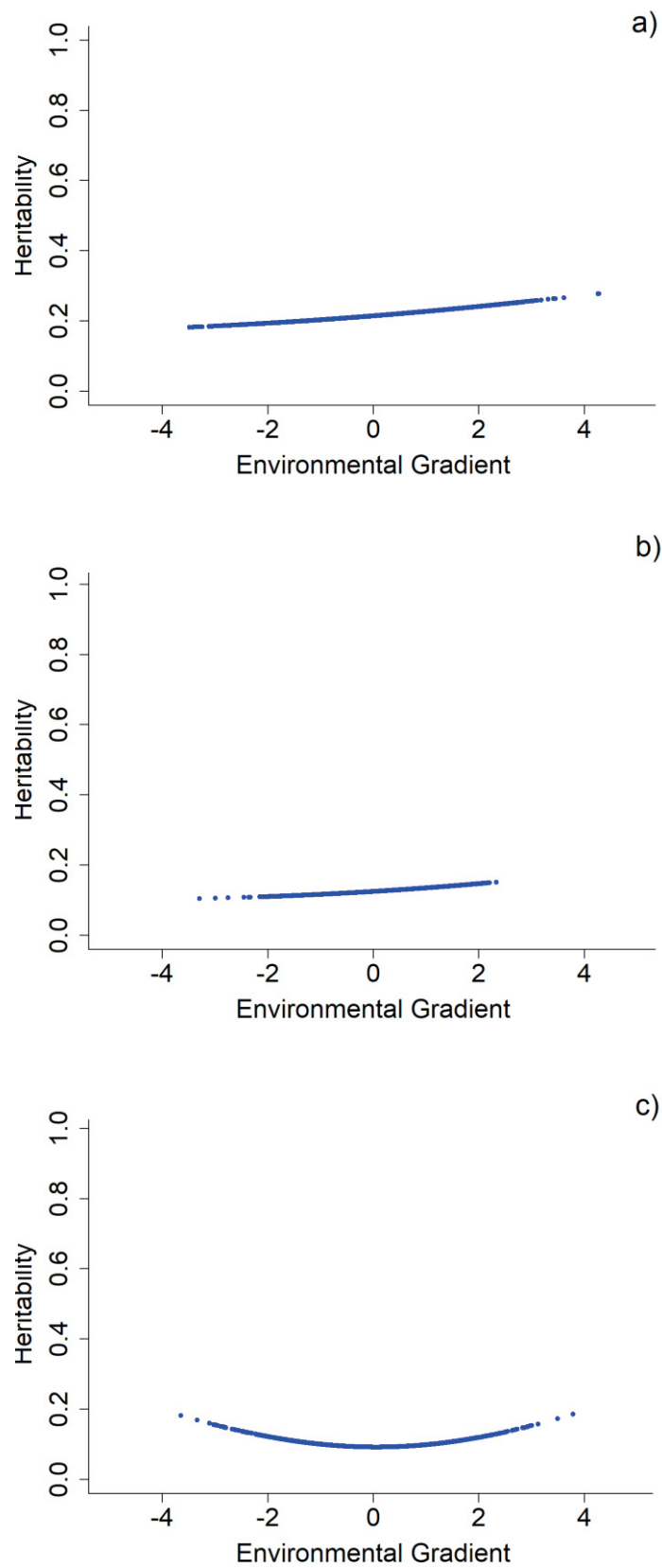


Figure 2 Heritability estimates for milk yield in the first (a), second (b), and third (c) lactations in Holstein cattle in the state of Paraná across environmental gradients.

As shown in Table 3, the heritability of MY in the first lactation within the least challenging environment was moderate (0.28), whereas it was lower (0.18) in the most challenging environment.

Table 3 - Heritability estimates for 305-day corrected milk yield (MY305), fat yield (FY305), and protein yield (PY305) in Holstein cattle in the state of Paraná, for the environmental gradients with the lowest and greatest challenge

Trait	Lactation number	Heritability $\pm$ standard error	
		Lowest challenge	Greatest challenge
MY305 (kg)	1	0.28 $\pm$ 0.003	0.18 $\pm$ 0.002
	2	0.15 $\pm$ 0.003	0.11 $\pm$ 0.002
	3	0.19 $\pm$ 0.009	0.18 $\pm$ 0.008
FY305 (kg)	1	0.18 $\pm$ 0.002	0.28 $\pm$ 0.003
	2	0.18 $\pm$ 0.004	0.15 $\pm$ 0.003
	3	0.09 $\pm$ 0.004	0.11 $\pm$ 0.005
PY305 (kg)	1	0.18 $\pm$ 0.002	0.15 $\pm$ 0.002
	2	0.11 $\pm$ 0.002	0.10 $\pm$ 0.002
	3	0.15 $\pm$ 0.006	0.17 $\pm$ 0.007

Heritability values for MY in the second and third lactations were of low magnitude, irrespective of the environmental challenge. For FY, the estimates of additive genetic variance in the first (Fig. 3a) and third (Fig. 3c) lactations were similar, with a decrease in variance noted in less challenging environments.

Conversely, an increase in additive genetic variance for FY was observed in the second lactation (Fig. 3b) as the environment improved. The environmental variance for FY in the first and third lactations (Fig. 3d and 3f) increased in less challenging environments. However, the environmental variance for FY in the second lactation decreased as conditions improved.

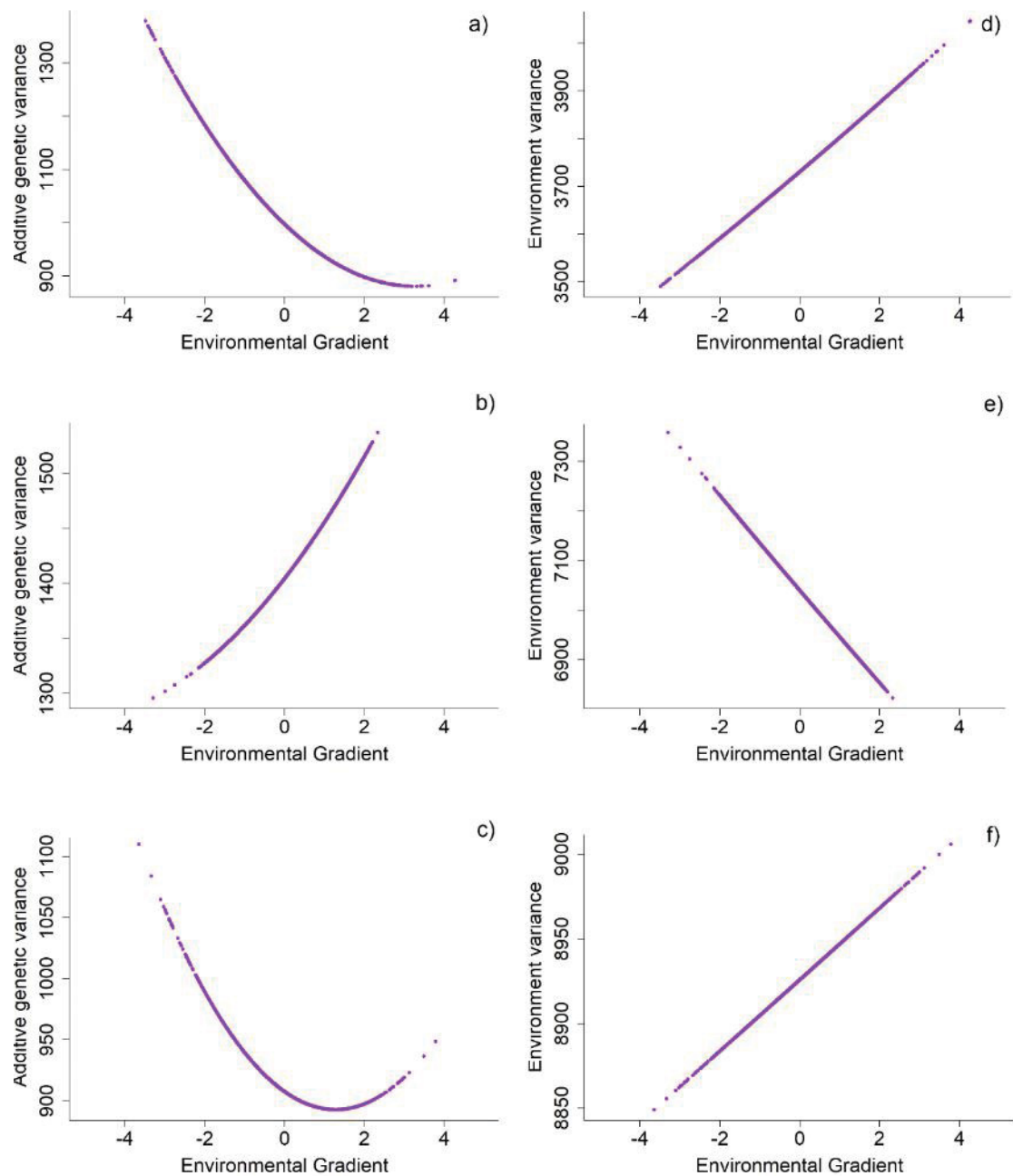


Figure 3 Additive genetic and environmental variances for 305-day corrected milk fat yield in the first (a, d), second (b, e), and third (c, f) lactations in Holstein cattle in the state of Paraná.

Heritability estimates for FY across environmental gradients varied from low to moderate, as depicted in Figure 4 and Table 3. In the third lactation (Fig. 4c), heritability for FY was higher in the least challenging environments compared to the most challenging ones.

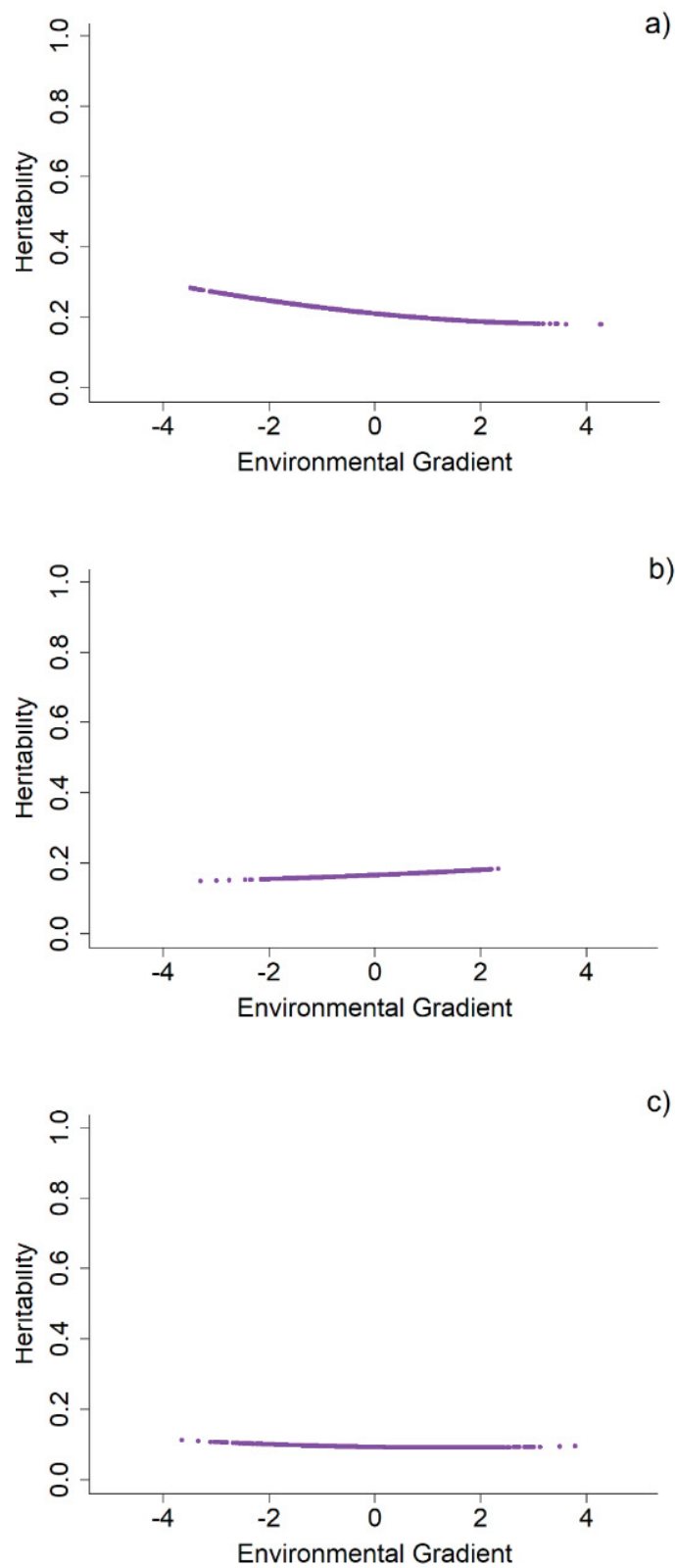


Figure 4 Heritability estimates for milk fat yield in the first (a), second (b), and third (c) lactations in Holstein cattle in the state of Paraná across environmental gradients.

Regarding PY, Figure 5a shows that additive genetic variance increased as the environmental challenge decreased in the first lactation. However, for the second- and third-lactation animals (Fig. 5b and 5c, respectively), a decrease in additive genetic variance was noted as the environmental challenge lessened, with a subsequent increase observed as conditions approached the least challenging gradient. The environmental variance for PY in first- and third-lactation animals (Fig. 5d and 5f, respectively) increased in improved environments. Nonetheless, this trend was not seen for the environmental variance of PY in second-lactation animals (Fig. 5e), which decreased in less challenging environments.

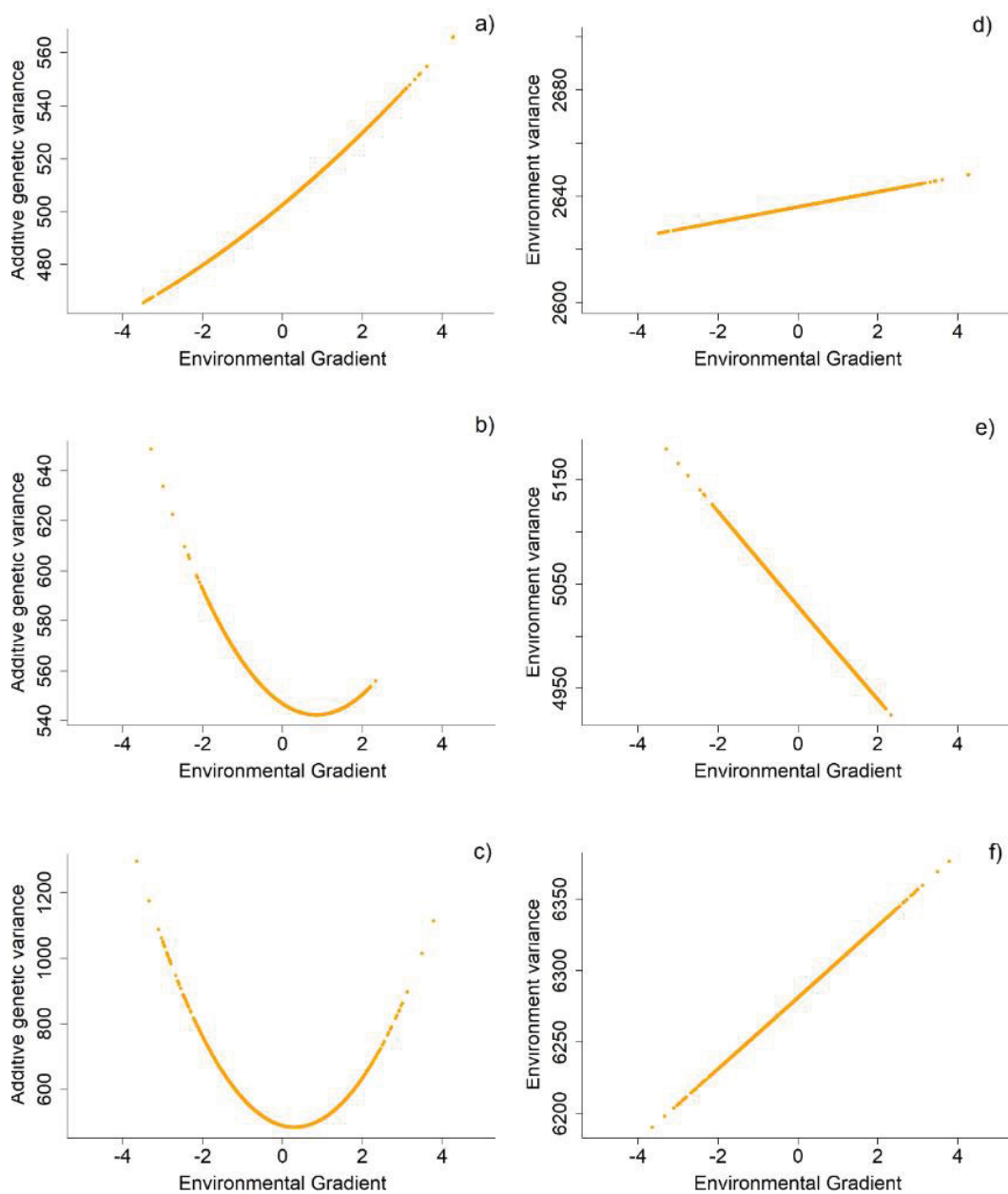


Figure 5 Additive genetic and environmental variances for 305-day corrected milk protein yield in the first (a, d), second (b, e), and third (c, f) lactations in Holstein cattle in the state of Paraná.

Heritability estimates for PY in the first and second lactations were marginally higher in environments posing the least challenge (Fig. 6a and 6b).

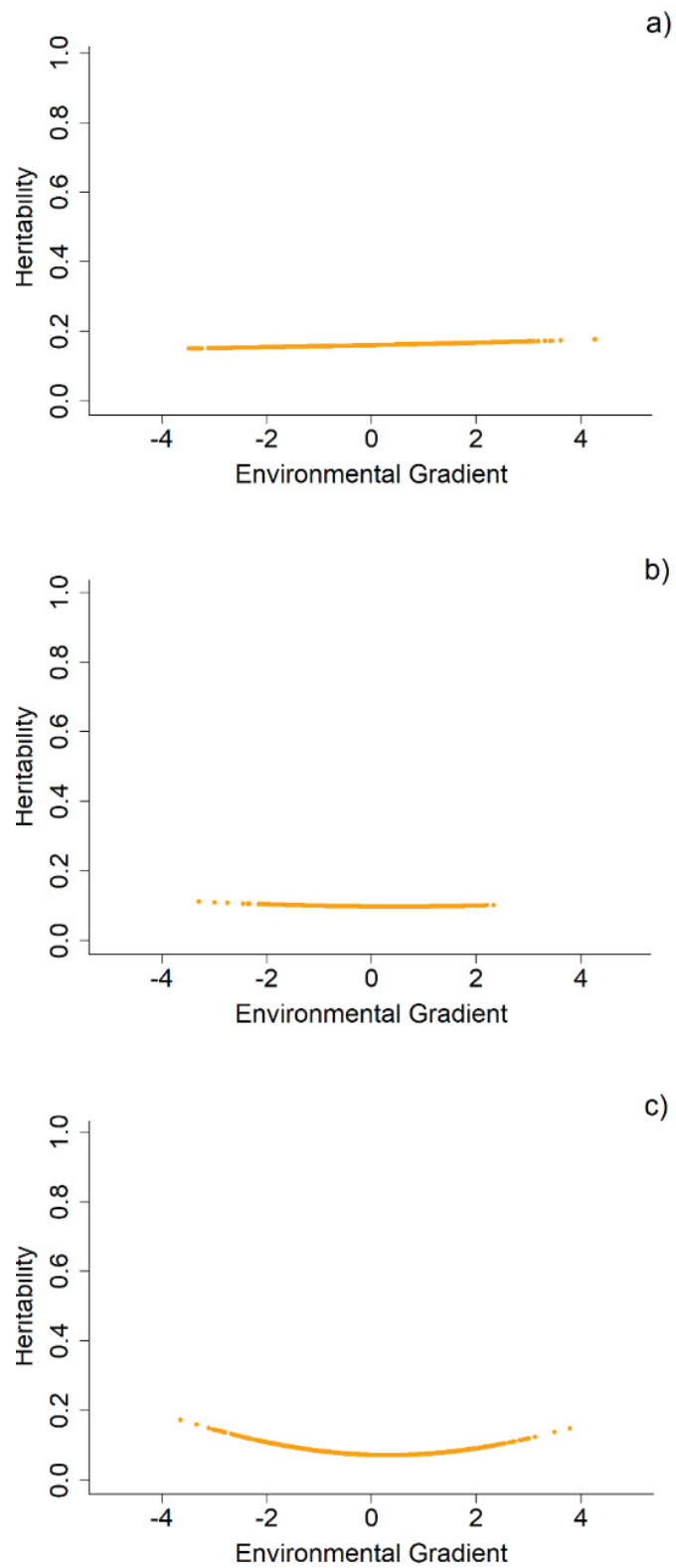


Figure 6 Heritability estimates for milk protein yield in the first (a), second (b), and third (c) lactations in Holstein cattle in the state of Paraná across environmental gradients.

Table 4 details the correlations among breeding values derived under varying environmental challenges: high, medium, and low.

Table 4 - Spearman correlation between the breeding values of 305-day corrected milk yield (MY305), fat yield (FY305), and protein yield (PY305) in Holstein cattle in the state of Parana, as a function of environmental gradients (EG)

Trait	Lactation number	EG	Intermediate	Lowest
MY305 (kg)	1	Greatest	0.9991	0.9966
		Intermediate	-	0.9991
	2	Greatest	0.9992	0.9974
		Intermediate	-	0.9994
	3	Greatest	0.9295	0.7200
		Intermediate	-	0.9084
FY305 (kg)	1	Greatest	0.9967	0.9785
		Intermediate	-	0.9918
	2	Greatest	0.9999	0.9996
		Intermediate	-	0.9999
	3	Greatest	0.9986	0.9940
		Intermediate	-	0.9983
PY305 (kg)	1	Greatest	0.9999	0.9997
		Intermediate	-	0.9999
	2	Greatest	0.9989	0.9954
		Intermediate	-	0.9987
	3	Greatest	0.9340	0.6659
		Intermediate	-	0.8617

P < 0,001 Ho: $\rho \neq 0$.

In the case of MY during the first and second lactations, the genetic correlations were strong, suggesting no genotype-environment interaction (GEI). However, Figures 7a and 7b display an increase in genotype expression variability for the MY trait as environmental conditions improved.

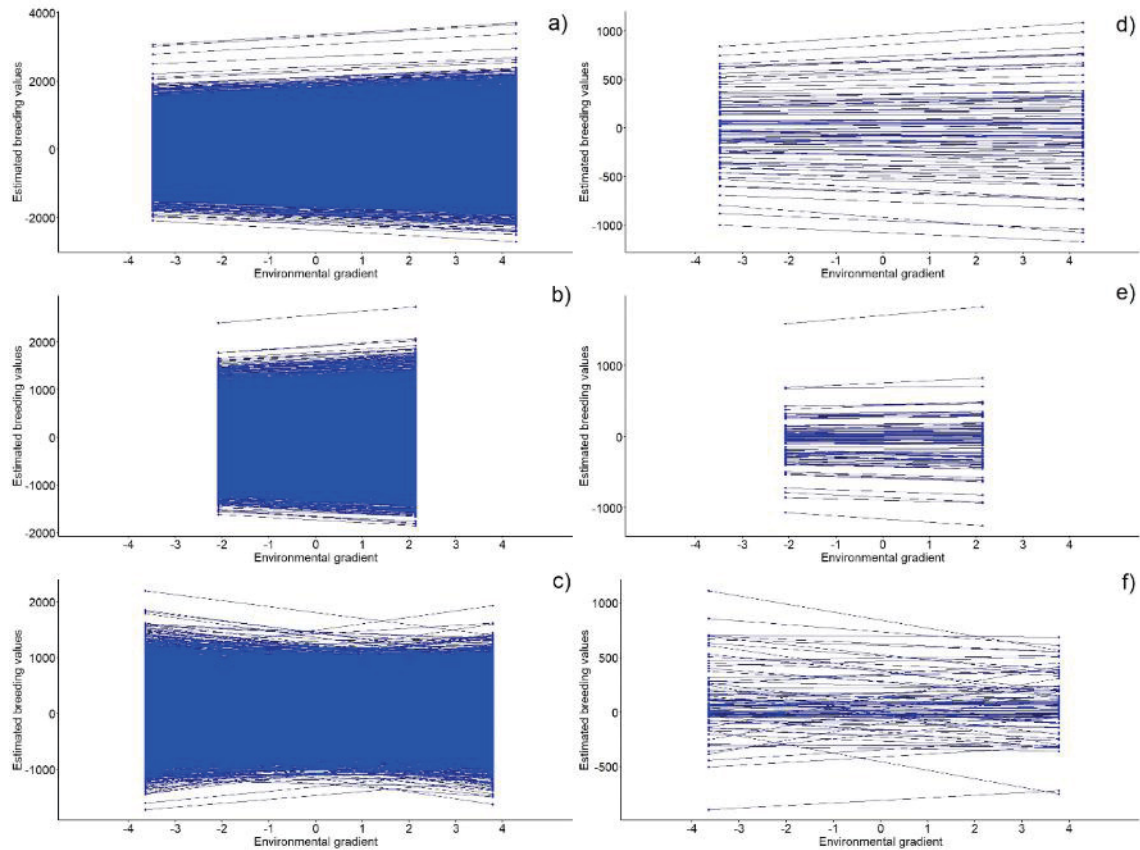


Figure 7 Reaction norms of estimated breeding values for 305-day corrected milk yield in Holstein cattle as a function of environmental gradients. (a, b, c) All animals in the analyzed population; and (d, e, f) Only for sires with more than 500 daughters distributed across environmental gradients.

In contrast, the correlation between the estimated breeding values for MY in the third lactation was 0.72 across the most and least challenging environments (Table 4), hinting at the presence of GEI between these environmental extremes. This is further evidenced by the variation in genotype responses to MY across different environmental gradients, as depicted in Figures 7c and 7f, indicating that genotype performance varied with the environment, which could signify GEI.

For fat yield (FY), the breeding value correlations were consistently strong and positive across all lactations, as reported in Table 4. This uniformity suggests breeding value stability across environments of varying challenge levels.

Nevertheless, a reduction in genotype response variability was observed in the least challenging environment for FY in the first lactation (Fig. 8a and 8d). In contrast, an increase in genotype response variability between the most and least challenging environments was noted for FY in the second lactation (Fig. 8b and 8e).

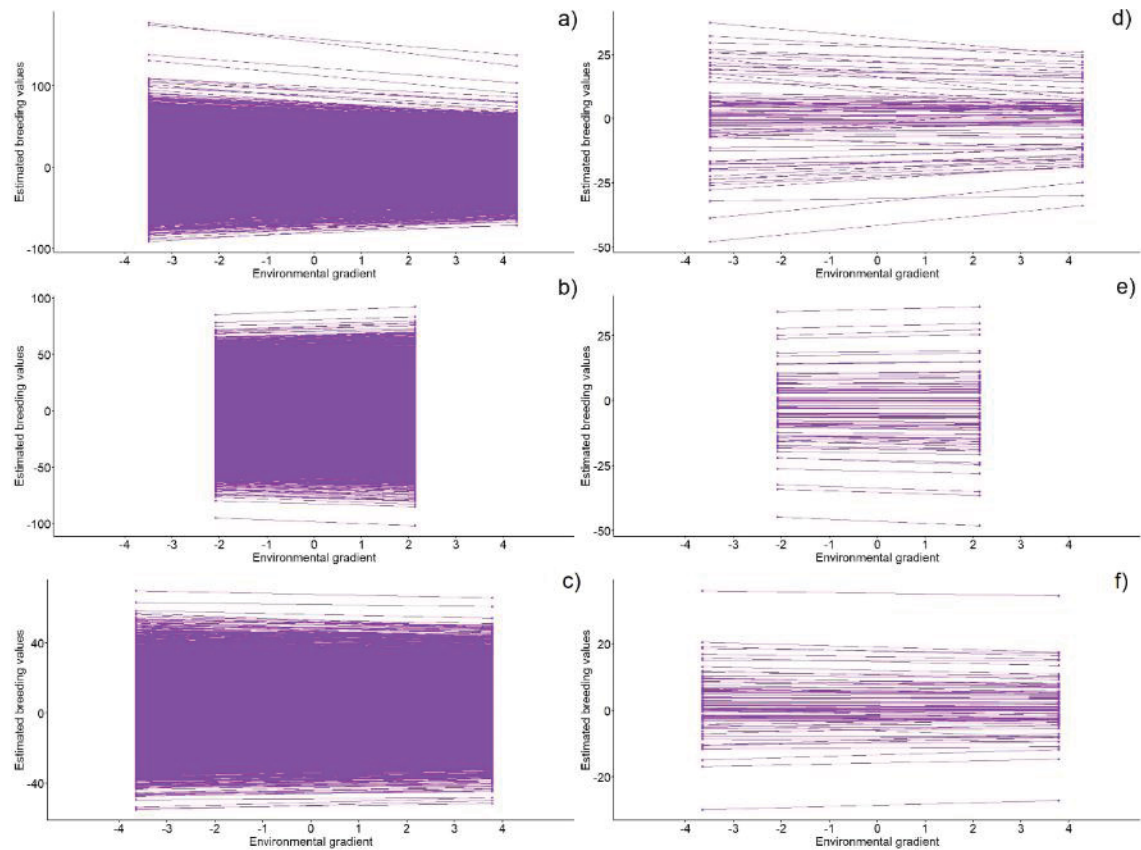


Figure 8 Reaction norms of estimated breeding values for 305-day corrected milk fat yield in Holstein cattle as a function of environmental gradients. (a, b, c) All animals in the analyzed population; and (d, e, f) Only for sires with more than 500 daughters distributed across environmental gradients.

For PY in the first and second lactations, correlations remained strong and positive (Table 4). However, for the third lactation, the correlation between breeding values for PY in the highest- and lowest-challenge environments was 0.67, suggesting potential GEI. This is supported by Figures 9c and 9f, where breeding values for PY showed varying response patterns across the environmental gradients.

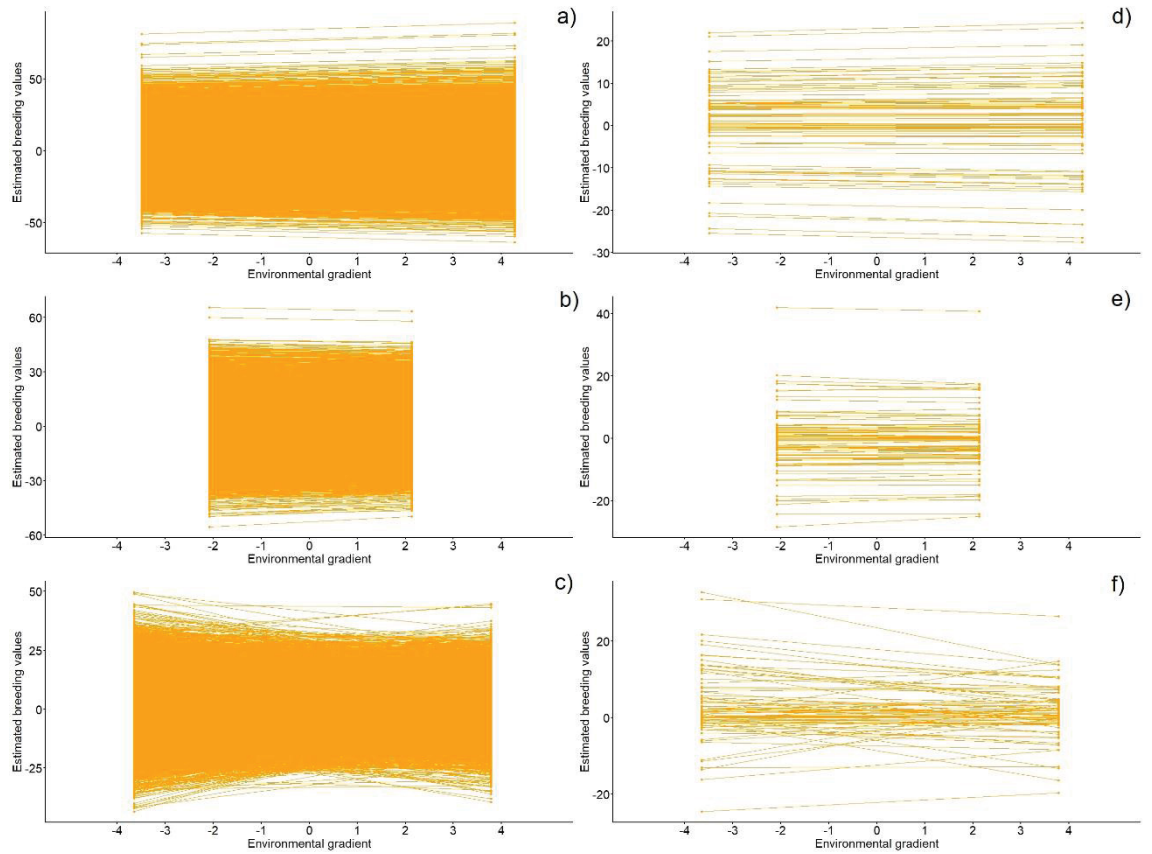


Figure 9 Reaction norms of estimated breeding values for 305-day corrected milk protein yield in Holstein cattle as a function of environmental gradients. (a, b, c) All animals in the analyzed population; and (d, e, f) Only for sires with more than 500 daughters distributed across environmental gradients.

4.4 DISCUSSION

The MY305 averages increased across lactations, reaching 9,586.97 kg in the first lactation, 11,127.77 kg in the second, and 11,251.83 kg in the third (Table 1). According to Siewert et al. (2019), the lower initial milk production observed in first-lactation cows may be related to additional stress during milking, as it is a new experience for primiparous cows. Evangelista et al. (2024), in a study on Holstein cattle in southern Brazil, observed that milk production was 9.23% and 7.34% lower in first-lactation cows compared to third- and second-lactation cows, respectively. The authors attributed this result to the fact that primiparous cows are still in a developmental phase, with nutrients being directed toward growth rather than milk production. Similarly, fat production increased from 341.64 kg in the first lactation to 393.75 kg in the second and 393.53 kg in the third, while protein production followed a similar pattern,

with averages of 304.21 kg in the first lactation, 354.28 kg in the second, and 353.88 kg in the third (Table 1). According to Nogara et al. (2024), when evaluating different Holstein cattle farming systems in southern Brazil, they observed that milk fat production was higher in the second and third lactations (3.65% and 3.64%, respectively) compared to the first lactation (3.59%). Regarding protein production, there was a significant difference between lactations, with the highest percentage observed in the second lactation (3.41%) and the lowest in cows with more than three lactations (3.30%). The authors concluded that factors such as the production system (confinement or pasture) and nutrition can influence production differences, especially in milk solids.

The observed increase in milk, fat, and protein yields with the reduction in environmental challenges aligns with expectations, as demonstrated in Table 2. This correlation was established using the contemporary group solutions for milk production to define the environmental gradient. Contemporary groups (CGs) are frequently used as environmental descriptors in the absence of direct data, such as temperature, humidity, or nutritional levels (Calus et al., 2002). CGs are derived from phenotypic data and reflect the management and environmental conditions to which the animals were exposed (Calus et al., 2002; Carneiro et al., 2019). In this context, using the best linear unbiased estimates (BLUE) of CG effects allows for the consideration of various management and environmental conditions, providing an efficient approach to modeling animal responses to environmental variation through reaction norm models (RNMs) (Falconer, 1990). However, one limitation of using CGs as environmental descriptors is the need to remove outlier data, as extreme records can affect reaction norm estimates (Calus et al., 2002). Additionally, the use of CG assumes homogeneity within groups concerning the environmental conditions to which the animals were exposed (Carneiro et al., 2019), which warrants their use as an environmental descriptor.

Consequently, it can be deduced that less challenging environments may present conditions conducive to enhancing these traits. Such environments likely feature reduced heat stress and superior pasture quality among other beneficial factors for milk and its solid components production (Bohlouli and Alijani, 2012; Mwendia et al., 2018; Ramírez-Rivera et al., 2019). Conversely, more demanding environments may present obstacles that curtail the productive capabilities of animals. Chen et al. (2022) highlighted that thermal stress could negatively impact the milk yield of both primiparous and multiparous cows.

Variations in additive genetic variability in response to environmental gradients were noted across all examined traits. This phenomenon, as discussed by Bowman (1972), may indicate the presence of genotype-environment interactions (GEIs), where certain genes may

be more readily expressed or suppressed due to environmental influences (Mota et al., 2020; Zamorano-Algandar et al., 2023). Notably, in more favorable settings (Fig. 1a, 1b, 3b, and 5a), additive genetic variations were more pronounced.

Some studies indicate an increase in additive genetic variances under improved environmental conditions, suggesting that genetic differences between animals become more evident in favorable scenarios (Mulim et al., 2020; Prescott et al., 2024; Chiaia et al., 2015). This occurs because, in environments with fewer restrictions, animals can better express their genetic potential, leading to greater additive genetic variation (Raidan et al., 2016; Silva-Neto et al., 2024). This can be explained by the greater expression of favorable genes, which are activated when there are no environmental limitations restricting animal performance. For example, Lesta et al. (2024) observed that nutritional supplementation with optimal amino acid levels significantly increased dairy cow productivity, highlighting how favorable environmental factors can enhance genetic expression and, consequently, productive performance. This finding aligns with underlying mechanisms of GEI, such as protein turnover, which regulates essential functions like homeothermy, reproduction, and immune responses, as well as the plasticity of the hypothalamic-pituitary-adrenal axis, which influences metabolism, the immune system, and stress responses, contributing to organismal robustness and resilience (Rauw, 2012; Mormède et al., 2011). Another relevant mechanism in GEI is epigenetic markers, such as DNA methylation, which allow organisms to adjust their environmental responses more efficiently and, in some cases, pass these adaptations on to future generations, reinforcing epigenetic inheritance (Jablonka & Lamb, 2002). This complex interaction between genotype and environment is essential for animal adaptation to different environmental conditions and for the development of genetic improvement strategies that consider epigenetic influences (Silva-Neto et al., 2024).

On the other hand, less challenging environments do not inherently ensure superior performance, as some animals may exhibit superior productivity under more adverse conditions (Nascimento et al., 2022). In this study, it was noted that animals in their third lactation (Fig. 1c, 3c, and 5c) showed a more robust expression of additive genetic variability in challenging environments for all evaluated traits (MY, FY, and PY). Sigdel et al. (2019) reported that under stress conditions, additive genetic variances for milk components in multiparous cows increased compared to those in primiparous cows. Our findings corroborate this, suggesting that multiparous cows can leverage their genetic potential even when subjected to challenging environments. Supporting this observation, Proudfoot and Huzzey (2022) found that

primiparous cows face greater adaptation challenges in competitive environments compared to their multiparous counterparts.

It was also observed that additive genetic variances were heightened for MY and PY during the first and second lactations, and for FY in the second lactation, in less challenging environments. In this respect, it is noteworthy that cows in their initial lactation cycles may require less stressful conditions to fully manifest their genetic potential. This necessity could be attributed to the adaptation challenges of younger cows in harsher environments and the possibility that they have not yet attained full maturity. This immaturity could lead to increased energy demands and hinder their ability to fully express their productive potential in less favorable environments (Morales Piñeyrúa et al., 2018).

Heritability estimates for all analyzed traits ranged from low to moderate (Table 3). Moreira et al. (2019) observed similar heritability ranges in Holstein cattle across three Paraná regions, with heritability values ranging from 0.16 to 0.21 for MY, 0.17 to 0.25 for FY, and 0.10 to 0.17 for PY. They posited that selecting based on these traits could lead to genetic improvement. Our findings align with this perspective, suggesting that direct selection for MY, FY, and PY would provide genetic gain, independent of the selection environment, given the heritable nature of these traits.

In less challenging environments, heritability estimates showed low magnitude, except for MY305 in the first lactation, which exhibited moderate heritability. According to Raidan et al. (2016), higher heritability in favorable environments can be attributed to the reduced influence of unpredictable environmental factors, such as management, nutrition, and climate, allowing genetic variation to be more clearly expressed. This suggests that selection processes could be more effective when conducted in such environments.

Sigdel et al. (2019) reported analogous findings, observing a decline in heritability in heat-stressed environments over time. This trend may be attributed to cows becoming increasingly sensitive to stress in subsequent lactations (Müschner-Siemens et al., 2020; de Paula et al., 2023). Thus, in the initial lactations, more favorable conditions may facilitate the expression of genetic potential, leading to higher heritability estimates for the traits under study. However, this trend does not extend to cows in their third lactation; despite their ability to express their breeding values, the amplified influence of the environment tends to diminish heritability estimates.

According to Robertson (1959), for the GEI effect to be considered relevant, the genetic correlation should be below 0.80. In this study, genetic correlations between breeding values across the lowest and highest challenge gradients (Table 4) were lower than 0.80 exclusively

for MY and PY during the third lactation. Hence, the genetic correlation coefficients exceeding 0.80 obtained for some traits imply that the progeny of bulls exhibit similar performance across varied environmental gradients, suggesting an absence of GEI. The small environmental variability and the homogeneity of production systems within this study's region could account for these findings. Despite climatic differences across Paraná, the variation between areas with the highest herd densities is small, as reported by Moreira et al. (2019). Such slight climatic disparities may have constrained the assessment of environmental impacts on the genotypes regarding milk and solids production in Holstein cattle within Paraná. However, in addition to climatic factors, it is essential to consider the environmental influences within the herd, such as differences in management practices, feeding regimes (feedlot or pasture), and animal comfort strategies in the effects of GEI (Tiezzi et al., 2017). In this study, the analyzed region stands out for being more technologically advanced, with a higher level of organization, training, and management, as well as incentives for investment in sectoral improvements. This scenario is mainly driven by the technical assistance provided by some cooperatives, which encourage the adoption of best practices and innovation in the productive sector (Botaro et al., 2016; Telles et al., 2020). These factors may contribute to reducing environmental variability and masking the GEI effects, which could explain the high genetic correlations observed in this study.

Nonetheless, the analysis of MY and PY in the third lactation reveals genetic correlation estimates that indicate the occurrence of GEI across the most contrasting environmental gradients. This observation might stem from the fact that, by the third lactation, animal performance is more influenced by environmental factors due to physiological strain from previous lactations and the heightened production in multiparous cows compared to their primiparous counterparts. This could lead to increased vulnerability to environmental factors, such as higher instances of mastitis and more pronounced heat stress owing to increased milk production (Steeneveld et al., 2008; Bernabucci et al., 2014). Corroborating the present findings, Mulim et al. (2021) reported genetic correlations of 0.87 to 1.0 (MY), 0.89 to 1.0 (FY), and 0.81 to 1.0 (PY) in first-lactation primiparous Holstein cows in the southern region of Brazil across different ambient temperatures, with no GEI detected for these first-lactation animals. Conversely, de Paula et al. (2009), examining the GEI effect on Holstein cows from the 1st to 10th lactation in the state of Paraná, found MY correlations ranging from 0.41 to 0.78, indicating GEI presence, particularly between extreme environmental gradients.

The evidence points to GEI for MY and PY in the third lactation, aligning with expectations since the RNM already suggested genotype reclassification across environmental gradients. While genetic correlation estimates mostly indicate a lack of GEI for most traits, the

RNM has unveiled variances in breeding values across environmental gradients, notably under improved conditions. This means that the genotypes for MY in the first and second lactations, FY in the second and third lactations, and PY in the first lactation (Fig. 7a; 8b and 9a) were better expressed under less challenging environmental gradients. Schmid et al. (2021), analyzing GEI across different environmental levels for FY in Brown Swiss cattle, observed breeding value variance differences but no genotype reclassification across gradients. Even with minor breeding value variance shifts between environmental gradients and the absence of genotype reclassification, selection for these traits remains viable across both the most and least challenging environmental gradients.

However, in the case of FY during the first lactation (Fig. 8a), reclassification of certain genotypes across various environments was noted, notwithstanding the substantial genetic correlation of 0.97 between the most and least challenging gradients (as depicted in Table 3).

Significant alterations in the variance of breeding value estimates and in the ranking of genotypes were particularly pronounced for MY and PY during the third lactation (Fig. 7c and 9c). As previously indicated, these two traits were anticipated to exhibit similar behavior, attributed to the potential influence of genes with a pleiotropic effect. This hypothesis is corroborated by the robust genetic correlation of 0.95 (± 0.03) between MY and PY from the first to third lactations in Holstein cattle (Liu et al., 2014). In the third lactation, a broader variance in genotypes was observed under the most challenging environmental gradient. This variation can be ascribed to the unique resilience of certain genotypes to suboptimal environments (Urruty et al., 2016). Conversely, in less challenging environments, genotypes tend to converge towards the mean, irrespective of each animal's breeding value, due to the reduced impact of such environments on the expression of these traits.

The little evidence of GEI effects on MY and PY in the first and second lactations, as well as for FY across all lactations, might be explained by the data concentration in the central eastern region of the state. This area, hosting significant dairy operations and the largest herds (de Paula et al., 2009; Moreira et al., 2019; Mulim et al., 2021). Environmental similarity may have limited the detection of GEI effects, as the relatively narrow variation in environmental challenges was likely insufficient to induce significant changes in genetic expression. According to Mulim et al. (2020), temperatures in southern Brazil range from 17.0 °C to 19.5 °C. Despite climatic differences within the region, the relative thermal stability was not enough to produce significant genetic effects on milk production in Holstein cattle (Montaldo et al., 2015). Consequently, the low thermal variation may have attenuated the differences in environmental challenges faced by the animals, potentially masking GEI effects in this region.

A possible limitation of this study is the geographic restriction of the data to the analyzed region, where environmental homogeneity may have reduced phenotypic and genetic variability, masking GEI effects, especially in earlier lactations. Differences in management, feed quality, and stress conditions may not have been adequately captured. Studies conducted in regions with greater climatic variation and different production systems could provide a broader perspective on GEI effects.

4.5 CONCLUSION

In conclusion, the study found no evidence of genotype-environment interaction on fat yield, regardless of the parity. No genotype-environment interaction effects were observed on milk or protein yields in the first and second lactations. However, the third lactation demonstrated genotype-environment interaction influences on milk and protein yields among Holstein cattle in Paraná, particularly under extreme environmental gradients. Consequently, selecting for milk, protein, and fat yields in the first lactation may be the best strategy, as the genotype-environment interaction effect was not relevant. The absence of GEI in the first lactation for milk, fat, and protein production suggests that a single genetic selection program would be sufficient for the Holstein herd in this region, ensuring greater efficiency and lower cost. However, the presence of GEI in the third lactation, especially under extreme environmental gradients, indicates that environmental factors become more important as animals age. Therefore, genetic selection should prioritize sires whose daughters maintain high milk and solid production even under adverse conditions.

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5 CAPÍTULO IV - INFLUENCE OF DIFFERENT ENVIRONMENTAL CHALLENGES ON THE EXPRESSION OF REPRODUCTIVE TRAITS IN HOLSTEIN CATTLE IN SOUTHERN BRAZIL

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ABSTRACT

The aim of this study was to assess the impact of genotype x environment interaction (GEI) on the manifestation of traits such as age at first calving (AFC), age at first service (AFS), and calving interval (CI) through the application of the reaction norm model in Holstein cattle raised in Paraná state, Brazil. Utilizing data from the milk testing service of the Paraná Association of Holstein Cattle Breeders (APCBRH), this study analyzed records from 179,492 animals undergoing their first, second, and third lactations from the years 2012 to 2022. These animals were part of 513 herds spread across 72 municipalities in Paraná. The environmental gradient was established by normalizing contemporary group solutions, derived from the animal model, with the 305 day corrected milk yield serving as the dependent variable. Subsequently, reaction norms were determined utilizing a Random Regression Model. Spearman's correlation was then applied to compare the estimates of breeding values

across different environmental gradients for the studied traits. The highest EG (+ 4) indicates the least challenging environments, where animals experience better environmental conditions. Conversely, lower EG (-4) values represent the most challenging environments, where animals endure worse conditions. The only trait that exhibited a moderate heritability magnitude was AFC (0.23) in the least challenging environmental condition. The other traits were classified as having low heritability magnitudes regardless of the evaluated environmental gradient. While minimal evidence was found for the influence of GEI on CI, a clear GEI effect was observed for AFC and AFS across all environmental gradients examined. A reversal in genotype ranking occurred under extreme environmental conditions. The findings suggested that the best performing genotype under one environmental gradient may not necessarily excel under another.

Keywords: Age at first calving, Calving interval; Dairy cattle; Environmental gradient; Estimated breeding values and Reaction norms.

5.1 INTRODUCTION

In dairy farming, fertility related traits are of significant importance due to their direct link with reproductive management, veterinary treatments, involuntary culling, and ultimately, farm profitability (González Recio et al. 2004). However, it is important to acknowledge that many herds prioritize increasing milk yield, which may negatively impact cow fertility owing to unfavorable genetic correlations between these traits (Sewalem et al. 2010; Canaza Cayo et al. 2018). Moreover, the selection for improved fertility is complex; the low heritability of these traits (Montaldo et al. 2017; Brzáková et al. 2019; Muuttoranta et al. 2019) poses a great challenge in achieving substantial genetic progress within breeding programs for this species.

An additional consideration in the selection for reproductive traits is the impact of genotype x environment interaction (GEI). GEI refers to the variance in genotype expression under diverse environmental conditions, potentially leading to alterations in phenotype classification, affecting genetic parameters, and altering breeding value estimates of individuals (Streit et al. 2012; Montaldo et al. 2017). These shifts present considerable obstacles in breeding stock selection within breeding programs (de Araújo et al. 2022), as selection responses may differ depending on the environment where the breeders were originally selected.

However, identifying robust genotypes, that is, those that maintain good performance even when exposed to challenging environments, could be a strategic approach in individual selection to enhance genetic gains (Chen et al. 2021). To identify these genotypes, GEI effects can be analyzed by assessing the performance of progenies from the same sire across varied environments. Reaction norm models (RNM) have been employed to ascertain genotype responses across different environmental conditions (Tiezzi et al. 2017; Mota et al. 2020; Schmid et al. 2021; Toro Ospina et al. 2023).

Despite the recognized significance of GEI on reproductive traits, the literature addressing this topic remains sparse. Furthermore, one implication of conducting this study is that, in Brazil, about 94% of the total semen used is imported, primarily from North American and European countries (ASBIA 2019). As a result, the genetic material originates from countries with temperate climates, starkly different from the climate in Brazil. Most Holstein cattle in Brazil are raised in the southeast (29%) and south (69%) regions, characterized by tropical and subtropical climates, respectively (Silva et al. 2021). These discrepancies between the selection and breeding environments underscore the need to assess the presence of GEI to make informed decisions about alternative strategies for selecting the best bulls for national production systems and to achieve the expected genetic response from imported genotypes in the dairy production conditions of each country. Another important consideration is that although the Multiple Across Country Evaluation (MACE) methodology, used by Interbull to evaluate the genetic performance of animals in different countries, is established in highly developed nations, it is not yet available in tropical countries like Brazil (Toro Ospina et al. 2023). Thus, ignoring GEI effects can lead to an underestimation of predicted genetic values, resulting in biased estimates, especially in breeding programs involving animals raised in highly diverse environments (Streit et al. 2012).

Given the above considerations, this study aimed to reveal the GEI effect on age at first service (AFS), age at first calving (AFC), and calving interval (CI) in Holstein cattle, utilizing reaction norm models.

5.2 MATERIALS AND METHODS

The study did not necessitate approval from the Animal Ethics and Use Committee (CEUA) as it utilized data from an already established database.

5.2.1 DATA

The study utilized data provided by the Paraná Association of Holstein Cattle Breeders (APCBRH), headquartered in Curitiba, Paraná, Brazil. This dataset included records from 378,000 animals across their first, second, and third lactations, from the years 2012 to 2022. These animals were part of 513 herds located across 72 municipalities within the state of Paraná, Southern Brazil (tropical and subtropical climate), where the genotypes, mainly those of bulls, originate from temperate climate regions (United States and Canada).

The dataset was processed using the statistical software R (R Core Team 2023), employing both the standard and the ‘dplyr’ packages (Wickham et al. 2019). Criteria for data curation involved excluding records of females with AFC less than 600 days or more than 1,080 days, AFS less than 330 days or more than 700 days, and CI less than 300 days or more than 1,200 days. The exclusion was carried out by visually inspecting the values that appeared as outliers in the graph. The contemporary group (GC) was formed based on the variables: herd, year, and calving season, and CGs comprising fewer than 10 animals were excluded. Following data editing, the remaining dataset encompassed records for 179,492 animals, including 74,290 records for AFC, 67,965 for AFS, and 37,237 for CI (interval between the first and second calvings; and between the second and third calvings).

5.2.2 DETERMINATION OF THE ENVIRONMENTAL GRADIENT

The solutions to the Animal Models were estimated using AIREMLF90 software (Misztal et al. 2018). We chose not to use the BLUE of CG effects for reproduction traits (AFC, AFS, and CI) as the environmental descriptor to avoid bias in reaction norm estimates that may occur when the environmental descriptor needs to be derived from the same phenotypic data (Su et al. 2006; Cardoso and Tempelman 2012). Thus, in the applied model, the CG effect on MY305 was treated as a fixed factor, while linear and quadratic effects of cow age were included as covariates, and the direct additive genetic effect was modeled as a random factor. The MY305 means from the first to the third lactation order across the environmental gradients were 9,987.11 to 14,438.95 (lowest challenge); 8,848.56 to 10,437.54 (intermediate challenge); and 8,332.98 to 12,142.21 (highest challenge).

To determine the environmental gradient (EG), the solutions for CG were standardized using the following equation:

$$EG = \frac{GC_{sol} - GC_{mean}}{GC_{sd}}$$

where, EG = environmental gradient; CGsol = solution for each CG obtained by the animal model; CGmean = mean of CG solutions; and CGsd = standard deviation of CG solutions. By employing MY305 to estimate GE as a contemporary group solution, it was anticipated that the highest EG (+ 4) would correspond to the least challenging environments, namely, those where animals experienced better conditions for milk production expression. Conversely, environments with a lower EG (-4) pose the greatest challenges for animals, leading to potentially reduced milk production in individuals raised in these conditions.

5.2.3 REACTION NORM MODEL (RNM)

After determining the environmental gradient, the RNM was used to estimate the variances and covariances for reproductive traits (AFC, AFS, and CI) using BLUPF90 + software (Misztal et al. 2018) through a single trait analysis. The estimated breeding values (EBVs) for these reproductive traits were also calculated at this stage. According to Chiaia et al. (2015), the RNM through random regression is described as follows:

$$Y_{ij} = F_{ij} + \sum_{m=0}^{kb-1} \beta_m \varphi_m(t_{ij}) + \sum_{m=0}^{ka-1} \alpha_{im} \varphi_m(t_{ij}) + e_{ij}$$

where, Y_{ij} = is the observation of the progeny of animal i in environment j ; F_{ij} = fixed effects (CG); β_m = average population trajectory; t_{ij} = standardized environment levels (EG); φ_m = linear Legendre polynomial; α_{im} = individual random regression coefficient of the direct genetic effect; kb and ka = orders of the corresponding polynomials; and e_{ij} = random residual effect. The variance components were estimated using mixed model equations for AFC, AFS, and CI through BLUPF90 + software (Misztal et al. 2018). The additive genetic variance was derived from the equation:

$$Var(a)|EG) = \sigma^2_{ab0} + \sigma^2_{ab1} \cdot EG^2 + 2 \cdot EG \cdot \sigma_{b0,b1}$$

where, $(\text{Var}(a)|EG)$ = additive genetic variance per EG; b_0 and b_1 = intercept and slope of the RNM, respectively; σ^2_{ab0} = additive genetic variance for the intercept; σ^2_{ab1} = additive genetic variance for the slope; EG = environmental gradient, as defined previously; $\sigma_{b0,b1}$ = covariance between the intercept (b_0) and the slope (b_1).

Considering that heteroscedastic reaction normal model performs better than homoscedastic model (Carvalho et al. 2019), the environmental variance was considered as heterogeneous in this analysis. According to Mulder et al. (2007), genetic heterogeneity of environmental variance may indicate genetic variations in environmental sensitivity. Additionally, this genetic heterogeneity of environmental variance can be leveraged to explore more resilient or stable genotypes. Thus, the environmental variance was obtained using the following equation:

$$(\text{Var}(e)|EG) = \exp(z_0 + z_1 \cdot EG)$$

where $(\text{Var}(e)|EG)$ = residual variance per EG; $\exp$ = exponential function to transform the values of the residual coefficients, obtained through the logarithmic function; z_0 = intercept of the residual function for the traits; z_1 = slope of the residual function for the traits in the RNM, considering heterogeneous residual variance; and EG = environmental gradient.

The heritability coefficients (h^2) were estimated by the following equation:

$$(h^2|EG) = \frac{(\text{Var}(a)|EG)}{(\text{Var}(a)|EG) + (\text{Var}(e)|EG)}$$

where, $(h^2|EG)$ = heritability per EG; $(\text{Var}(a)|EG)$ = additive genetic variance per EG; and $(\text{Var}(e)|EG)$ = residual variance per EG.

Rank correlation between EBVs across environmental gradients the estimated breeding values (EBVs) for all animals in this study were determined following the RNM analysis using the equation:

$$\text{EBVi}|EG = b_{0i} + b_{1i} \cdot EG$$

where, $\text{EBVi}|EG$ = estimated breeding values for each animal; b_{0i} = intercept of the reaction norm for animal i ; and b_{1i} = slope of the reaction norm for animal i ; and EG = environmental gradient. The Spearman correlation between the EBVs of the traits obtained at

the highest, intermediate, and lowest environmental gradients was estimated using R software (R Core Team 2023) with the ‘corrplot’ function (Wei et al. 2017). To create plots of additive genetic variance, environmental variance, heritability, and EBVs across the environmental gradients (EGs), the ‘ggplot2’ package of R software was used (Wickham 2011).

5.3 RESULTS

The descriptive statistics for AFC, AFS, and CI in Holstein cattle from Paraná are summarized in Table 1.

Table 1 Descriptive statistics for age at first service (AFS), age at first calving (AFC) and calving interval (CI) of Holstein cattle in the state of Paraná, Brazil.

Trait	^A N	Mean ± Standard deviation	Minimum	Maximum
AFS (days)	67.295	453,13 ± 60.45	330	700
AFC (days)	74.290	753,87 ± 73.30	631	1073
CI (days)	37.237	423,27 ± 78.99	300	1175

^AN.: number of animals

Table 2 displays the mean values for AFC, AFS, and CI across the lowest, medium, and greatest challenge environmental gradients.

Table 2 - Mean values for age at first service (AFS), age at first calving (AFC) and calving interval (CI) of Holstein cattle as a function of the environmental gradient (EG).

Trait	Environmental gradient		
	Lowest challenge	Intermediate challenge	Greatest challenge
AFS (days)	470,54	468,57	473,00
AFC (days)	751,00	762,71	816,50
CI (days)	413,00	417,00	425,16

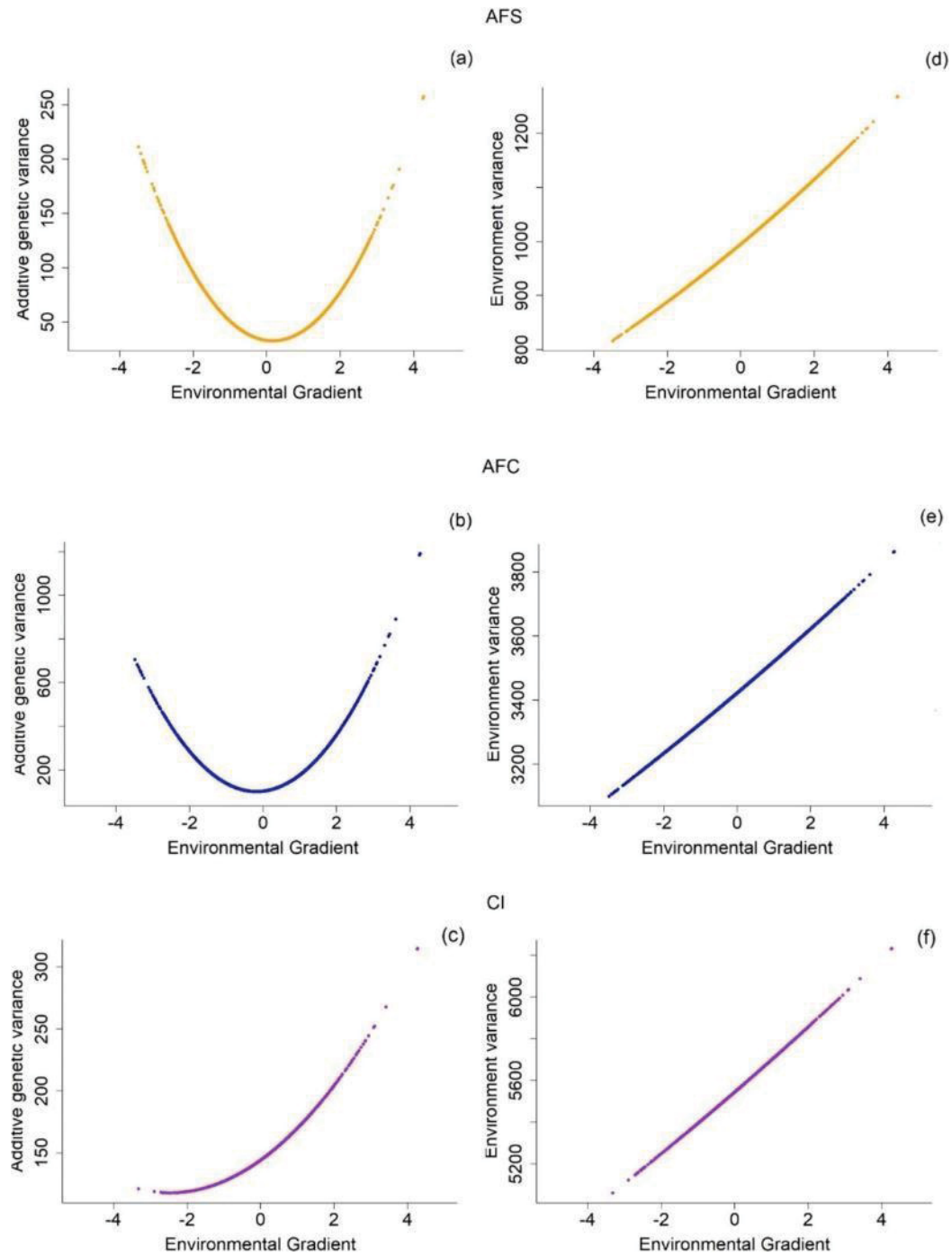


Figure 1 Additive genetic and environmental variances for age at first service (orange), age at first calving (blue), and calving interval (purple) of Holstein cattle across environmental gradients in the state of Paraná, Brazil. (a, b, c) Represent additive genetic variances, while (d, e, f) correspond to environmental variances.

5.3.1 HERITABILITY

Figure 2 illustrates heritability estimates for reproductive traits, indicating that heritability for AFC (Fig. 2b) was highest in the least challenging environmental gradient.

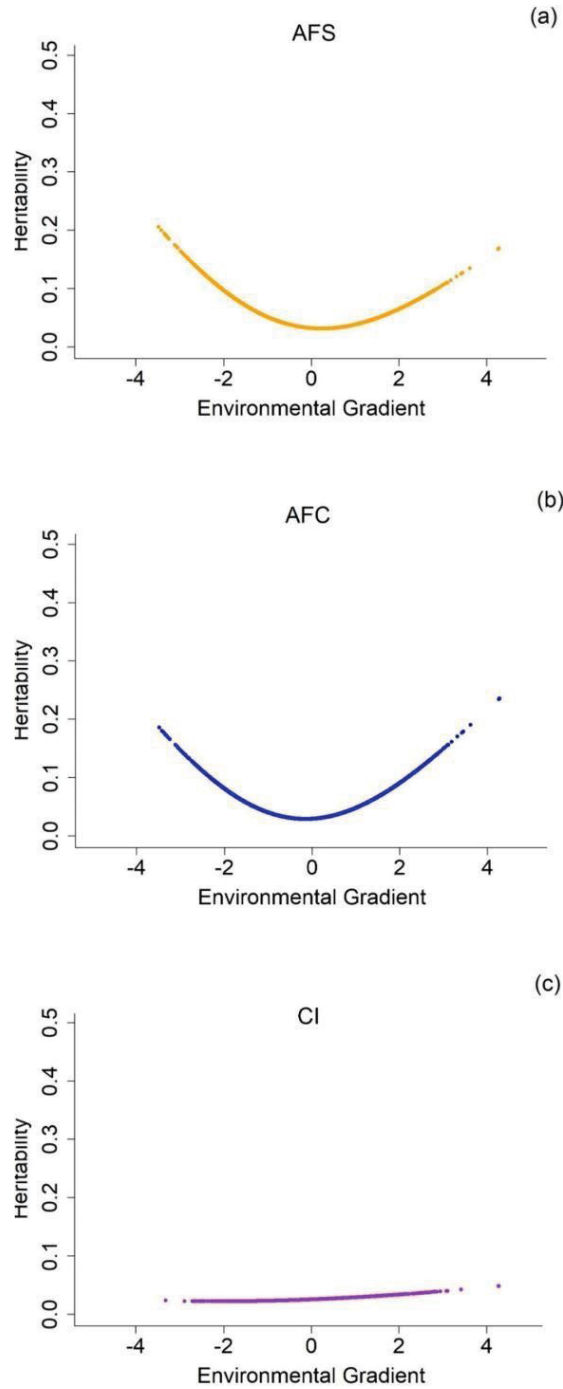


Figure 2 Heritability for reproductive traits: (a) age at first service (orange), (b) age at first calving (blue), and (c) calving interval (purple) of Holstein cattle across environmental gradients in the state of Parana, Brazil.

Moreover, Table 3 reveals variations in heritability magnitude for AFC across extreme environmental gradients, with moderate heritability (0.23) in the least challenging environment and low magnitude heritability (0.18) in the most challenging one. For the AFS trait (Fig. 2a), heritability was higher in the most challenging environment compared to the least challenging environmental gradient. As shown in Table 3; Fig. 2c, heritability estimates for CI were low across all environmental gradients.

Table 3 - Heritability estimates for age at first service (AFS), age at first calving (AFC) and calving interval (CI) in days of Holstein cattle in the environmental gradients (EG) with lowest and greatest challenge in the state of Paraná, Brazil.

Trait	Heritability $\pm$ Standard error	
	Lowest challenge	Greatest challenge
AFS	0.17 (0.02)	0.20 (0.03)
AFC	0.23 (0.03)	0.18 (0.02)
CI	0.05 (0.01)	0.02 (0.004)

5.3.2 RANK CORRELATION BETWEEN EBVS ACROSS ENVIRONMENTAL GRADIENTS

Table 4 provides the correlations between breeding values estimated in the most, intermediate, and least challenging environmental gradients. Figure 3a and b, and 3c depict reaction norm plots for all evaluated animals, while Fig. 3d and e, and 3f include only bulls with more than 500 daughters.

Table 4 - Correlation between the rankings of breeding values for age at first service (AFS), age at first calving (AFC) and calving interval (CI) of Holstein cattle across environmental gradients (EG) in the state of Paraná, Brazil.

Trait	EG	Intermediate	Lowest
AFS	Greatest	0.5671*	-0.5056*
	Intermediate	-	0.2980*
AFC	Greatest	0.4984*	-0.6035*
	Intermediate	-	0.2664*
CI	Greatest	0.9903*	0.9683*
	Intermediate	-	0.9931*

*Spearman's correlation $P < 0.001$

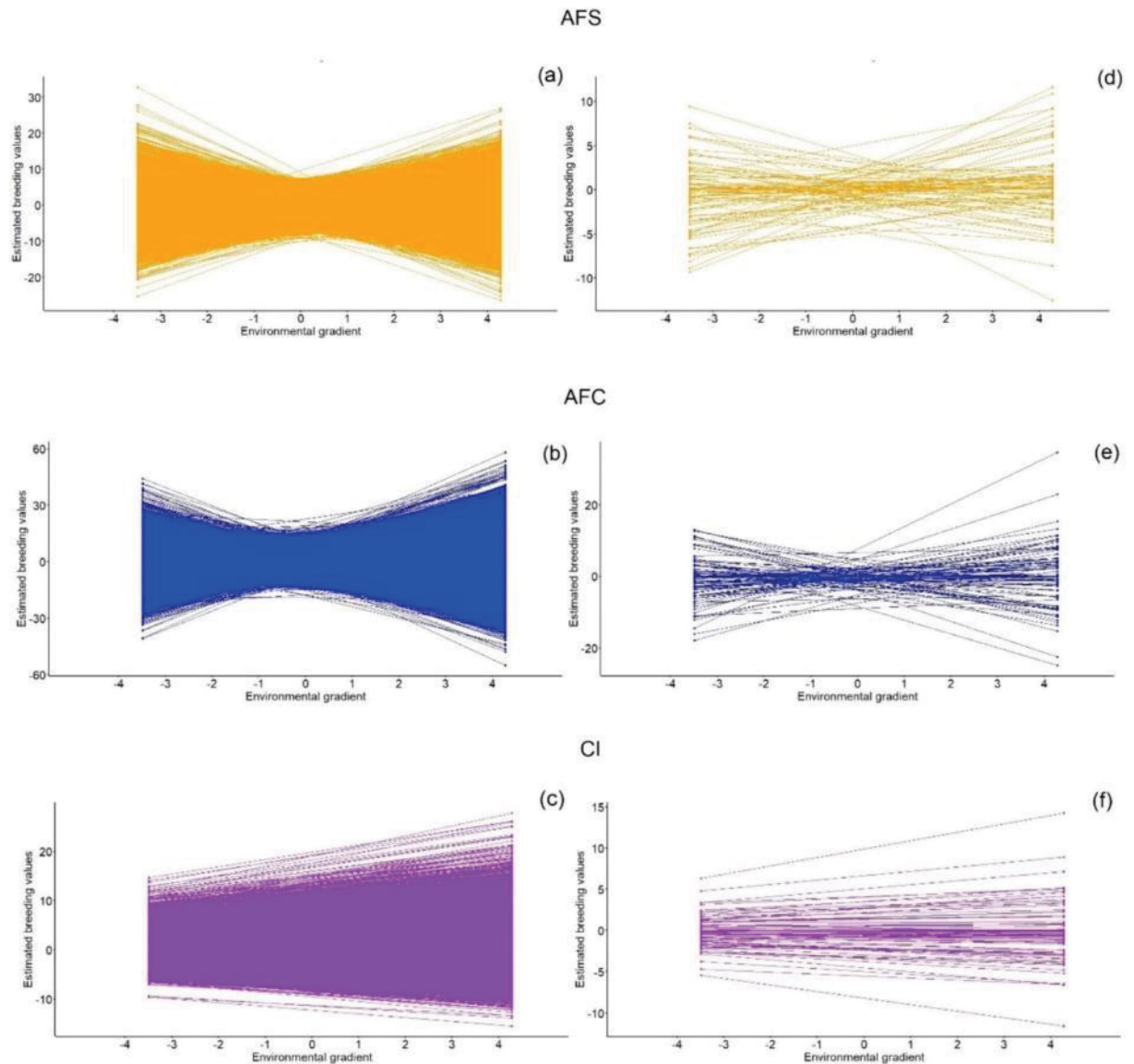


Figure 3 Reaction norms of estimated breeding values for reproductive traits: age at first service (orange), age at first calving (blue), and calving interval (purple) (a, b, c) For all animals in the analyzed population; and (d, e, f) Only for sires with more than 500 daughters distributed across environmental gradients.

5.4 DISCUSSION

There is a widely recognized negative genetic correlation between productivity and fertility, where the selection of more productive cows has resulted in a decline in fertility (Pryce et al. 2004). Therefore, the results presented in this study were expected, as the solutions of the GC for MY305 were used to determine the EG. Consequently, cows in more challenging environments have lower MY305, while cows in less challenging environments

tend to produce more milk. As a result, the averages of reproductive traits increased from the least challenging environment to the most challenging environment.

We observed changes in additive genetic variability for all reproductive traits across EG, which may indicate the presence of GEI effect (Bowman 1972). This suggests that in the more favorable environment, the additive genetic variances were greater than in less favorable environments, allowing the animals to fully express their genetic potential (Lemos et al. 2015). In our results, AFC and CI presented more pronounced differences in additive genetic variation between environments. Therefore, cows raised in more favorable environments will have more chances to express their genetic potential for those traits. Certain genes may be more readily activated or suppressed in response to environmental changes, which may explain the difference in genetic variability across environments (Mota et al. 2020; Zamorano Algandar et al. 2022). The environmental variance for all reproductive traits followed a consistent pattern; in the most favorable environments with fewer challenges, the environmental variance was smaller compared to the more challenging environments, which showed greater environmental variability. This aligns with the findings of Wahinya et al. (2020), who observed reduced environmental variance in more favorable settings for the CI and AFC traits in Holstein cattle in Kenya.

The moderate estimate of heritability observed for AFS and AFC across environments indicates that direct selection will result in genetic gain for those traits. On the other hand, CI had low estimates of heritability across different environments. The variability of heritability estimates across environmental indicate the need to consider environmental factors in the selection of breeding stock to enhance the accuracy of results for reproductive traits (Shi et al. 2021; Chen et al. 2021). However, despite the significant environmental influence on these traits, genetic progress can still be achieved by selecting animals that are better adapted to the breeding environment (Muuttoranta et al. 2019).

The GEI effect is considered relevant when the genetic correlation falls below 0.80 (Robertson 1959). Our results indicate that the correlation between EBVs in the lowest and highest gradients only exceed 0.80 for CI, suggesting a similar expression of this trait across different environmental gradients and indicating a weak GEI effect on this trait. The correlation between EBVs in the extreme environmental gradients was negative for both AFC and AFS, indicating that genotypes with better performance in less challenging environments underperform in more challenging ones. The observed negative correlations between extreme environmental gradients highlight a pronounced GEI and suggest that genotypes related to AFC and AFS are highly plastic in response to environmental changes (Tiezzi et al. 2017).

This genotype adaptability further affects breeding stock selection, given the significant role of GEI in evaluating the performance of candidate breeding animals. This is particularly pertinent in regions with extensive environmental variability, such as Brazil (Nascimento et al. 2022). Such environmental diversity makes it challenging to select genotypes that are suitable for all types of environments, which would only be viable if the rearing environment matched the selection environment. However, in practice, this often does not occur, as many countries, including Brazil, import genetic material from bulls in other nations, such as the United States and Canada.

One of the main implications of selecting robust genotypes is the lack of selection programs that consider both the selection and breeding environments of these genotypes. To overcome this challenge, the Interbull organization was created to analyze bulls in different countries and provide the best bull according to each country. Thus, by accounting for environmental effects, it could reduce their influence in gene expression for economically important traits (Hayes et al. 2016). Nevertheless, although this is a reality in highly developed countries, there is no availability of a similar model to Interbull that allows obtaining similar results in tropical countries (Toro Ospina et al. 2023). Despite these implications, some short-term solutions can be implemented based on the findings of this research. For example, due to the low heritabilities of reproductive traits, especially CI, investing in environmental adaptations to improve reproductive performance could be beneficial. Such improvements could include thermal stress reduction through fans and sprinklers, as well as optimal feeding (both in quantity and quality) (Saizi et al. 2019). Although these methods may be effective in the short term, our results demonstrate that genetic improvement will not happen effectively due to incorrect genotype selection, as shown by changes in genotype rankings across environmental gradients. Such mismatches can lead to diminished genetic gains in reproductive traits in Holstein cattle. Therefore, it is important to pay close attention to both the environment in which the sires are selected and the environment where the offspring will be raised, particularly for AFS and AFC. This approach enables the selection of animals that are well suited to various environmental challenges, especially in large countries like Brazil, where breeding environments are highly diverse.

In conclusion, our findings indicate the presence of GEI for reproductive traits in Holstein cattle raised in Brazil. Furthermore, it emphasizes the need for these countries to participate in international genetic evaluations, such as the Interbull assessment. One of the main reasons for this is that Brazil is a major importer of Holstein genetic material and could benefit significantly from an international evaluation of the genetic quality of imported semen.

This study highlights the significance of both national and international genetic evaluation systems in selecting the best genotypes for Brazilian regions and advancing genetic progress in reproductive traits.

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6 CAPÍTULO V – ANÁLISE GENÉTICA DA RESILIÊNCIA DE VACAS PRIMÍPARAS DA RAÇA HOLANDESA

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RESUMO

A seleção para aumento da produção de leite em bovinos, frequentemente priorizada em programas de melhoramento de bovinos leiteiros, afetou negativamente outras características de importância econômica, como as relacionadas à saúde e fertilidade, o que tornou os animais menos resilientes a perturbações ambientais. Este estudo teve como objetivos estimar o coeficiente de herdabilidade para resiliência avaliada por diferentes indicadores: 1) logaritmo natural da variância (LnVar), 2) autocorrelação (Auto) e 3) assimetria (Assim), além de estimar as correlações genéticas entre a resiliência e as características produtivas, de saúde e fertilidade em vacas primíparas da raça Holandesa. Para isso, foram utilizados dados de 45.292 vacas da raça Holandesa de primeiro parto, coletados entre 2012 e 2022 em 237 rebanhos no Paraná, Brasil. Inicialmente, os dados da produção de leite no dia do controle leiteiro foram ajustados por quatro métodos a fim de estimar a curva esperada, a partir da qual foram gerados os desvios de produção de leite. Esses desvios foram então utilizados para calcular os indicadores de

resiliência (LnVar, Auto e Assim). A análise genética foi realizada por meio do método REML, para estimar herdabilidade da resiliência (por meio de cada um dos indicadores considerados) e correlações genéticas entre a resiliência e características produtivas: produção de leite aos 305 dias (PL305), produção de proteína (PP305), produção de gordura (PG305), reprodutivas: idade ao primeiro parto (IPP), idade ao primeiro serviço (IPS) e de saúde: contagem de células somáticas (CCS). Os coeficientes de herdabilidade para resiliência, independentemente do indicador utilizado, foram de baixa magnitude. A produção de leite mais estável, indicada pelo LnVar, pode estar associada a maior capacidade de adaptação e resistência a distúrbios ambientais. Além disso, o indicador LnVar destacou-se por apresentar correlações genéticas de moderadas a altas com características produtivas. Portanto, dentre os indicadores avaliados, concluiu-se que o LnVar foi o indicador mais promissor para avaliar a resiliência na população estudada.

Palavras-chave: adaptação ambiental, bovinos leiteiros, microsensibilidade ambiental, novos fenótipos, indicadores de resiliência, variabilidade longitudinal.

6.1 INTRODUÇÃO

Ao longo dos anos, os programas de melhoramento de bovinos leiteiros priorizaram a maximização da produção de leite. No entanto, a ênfase na produção de leite pode resultar em consequências negativas em outras características de importância econômica, tais como: saúde, fertilidade e adaptabilidade (PRITCHARD et al., 2013). Talvez por essa razão, na atualidade, as populações de gado leiteiro tornaram-se menos resilientes, especialmente em ambientes subótimos com maior exposição a perturbações ambientais como, por exemplo, o microambiente de uma propriedade (Maskal et al., 2023).

Animais resilientes podem ser definidos como aqueles que recuperam rapidamente o seu nível de desempenho, ou cujo desempenho não é prejudicado, quando expostos a perturbações ambientais (Berghof et al., 2019). De acordo com Poppe et al. (2020), uma vaca é considerada resiliente quando consegue lidar com desafios ambientais, como: patógenos ou ondas de calor, mantendo níveis adequados de produção.

Entretanto, devido a sua complexidade e a diversidade de perturbações que podem ocorrer em um microambiente, a resiliência não é direta e facilmente mensurável. Porém, espera-se que haja variabilidade genética e que, por essa razão, seja possível realizar seleção de indivíduos por meio de características indicadoras de resiliência.

Algumas características têm sido usadas para avaliar a resiliência em bovinos leiteiros como, por exemplo, os registros mensais da produção de leite (Elgersma et al., 2018). Segundo Chen et al. (2023), esses registros são fundamentais para mensurar com precisão a resiliência partindo do princípio de que as vacas estão constantemente sujeitas a perturbações desconhecidas, o que gera flutuações na produção de leite. O padrão de flutuação fornece informações valiosas sobre a resiliência do animal, pois vacas que apresentam pequena variação na produção de leite são consideradas menos impactadas por perturbações do que aquelas com flutuações mais acentuadas (Poppe et al., 2020). Além disso, abordagens analíticas, como a avaliação da variância, autocorrelação e assimetria dos desvios de produção de leite, estão sendo utilizadas como indicadores de resiliência animal (Berghof et al., 2019 e Scheffer et al., 2018).

Embora promissoras, as validações desses indicadores de resiliência frente a respostas às perturbações permanecem desafiadoras, principalmente devido à limitação de dados sobre as condições específicas dessas perturbações (Poppe et al., 2020). As estimativas de parâmetros genéticos podem auxiliar na compreensão mais aprofundada dos mecanismos biológicos subjacentes que influenciam a resiliência.

Portanto, os objetivos neste estudo foram estimar as herdabilidades para resiliência, por meio dos indicadores: variância, autocorrelação e assimetria dos desvios de produção de leite, além das correlações genéticas entre a resiliência, em função dos indicadores, e as características produtivas (produção de leite aos 305 dias – PL305, produção de proteína aos 305 dias – PP305 e produção de gordura aos 305 dias – PG305), de fertilidade (idade ao primeiro parto - IPP e idade ao primeiro serviço - IPS) e saúde (contagem de células somáticas - CCS) para vacas Holandesas primíparas criadas em clima subtropical no Brasil.

6.2 MATERIAL E MÉTODOS

A aprovação do comitê de ética e uso de animais (CEUA) não foi necessária, pois todas as informações foram obtidas a partir de um banco de dados preexistente.

6.2.1 DADOS

Os dados utilizados foram fornecidos pelo serviço de controle leiteiro da Associação Paranaense de Criadores de Bovinos da Raça Holandesa (APCBRH). A base de dados abrangiu

informações de 237 rebanhos no estado do Paraná, totalizando 378.000 vacas da raça Holandesa em primeira, segunda e terceira ordens de lactação, com registros coletados entre 2012 e 2022.

Os indicadores de resiliência foram calculados para 45.292 vacas Holandesas de primeira cria e seguiu duas etapas: (1) ajuste das curvas de lactação individuais e (2) definição dos indicadores de resiliência com base nos desvios em relação às curvas de lactação.

6.2.2 AJUSTE CURVAS DE LACTAÇÃO INDIVIDUAIS

Para o ajuste das curvas de lactação individuais foram utilizados 4 métodos, sendo dois métodos não paramétricos (média e mediana móvel) e dois baseados em modelos (modelo de curva de lactação de Wilmink (Wilmink, 1987) e modelo de curva de lactação baseado em regressão polinomial de quarta ordem, como proposto por Poppe et al. (2020).

O ajuste das curvas de lactação individuais para cada vaca, com base nos registros de produção de leite do controle leiteiro oficial, teve como objetivo obter a produção de leite esperada em cada fase da lactação de acordo com os dias em leite (DEL). Dessa forma, cada vaca apresentou uma curva de lactação observada (baseada no controle leiteiro oficial) e uma curva de lactação predita (gerada pelos métodos de ajuste), que representa a produção mais próxima possível da que seria alcançada na ausência de perturbações. A partir dos desvios entre a produção observada e a esperada foi possível estimar os indicadores de resiliência.

6.2.3 AJUSTE NÃO PARAMÉTRICO (MÉDIA MÓVEL E MEDIANA MÓVEL)

Foram usados dois métodos não paramétricos a média móvel e a mediana móvel para ajustar as curvas de lactação, em que para ambos os métodos foram utilizados dois controles leiteiros de intervalo. Desse modo, cada produção de leite esperada para um determinado controle leiteiro foi a média da produção de leite dos 30 dias anteriores (1 controle leiteiro anterior) e dos 30 dias posteriores (1 controle leiteiro posterior). O mesmo foi realizado para a mediana móvel, porém, a produção de leite esperada para um determinado controle leiteiro foi a mediana da produção de leite dos 30 dias anteriores e dos 30 dias posteriores. Para realizar esse ajuste para a média móvel e mediana móvel foi aplicada a função `rollapply` do pacote `zoo` do software R (Zeileis; Grothendieck, 2005). A principal vantagem de usar a média móvel e a mediana móvel é a flexibilidade, uma vez que as produções esperadas são calculadas com base apenas nos pontos de dados próximos no tempo.

6.2.4 AJUSTE BASEADO NO MÉTODO DA CURVA DE LACTAÇÃO DE WILMINK

O método baseado no modelo de curva de lactação de Wilmink (Wilmink, 1987) foi dado por:

$$\text{Desempenho}_t = \beta_0 + \beta_1 t + \beta_2 e^{-0.05t} + e$$

em que:

Desempenho_t = produção de leite observada no dia do teste t ,

β_0 = nível de produção,

β_1 = diminuição da produção após o pico de produção,

β_2 = aumento na produção de leite no início da lactação,

t = dia do teste,

e = resíduo.

Os coeficientes de regressão, para calcular as curvas de lactação esperadas, foram estimados para cada vaca usando a função `lm` no software R (R Core Team, 2024).

6.2.5 AJUSTE BASEADO NO METÓDO DE REGRESSÃO POLINOMIAL DE QUARTA ORDEM

A regressão polinomial é comumente usada em análises de séries temporais (Brockwell; Davir, 2016). Da mesma forma, a maioria dos modelos de dia de teste usados em avaliação genética usam polinômios de Legendre por meio de regressão aleatória (Van Der Werf et al., 1998). No método baseado em regressão polinomial de quarta ordem usa-se um quantil de 0,7 da seguinte forma:

$$\text{Desempenho}_t = \beta_0 + \beta_1 t + \beta_2 t^2 + \beta_3 t^3 + \beta_4 t^4 + e$$

em que:

Desempenho_t = produção de leite observada no dia do teste t ,

β = nível de produção,

t = dia do teste,

e = resíduo.

De acordo com Poppe et al. (2020), a regressão quantílica estima a mediana ou outro quantil, e quando se utiliza um quantil maior do que 0,5, os valores baixos de produção têm menos impacto na curva prevista do que os valores altos, o que faz com que uma curva ajustada com um quantil superior a 0,5 represente melhor o potencial de produção de leite sem interferências. Para cada vaca, os coeficientes de regressão quantílica polinomial de quarta ordem foram estimados com o quantil 0,7, por meio do pacote quantreg (Koenker, 2024) do software R. A Figura 1 apresenta exemplos dos quatro diferentes métodos de ajuste da curva de lactação, juntamente com a curva de lactação observada para uma vaca.

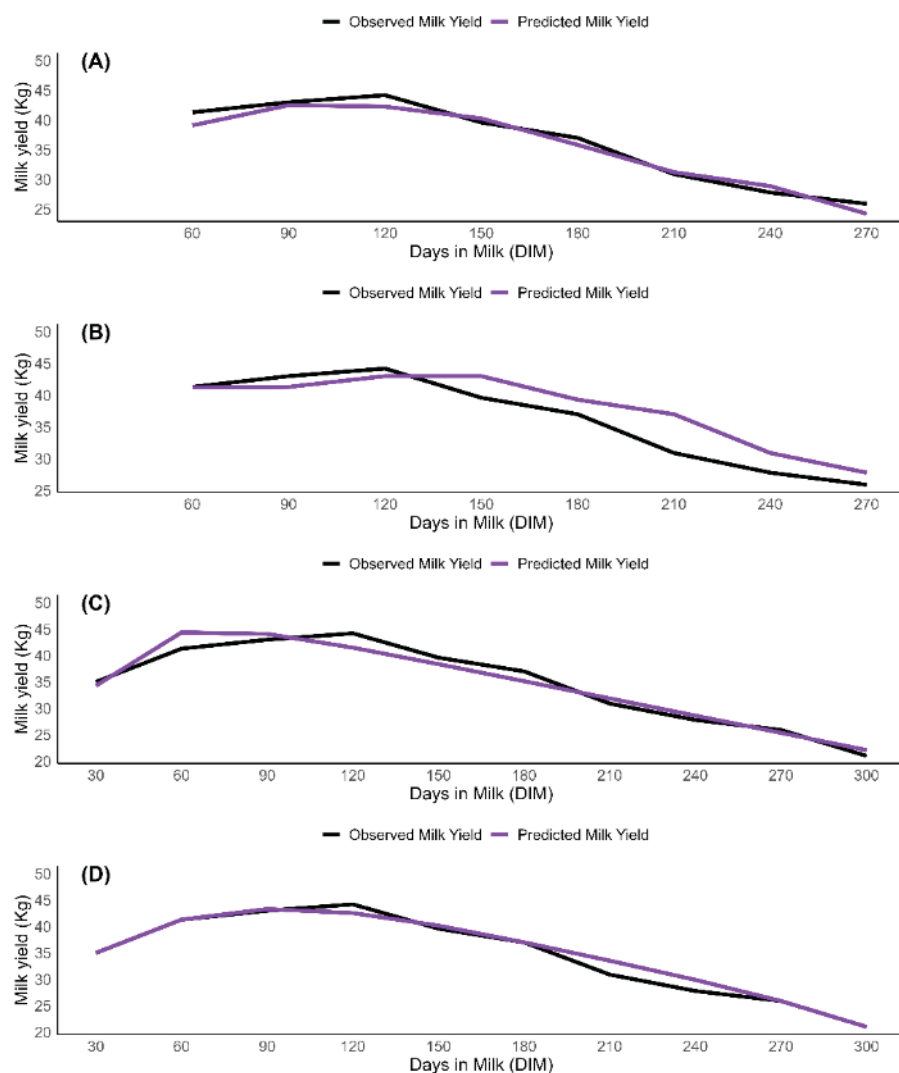


Figura 1. Exemplos dos métodos de ajuste de curva de lactação para uma vaca exemplo. As linhas pretas mostram a produção de leite observada, e as linhas roxas mostram a produção de leite prevista; (A) média móvel, (B) mediana móvel, (C) curva de Wilmink, (D) pol - regressão quantílica polinomial de quarta ordem.

6.2.6 DEFINIÇÃO E INTERPRETAÇÃO DOS INDICADORES DE RESILIÊNCIA COM BASE EM DESVIOS DAS CURVAS DE LACTAÇÃO

Assumiu-se que os desvios das curvas de lactação ajustados (produção – produção esperada) refletem as perturbações ambientais e, portanto, foram usados para calcular os três indicadores de resiliência: o log natural da variância (LnVar), a autocorrelação (auto) e a assimetria (Assim) dos desvios.

A variância dos desvios foi transformada em logaritmo natural (LnVar), para tornar a distribuição normal, o que foi confirmado após inspeção visual. Conforme relatado por Berghof et al. (2019), Elgersma et al. (2018), Poppe et al. (2020) e Scheffer et al. (2018), os indicadores proporcionam importantes interpretações sobre a resiliência dos animais. A variância (LnVar) reflete a amplitude das flutuações na produção de leite ao longo do tempo. Logo, valores elevados de LnVar indicam maior instabilidade, caracterizada por grandes desvios em relação à curva esperada e, dessa forma, a grande variação entre a curva observada e a esperada pode indicar que o animal é menos resiliente às perturbações do microambiente.

Em contraste, a Autocorrelação (Auto) expressa a regularidade na produção de leite ao longo do tempo. Valores elevados de autocorrelação sugerem períodos prolongados de desvios, tanto negativos quanto positivos, o que indica recuperação mais lenta após desafios e/ou perturbações do microambiente, o que está relacionado a uma menor resiliência.

Já, a Assimetria (Assim) descreve a distribuição dos desvios em relação à curva esperada de lactação. Quanto mais assimétrica for a diferença entre a curva observada e a esperada, menor será a resiliência do animal. Em resumo, valores elevados dos três indicadores demonstram menor resiliência.

6.2.7 EDIÇÃO DOS DADOS

A edição dos dados foi realizada pelo software estatístico R (R Core Team, 2023) por meio do pacote dplyr (Wickham et al., 2019). Inicialmente, foram utilizados dados de 378.000 vacas, e após o processo de edição, o arquivo passou a conter registros de 45.090 vacas (Tabela Suplementar 1). Os dados foram organizados conforme a estação do ano no dia do controle leiteiro, considerada da seguinte forma: verão (dezembro, janeiro e fevereiro), outono (março, abril e maio), inverno (junho, julho e agosto) e primavera (setembro, outubro e novembro). Para a definição dos grupos contemporâneos (GCs), foram levados em conta: rebanho, ano e estação do dia do controle leiteiro, sendo que, GC's com menos de 5 animais foram eliminados.

Para analisar a resiliência foram consideradas apenas vacas de primeiro parto, oficialmente registradas como Holstein, com registros de produção de leite entre 5 kg e 75 kg por controle leiteiro (CL), com mais de 10 CL e dias em leite (DEL) entre 60 dias e 500 dias. Foram criadas três variáveis de acordo com os indicadores de resiliência, de forma que cada vaca tivesse um indicador para cada método de ajuste da curva de lactação.

Para as análises das correlações genéticas entre os indicadores de resiliência e as características produtivas (PL305, PP305 e PG305), além de fertilidade (IPP e IPS) e de saúde (CCS), foram considerados os seguintes intervalos: idade ao primeiro parto (IPP) entre 600 e 1080 dias, idade ao primeiro serviço (IPS) entre 330 e 700 dias, e contagem de células somáticas (CCS) entre 20 mil e 1 milhão. A contagem de células somáticas foi transformada, conforme recomendado por Ali e Shook (1980), pela seguinte equação:

$$SCS = \log_2(CCS/100.000) + 3$$

As etapas de edição de dados, incluindo o número de registros restantes e a quantidade de vacas após cada etapa de edição, estão detalhadas na Tabela Suplementar 1.

6.2.8 PARÂMETROS GENÉTICOS

Os componentes de variância (variância genética aditiva - σ^2_a e variância ambiental - σ^2_e) e os parâmetros genéticos foram estimados usando Modelo Animal pelo método de máxima verossimilhança restrita (REML). Os coeficientes de herdabilidade para cada indicador de resiliência (LnVar, Auto e Assim) foram estimados por meio de análise unicaracterística, por meio do software BLUPF90+ (Misztal et al., 2022) de acordo com o seguinte modelo:

$$y = X\beta + Za + e$$

Em que: y = vetor das observações (indicadores de resiliência: LnVar, Auto ou Assim); β = vetor de efeitos fixos (grupo de contemporâneo contendo rebanho, ano e estação do dia do teste de controle leiteiro, idade no primeiro parto e DEL), a = vetor de efeitos genéticos aditivos diretos, X e Z = matrizes de incidência que conectavam os registros em y aos efeitos fixos e efeitos genéticos aditivos, respectivamente e e = vetor de resíduos aleatórios associados a cada observação.

As correlações genéticas entre os indicadores de resiliência e as características produtivas (PL305, PP305 e PG305), características de fertilidade (IPP e IPS) e de saúde (CCS), foram estimadas por meio do modelo animal misto bivariado:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

em que: y_1 e y_2 são os vetores de observações para as características 1 e 2, respectivamente; X_1 , X_2 , b_1 e b_2 são as matrizes de incidência e vetores de efeitos fixos das características 1 e 2, respectivamente; Z_1 e Z_2 são matrizes de incidência para o efeito genético aditivo das características 1 e 2; a_1 e a_2 são os vetores de efeitos aleatórios genéticos aditivos das características 1 e 2, e e_1 e e_2 são os vetores de efeitos residuais.

O vetor dos efeitos genéticos aditivos diretos (a) foi assumido como $N \sim (0, A \sigma^2_a)$, onde A é a matriz de parentesco entre os animais no arquivo de genealogia e σ^2_a é a variância genética aditiva direta. O vetor dos efeitos residuais (e) foi assumido como $N \sim (0, I \sigma^2_e)$, onde I é a matriz identidade cuja ordem é igual ao número de registros e σ^2_e é a variância ambiental.

6.3 RESULTADOS

A Tabela 1 apresenta as estatísticas descritivas dos indicadores de resiliência obtidos por meio de diferentes métodos de ajuste de curva de lactação. Para o LnVar, as médias variaram de 1,20 (modelo média móvel - mm) a 1,51 (modelo mediana móvel - ma). Para o indicador Auto, os valores médios oscilaram entre 0,28 (modelo mm) e 0,45 (modelo ma). Para a Assim, as médias variaram de 0,22 (modelo mm) a 0,33 (modelo Wilmink).

Tabela 1 Estatísticas descritivas para os indicadores de resiliência com base em diferentes métodos de ajuste de curva de lactação de vacas primíparas da raça Holandesa

Ind.	Curve	Média	Desvio	Mínimo	Máximo
LnVar	mm	1,20	0,35	0,80	1,59
	ma	1,51	0,36	1,27	1,80
	wil	1,38	0,33	1,08	1,66
	pol	1,41	0,35	1,04	1,78
Auto	mm	0,28	0,37	1,20	1,23
	ma	0,45	0,31	0,22	0,69
	wil	0,32	0,32	0,04	0,59
	pol	0,35	0,32	0,07	0,62
Assim	mm	0,22	0,58	-2,07	2,03
	ma	0,27	0,62	-2,19	2,17
	wil	0,33	0,58	-1,99	2,06
	pol	0,25	0,60	-2,14	2,06

Ind – indicador de resiliência; LnVar – logaritmo natural da variância dos desvios da produção de leite; Auto – autocorrelação dos desvios de produção de leite; Assim – assimetria dos desvios de produção de leite; mm – média móvel; ma – mediana móvel; wil – método de ajuste pela curva de Wilmink; pol – regressão quantílica polinomial de quarta ordem.

A Tabela 2 apresenta os componentes de variância genética aditiva (σ^2a), variância ambiental (σ^2e) e herdabilidade (h^2) dos indicadores de resiliência obtidos a partir de diferentes métodos de ajuste de curva de lactação.

Tabela 2 Componentes de variância e herdabilidades dos indicadores de resiliência com base em diferentes métodos de ajustes de curva de lactação

Ind.	Curve	σ^2a	σ^2e	$h^2 \pm ep$
LnVar	mm	0,0235 $\pm$ 0,002	0,1009 $\pm$ 0,002	0,19 $\pm$ 0,017
	ma	0,0099 $\pm$ 0,001	0,1144 $\pm$ 0,001	0,08 $\pm$ 0,012
	wil	0,0007 $\pm$ 0,001	0,0051 $\pm$ 0,002	0,12 $\pm$ 0,003
	pol	0,0134 $\pm$ 0,001	0,1031 $\pm$ 0,001	0,11 $\pm$ 0,014
Auto	mm	0,0089 $\pm$ 0,001	0,1244 $\pm$ 0,001	0,06 $\pm$ 0,011
	ma	0,0020 $\pm$ 0,000	0,0949 $\pm$ 0,001	0,02 $\pm$ 0,007
	wil	0,0040 $\pm$ 0,000	0,0944 $\pm$ 0,001	0,04 $\pm$ 0,009
	pol	0,0035 $\pm$ 0,000	0,0930 $\pm$ 0,001	0,05 $\pm$ 0,008
Assim	mm	0,0120 $\pm$ 0,008	0,2997 $\pm$ 0,010	0,04 $\pm$ 0,026
	ma	0,0164 $\pm$ 0,003	0,3693 $\pm$ 0,004	0,04 $\pm$ 0,009
	wil	0,0127 $\pm$ 0,003	0,3335 $\pm$ 0,004	0,04 $\pm$ 0,008
	pol	0,0119 $\pm$ 0,002	0,3494 $\pm$ 0,004	0,03 $\pm$ 0,008

Ind – indicador de resiliência; LnVar – logaritmo natural da variância dos desvios da produção de leite; Auto – autocorrelação dos desvios de produção de leite; Assim – assimetria dos desvios de produção de leite; mm – média móvel; ma – mediana móvel; wil – método de ajuste pela curva de Wilmink; pol - regressão quantílica polinomial de quarta ordem; σ^2a - variância genética aditiva; σ^2e - variância ambiental h^2 - herdabilidade, ep – erro-padrão.

Para o indicador LnVar, independentemente do método de ajuste da curva de lactação, as herdabilidades foram superiores às observadas para os demais indicadores de resiliência. Logo, o indicador de resiliência LnVar apresentou maior variabilidade genética do que os

demais indicadores estudados. Entre os métodos utilizados para ajustar a curva de lactação, a Média Móvel apresentou a maior variância genética aditiva ($\sigma^2_a = 0,0235 \pm 0,0022$) e a maior herdabilidade ($h^2 = 0,19 \pm 0,017$) quando comparado aos demais métodos.

Sendo assim, o indicador de resiliência LnVar foi escolhido para dar continuidade às análises de correlação genética entre a resiliência (LnVar) e as características produtivas, de saúde e fertilidade.

Na Tabela 3 estão as estimativas de correlação genética entre a resiliência (LnVar) e as características produtivas, de saúde e fertilidade de vacas primíparas da raça Holandesa, com base em diferentes métodos de ajuste de curva de lactação.

Tabela 3 Correlações genéticas $\pm$ desvio-padrão entre resiliência (indicador LnVar) e as características produtivas, de saúde e de fertilidade de vacas primíparas da raça Holandesa.

Ind.	Curve	PL305	PP305	PG305	SCS	IPP	IPS
Resiliência (LnVar)	mm	$0,59 \pm 0,04$	$0,47 \pm 0,02$	$0,37 \pm 0,01$	$0,08 \pm 0,01$	$0,11 \pm 0,03$	$0,09 \pm 0,03$
	ma	$0,52 \pm 0,02$	$0,37 \pm 0,03$	$0,18 \pm 0,01$	$0,17 \pm 0,05$	$0,10 \pm 0,01$	$0,04 \pm 0,02$
	wil	$0,50 \pm 0,03$	$0,37 \pm 0,02$	$0,23 \pm 0,03$	$0,18 \pm 0,04$	$0,02 \pm 0,01$	$0,04 \pm 0,01$
	pol	$0,42 \pm 0,03$	$0,30 \pm 0,02$	$0,15 \pm 0,03$	$0,17 \pm 0,06$	$0,11 \pm 0,02$	$0,07 \pm 0,03$

Ind – indicador de resiliência; LnVar – logaritmo natural da variância dos desvios da produção de leite; Auto – autocorrelação dos desvios de produção de leite; Assim – assimetria dos desvios de produção de leite; mm – média móvel; ma – mediana móvel; wil – método de ajuste pela curva de Wilmink; pol – regressão quantílica polinomial de quarta ordem; PL305 – produção de leite aos 305 dias; PP305- produção de proteína no leite aos 305 dias e PG305 – produção de gordura no leite aos 305 dias; SCS – pontuação de células somáticas; IPP – idade ao primeiro parto; IPS – idade ao primeiro serviço.

Independente do modelo utilizado para ajuste da curva de lactação, as correlações genéticas entre a resiliência e a PL305 foram positivas e altas. Isso indica que, a seleção para aumentar a produção de leite resultam em animais menos resilientes. A correlação genética entre resiliência e a PP305 dias foram todas positivas, porém, variaram de moderada a alta magnitude. E as correlações genéticas entre a resiliência e a PG305 foram positivas e variaram de baixa a moderada magnitude. Em relação as correlações genéticas entre a resiliência e as características de saúde e de fertilidade foram positivas e de baixa magnitude. Logo, a seleção para aumentar a produção de gordura e proteína pode resultar em animais menos resilientes.

A Tabela Suplementar 2 (Tabela S2) mostra as correlações genéticas dos demais indicadores com as características produtivas, saúde e de fertilidade. As correlações genéticas entre o indicador Auto e as características produtivas (PL305, PP305 e PG305) foram positivas, variando de baixa a moderada magnitude, enquanto as correlações entre o indicador Assim e

essas mesmas características foram positivas e de baixa magnitude. Para saúde e fertilidade, tanto o indicador Auto quanto o indicador Assim apresentaram correlações positivas de baixa magnitude.

6.4 DISCUSSÃO

Embora a análise realizada por meio de modelos de normas de reação seja comumente usada para identificar animais robustos em diferentes ambientes (Berghof et al., 2019), esta não captura as perturbações microambientais como, por exemplo, as variações que ocorrem no micro ambiente de uma propriedade. Desse modo, optou-se por utilizar os desvios da produção de leite entre a curva de lactação observada e a curva de lactação esperada, que são dados frequentemente mensurados e considerados mais eficazes para a avaliação da resiliência. Os desvios de produção de leite refletem a adaptação dos animais às flutuações do microambiente e permitem identificar com maior facilidade os animais capazes de manter níveis estáveis de produção, mesmo quando expostos a situações desafiadoras (Chen et al., 2023; Elgersma et al., 2018; Poppe et al., 2020).

6.4.1 COEFICIENTE DE HERDABILIDADE PARA A CARACTERÍSTICA RESILIÊNCIA AVALIADA POR MEIO DE DIFERENTES INDICADORES

Os coeficientes de herdabilidade estimados apresentaram baixa magnitude (0,03 a 0,19). O indicador LnVar foi o que apresentou maior estimativa de herdabilidade o que indica o potencial desse critério para avaliar a característica resiliência. Na literatura, Elgersma et al. (2018) e Poppe et al. (2020) investigaram o potencial do indicador de resiliência LnVar em bovinos da raça Holandesa, e estimaram herdabilidades de baixa a moderada magnitude. Os autores concluíram que esse indicador pode ser o mais promissor para avaliar a característica resiliência.

Os resultados obtidos no presente estudo sugerem que a seleção para resiliência, baseada no indicador LnVar, poderá promover progresso genético. De acordo com Elgersma et al. (2018), utilizar o LnVar, que se baseia na média dos desvios da produção de leite ao quadrado, pode ser eficaz para identificar flutuações significativas. Ainda segundo os autores, o LnVar dos desvios de produção de leite é uma medida robusta e eficaz para capturar a resiliência dos animais.

Os coeficientes de herdabilidade dos indicadores Auto e Assim foram baixos (0,02 e 0,06), o que refletiu menor variabilidade genética e maior influência de fatores ambientais. Herdabilidades semelhantes foram relatadas por Poppe et al. (2020) que estimaram herdabilidades baixas para os indicadores Auto (0,08 a 0,09) e Assim (0,009 a 0,01), quando comparados ao indicador LnVar. As baixas herdabilidades dificultam a utilização desses indicadores em programas de melhoramento genético, por serem ferramentas menos eficientes para serem usadas como critérios de seleção para resiliência. Dessa forma, de acordo com os resultados obtidos neste e em estudos anteriores, o LnVar parece ser o melhor indicador para obter progresso genético para resiliência.

6.4.2 CORRELAÇÃO DOS INDICADORES DE RESILIÊNCIA COM CARACTERÍSTICAS PRODUTIVAS, REPRODUTIVAS E DE SAÚDE

As correlações genéticas entre PL305 e a resiliência (LnVar) foram fortes e positivas (0,42 a 0,59), o que indica que a seleção para aumentar a PL305, levará ao aumento do LnVar, portanto resultará em animais menos resilientes. De acordo com Poppe et al. (2021) e Wang et al. (2024), os animais que apresentam produção de leite mais alta tendem a ter maior variação durante a curva de lactação, o que indica menor resiliência às perturbações microambientais.

Além disso, essa menor resiliência pode ser explicada pela alta demanda de recursos energéticos necessários para sustentar elevados níveis de produção, o que reduz o redirecionamento de energia para enfrentar perturbações ambientais e aumenta a susceptibilidade a doenças, devido a maior carga metabólica associada a produção intensiva de leite (Kašná et al., 2022).

Segundo Berghof et al. (2019), outra explicação está relacionada ao efeito de escala, onde vacas de alta produção podem sofrer maior queda na produção de leite em termos absolutos devido a mesma perturbação. No entanto, quando a perda é considerada como porcentagem da produção inicial, o impacto tende a ser proporcional entre vacas de alta e baixa produção, ou seja, embora a queda na produção de leite seja maior em vacas de alta produção, a proporção da perda é semelhante.

Outro ponto a ser considerado é que, como os indicadores de resiliência e a PL305 são baseados nas mesmas informações de lactação completa, é possível que ambos sejam parcialmente influenciados pelos mesmos genes (Kebler et al., 2024). Os resultados das

correlações genéticas entre resiliência, avaliada por meio do indicador LnVar, com a PL305 corroboram essa hipótese.

No entanto, há poucos estudos na literatura que estimaram correlações genéticas entre os indicadores de resiliência e características produtivas como PP305 e PG305, para que se chegue a resultados conclusivos. De acordo com Önder et al. (2023), a correlação genética entre a PL305 e a PP305 (0,81) é mais forte do que entre a PL305 e a PG305 (0,32). Talvez esse resultado possa explicar o porquê a PP305 apresentou correlação mais forte com o LnVar (0,30 a 0,47) do que a correlação da PG305 (0,15 a 0,37).

As correlações genéticas positivas e altas identificadas neste estudo entre o indicador LnVar e a PL305, juntamente com as correlações genéticas frequentemente desfavoráveis entre a produção de leite e as características de saúde e reprodução (Windig et al., 2006), sugerem que o impacto genético em características de saúde e de fertilidade pode estar mais relacionado ao volume de produção do que à variabilidade na produção de leite em si. Sendo assim, esse resultado sugere que a maior produção pode influenciar de forma mais significativa a saúde e a fertilidade do que as flutuações na produção de leite.

Além disso, as correlações genéticas entre a resiliência (indicador LnVar) e as características CCS, IPP e IPS foram, em sua maioria, de baixa a moderada magnitude. Na literatura, em estudos que investigaram indicadores de resiliência, os autores estimaram correlações genéticas dos indicadores de resiliência com características de saúde e reprodutivas de magnitude moderada (Elgersma et al., 2018; Putz et al., 2019; Poppe et al., 2020) e concluíram que o LnVar mais baixo está geneticamente associado a melhor saúde do úbere e melhor fertilidade, mantendo o mesmo nível de produção de leite. É importante ressaltar que, os resultados indicaram valores baixos de LnVar estão associados a melhor saúde e maior eficiência reprodutiva.

Em relação aos demais indicadores de resiliência avaliados (Auto e Assim), ambos apresentaram correlações genéticas de moderadas a fortes com características produtivas PL305, PP305 e PG305 (Tabela Suplementar 2). Neste estudo, a correlação genética entre o indicador de resiliência Auto e a CCS foi positiva, mas de baixa magnitude, o que indica que um valor baixo de autocorrelação está associado a menor resiliência, porém a melhor saúde do úbere. A associação entre a resiliência, por meio do indicador Auto, e a saúde do úbere pode ser explicada pela correlação genética positiva entre resistência à mastite e taxa de recuperação (Welderufael et al., 2018). Kok et al. (2021) estimaram autocorrelação menor em vacas com mastite precoce e tardia em comparação com vacas que não foram identificadas com mastite.

Dessa forma, a autocorrelação pode estar mais relacionada ao tempo de recuperação do animal, uma hipótese já levantada nos manuscritos de Poppe et al. (2020) e Elgersma et al. (2018).

O indicador de resiliência baseado na assimetria dos desvios de produção de leite apresentou menor variação genética e maior ruído, o que resultou em baixa herdabilidade. As correlações genéticas com características de saúde (CCS) e fertilidade (IPP e IPS) foram fracas ou inconsistentes. Desse modo, este não foi um bom indicador de resiliência animal. Corroborando os resultados do presente estudo, Poppe et al. (2020) identificaram herdabilidades de baixa magnitude e correlações genéticas inesperadas com as características de saúde e fertilidade, e também concluíram que o indicador de assimetria foi o menos promissor para avaliar a resiliência.

6.4.3 QUAL MÉTODO DE AJUSTE DE CURVA FOI MAIS ADEQUADO?

Devido às estimativas de herdabilidade de resiliência e correlações genéticas entre a resiliência e as características produtivas (PL305, PG305 e PP305), o LnVar destacou-se como o indicador de resiliência mais promissor. No entanto, também deve-se definir qual método de ajuste de curva foi o melhor. Os quatro métodos de ajuste da curva de lactação utilizados geraram resultados semelhantes, o que demonstra que, para esse indicador, a escolha do método de ajuste não pareceu ser um fator determinante. Contudo, pequenas diferenças nos parâmetros genéticos foram observadas. Inicialmente, o modelo que utilizou a média móvel (mm) pareceu ser a melhor opção quando o objetivo principal é maximizar a produção de leite e sólidos, embora seja preciso considerar a possível influência indireta de características de saúde. Porém, se a prioridade for minimizar essas influências, o modelo Wilmink pode ser uma alternativa válida, mesmo com a pequena redução observada nas correlações entre a resiliência (LnVar) com as características produtivas.

6.4.4 SELEÇÃO DE ANIMAIS RESILIENTES COM BASE NA PRODUÇÃO DE LEITE

A escolha de animais resilientes deve considerar a capacidade de adaptação às variações ambientais. Vacas de alta produção geralmente apresentam maior variabilidade na produção de leite, o que pode indicar menor resiliência devido à maior demanda energética, dificultando a adaptação a estresses ambientais e metabólicos (Kašná et al., 2022). No entanto, vacas com

produção moderada tendem a ser mais resilientes, pois equilibram melhor a produção com as necessidades metabólicas, favorecendo a adaptação a flutuações ambientais (Elgersma et al., 2018; PUTZ et al., 2019). Além disso, vacas de alta produção podem ser mais suscetíveis a doenças e a apresentar pior desempenho reprodutivo (POPPE et al., 2021).

Portanto, a resiliência dos animais pode ser melhorada ao selecionar aqueles que têm maior capacidade de manter níveis estáveis de produção de leite ao longo do ciclo de lactação. Isso está diretamente relacionado com o indicador LnVar, já que este foi capaz de capturar a variação na produção de leite com maior precisão. Desse modo, a seleção de vacas que apresentam menor variabilidade na produção de leite pode ser uma estratégia eficaz para melhorar a resiliência.

6.5 CONCLUSÕES

Embora os coeficientes de herdabilidade para resiliência tenham sido de baixa magnitude, independente do indicador de resiliência utilizado, foi possível identificar variabilidade genética, sendo que, o LnVar foi o que se destacou. Logo, espera-se que a seleção para essa característica seja possível. As correlações genéticas indicaram que a seleção para maior produção de leite (PL305), proteína (PP305) e gordura (PG305) pode resultar em animais menos resilientes. O indicador LnVar mostrou-se uma ferramenta viável para avaliar a resiliência em vacas Holandesas primíparas criadas em clima subtropical no Brasil. Esses resultados são relevantes para programas de melhoramento genético, pois fornecem informações para equilibrar a produtividade e a capacidade de adaptação dos animais a diferentes condições ambientais.

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Tabela Suplementar 1 Números de registros e de vacas após cada etapa de edição de dados.

Etapas de edição	Número de registros	Número de vacas
Banco de dados original	5.844.660	378.000
Vacas de 1ª Ordem de lactação	1.563.392	101.722
Vacas oficialmente registradas (pedigree)	1.519.183	98.390
Exclusão dos registros produção de leite mínimo 5 kg e máximo 75kg cada CL, mínimo de 10 CL	671.358	53.891
Exclusão de vacas com DEL menor que 60 dias e maior que 500 dias	563.073	45.292
Exclusão dos GC com menos de 5 animais	561.044	45.090
Registros diários de produção de leite aos indicadores de resiliência	45.090	45.090
Exclusão de registros de IPP menor que 600 dias e maior do que 1080 dias	40.167	40.167
Exclusão de registros de IPS menor que 330 dias e maior do que 700 dias	21.700	21.700
Exclusão registros de CCS menor que 20 mil e maior do que 1 milhão	21.007	21.007

Tabela Suplementar 2 Correlações genéticas entre os indicadores de resiliência Autocorrelação e Assimetria e as características produtivas, de saúde e de fertilidade em vacas primíparas da raça Holandesa

Ind.	Curve	PL305	PP305	PG305	CCS	IPP	IPS
Auto	mm	0,59 ± 0,04	0,47 ± 0,02	0,37 ± 0,01	0,06 ± 0,03	0,19 ± 0,06	0,11 ± 0,05
	ma	0,52 ± 0,02	0,37 ± 0,03	0,18 ± 0,01	0,19 ± 0,01	0,10 ± 0,04	0,03 ± 0,01
	wil	0,50 ± 0,03	0,37 ± 0,02	0,23 ± 0,03	0,17 ± 0,06	0,05 ± 0,01	0,12 ± 0,03
	pol	0,42 ± 0,03	0,30 ± 0,02	0,15 ± 0,03	0,17 ± 0,07	0,02 ± 0,01	0,06 ± 0,03
Assim	mm	0,25 ± 0,05	0,13 ± 0,04	0,12 ± 0,03	0,09 ± 0,04	0,10 ± 0,01	0,11 ± 0,05
	ma	0,16 ± 0,04	0,11 ± 0,04	0,08 ± 0,01	0,07 ± 0,02	0,06 ± 0,01	0,03 ± 0,01
	wil	0,19 ± 0,06	0,16 ± 0,03	0,12 ± 0,02	-0,09 ± 0,02	-0,02 ± 0,01	0,02 ± 0,01
	pol	0,19 ± 0,07	0,14 ± 0,08	0,10 ± 0,08	0,03 ± 0,01	0,09 ± 0,05	0,08 ± 0,02

Ind. – Indicador de resiliência; Auto – autocorrelação dos desvios de produção de leite; Assim – assimetria dos desvios de produção de leite; mm – média móvel; ma – mediana móvel; wil – método de ajuste pela curva de Wilmink; pol – método de ajuste pelo polinômio de 4º ordem; PL305 – produção de leite aos 305 dias; PP305- produção de proteína no leite aos 305 dias e PG305 – produção de gordura no leite aos 305 dias; SCS – pontuação de células somáticas; IPP – idade ao primeiro parto; IPS – idade ao primeiro serviço.

7. CONSIDERAÇÕES FINAIS

Em bovinos leiteiros da raça Holandesa, o efeito da Interação Genótipo x Ambiente (IGA) mostrou impacto significativo em características produtivas, especialmente em lactações mais avançadas, e também influenciou as características reprodutivas, principalmente, em gradientes ambientais extremos, ou seja, tanto em cenários de menor quanto de maior desafio ambiental. Dessa forma, um genótipo que se destacou em um ambiente pode não ser o mais eficiente em outro, o que reforça a necessidade de incorporar as informações sobre a IGA nos programas de melhoramento genético animal para selecionar indivíduos com genótipos mais adequados ao ambiente de produção.

Além disso, a adaptação dos animais está fortemente relacionada ao microambiente específico da propriedade, desse modo, é relevante identificar animais resilientes a essas condições para otimizar o desempenho. Contudo, a resiliência é uma característica complexa, de difícil mensuração. Por isso, adotar métodos alternativos que utilizem características mais fáceis de medir, como a produção de leite, pode ser uma estratégia eficaz para selecionar animais resilientes.

No entanto, uma das dificuldades em se trabalhar com essa característica está na disponibilidade de dados diários da produção de leite, que seria o mais adequado para melhor identificar a variação no desempenho dos animais. Porém, no Brasil, é mais frequente a obtenção de dados provenientes do controle leiteiro, realizado a cada 30 dias, o que torna mais difícil identificar com precisão a resiliência, devido ao intervalo de captação dos dados. Assim, quando houver maior disponibilidade de dados de produção diária de leite, será possível captar melhor os distúrbios ambientais e, conseqüentemente, a precisão dos resultados poderá aumentar e, dessa forma, as estratégias de seleção poderão ser refinadas.

Os resultados obtidos sugerem que, embora a seleção para resiliência possa afetar a produção de leite, animais resilientes tendem a direcionar parte de sua energia para a manutenção dessa característica. No entanto, esse equilíbrio na distribuição da energia permite que as vacas enfrentem desafios ambientais sem comprometer significativamente a sua performance. Nesse contexto, a resiliência pode gerar benefícios relevantes como a maior longevidade, redução de custos com manejo e tratamento de doenças, além de melhorias nos índices de fertilidade. A resiliência avaliada por meio do indicador LnVar, que reflete a capacidade dos animais de manter ou recuperar sua produção de leite após distúrbios ambientais, apresentou correlações genéticas favoráveis com características de saúde e fertilidade.

Os programas de melhoramento genético de bovinos leiteiros no mundo têm demonstrado sua importância e eficiência na seleção de características produtivas e reprodutivas. No entanto, as características de saúde ainda representam um desafio para os melhoristas que trabalham com essa espécie. Resultados como a correlação da resiliência com características de saúde demonstram o potencial do indicador LnVar para ser utilizado em programas de melhoramento genético, auxiliando no progresso de animais mais resilientes.

Diante das mudanças climáticas evidentes em todo o planeta, o grande desafio para as novas gerações de criadores, técnicos e cientistas será identificar e realizar a seleção de animais de genótipos mais robustos e resilientes. A compreensão e aplicação da IGA e dos indicadores de resiliência em programas de melhoramento genético animal permitirão a escolha de genótipos mais adequados e resilientes, o que permitirá melhores respostas às diferentes condições ambientais e às adversidades no ambiente de produção.

8. ANEXOS



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Breeding and genetics
Full-length research article

Bibliometric mapping of genotype × environment interaction in production animals

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ABSTRACT - The objective was to explore publications on the effects of genotype × environment interaction (GEI) in livestock farming. The dataset used for this analysis came from the Web of Science (WOS) database, and the search was carried out from the first article identified in the WOS database until the search date (August 17, 2023). A set of minimum parameters was defined, and then the data was processed using the VOSviewer® software. To generate visual representations in VOSviewer, fractional counting was used, in which the contribution of each article is divided proportionally based on the number of co-authors. Consequently, if an article has three authors, the weight of each author is calculated as 1/3. Brazil and the United States lead research on GEI, while India, China, and Uruguay are emerging countries on the subject. The most cited journals on GEI include the Journal of Animal Science, Journal of Dairy Science, Animal, Livestock Science, Journal of Animal Breeding and Genetics, and Revista Brasileira de Zootecnia. In Brazil, the research groups are at the forefront of publications related to GEI. Ongoing climate changes over the years have likely led to further investigations into this matter. In the Brazilian context, research groups from the São Paulo State University (UNESP), College of Agricultural and Veterinary Sciences - Jaboticabal, and the Faculty of Veterinary Medicine and Animal Science at the University of São Paulo (FZEA/USP, Campus Pirassununga) have played a prominent role in advancing this area of study. Furthermore, our bibliometric analysis revealed future trends in GEI publications, including an increasing integration of genomic information into research.

Keywords: beef cattle, climate challenges, cluster analysis, dairy cattle, timeline

1. Introduction

The majority of economically significant traits are under the influence of genetic and environmental factors, as well as the interaction between the two (Hay and Roberts, 2018). Genotype × environment interaction (GEI) constitutes a complex system that presents challenges for advancing genetics in livestock animals (Araújo et al., 2022). However, despite the potential influence of GEI on animal performance, most selection programs in Brazil do not incorporate this factor into their evaluations (de Paula Freitas et al., 2021). Neglecting GEI in selection makes it challenging to select animals that exhibit plasticity in the face of differing climatic challenges (Tiezzi et al., 2017).



Influence of different environmental challenges on the expression of reproductive traits in Holstein cattle in Southern Brazil

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Abstract

The aim of this study was to assess the impact of genotype-environment interaction (GEI) on the manifestation of traits such as age at first calving (AFC), age at first service (AFS), and calving interval (CI) through the application of the reaction norm model in Holstein cattle raised in Paraná state, Brazil. Utilizing data from the milk testing service of the Paraná Association of Holstein Cattle Breeders (APCBRH), this study analyzed records from 179,492 animals undergoing their first, second, and third lactations from the years 2012 to 2022. These animals were part of 513 herds spread across 72 municipalities in Paraná. The environmental gradient was established by normalizing contemporary group solutions, derived from the animal model, with the 305-day-corrected milk yield serving as the dependent variable. Subsequently, reaction norms were determined utilizing a Random Regression Model. Spearman's correlation was then applied to compare the estimates of breeding values across different environmental gradients for the studied traits. The highest EG (+4) indicates the least challenging environments, where animals experience better environmental conditions. Conversely, lower EG (-4) values represent the most challenging environments, where animals endure worse conditions. The only trait that exhibited a moderate heritability magnitude was AFC (0.23) in the least challenging environmental condition. The other traits were classified as having low heritability magnitudes regardless of the evaluated environmental gradient. While minimal evidence was found for the influence of GEI on CI, a clear GEI effect was observed for AFC and AFS across all environmental gradients examined. A reversal in genotype ranking occurred under extreme environmental conditions. The findings suggest that the best-performing genotype under one environmental gradient may not necessarily excel under another.

Keywords Age at first calving · Calving interval · Dairy cattle · Environmental gradient · Estimated breeding values · Reaction norms

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Introduction

In dairy farming, fertility-related traits are of significant importance due to their direct link with reproductive management, veterinary treatments, involuntary culling, and ultimately, farm profitability (González-Recio et al. 2004). However, it is important to acknowledge that many herds prioritize increasing milk yield, which may negatively impact cow fertility owing to unfavorable genetic correlations between these traits (Sewalem et al. 2010; Canaza-Cayo et al. 2018). Moreover, the selection for improved fertility is complex; the low heritability of these traits (Montaldo et al. 2017; Brzákova et al. 2019; Muuttoranta et al. 2019) poses a great challenge in achieving substantial genetic progress within breeding programs for this species.

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