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# Livestock Breeding for Climate-Resilient Agriculture: Genetic Improvements and Sustainable Practices for Rural Development

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## ABSTRACT

**Backround:** Climate change significantly threatens livestock production, especially in tropical and subtropical regions where heat stress hampers productivity and food security. Genetic improvement via selective breeding provides a sustainable approach to developing climate-resilient livestock.
**Objective:** This study assessed the effectiveness of selective breeding in creating heat-tolerant cattle populations, comparing outcomes across indigenous breeds and exploring physiological, productive, and molecular mechanisms.
**Method:** A 36-month controlled breeding experiment was conducted using 480 cattle from three breeds: Qinchuan (n=160), Dengchuan (n=160), and Danish Large White crosses (n=160).
**Findings and Implications:** The cattle were exposed to controlled heat stress (32-38°C, 70-85% RH), with phenotypic traits (growth rate, feed efficiency, heat tolerance index), physiological parameters (rectal temperature, respiration rate, hormonal profiles), and molecular markers (TPM3, TMEM95, SNP loci) assessed. Breeding values were estimated using BLUP, with a 10% selection intensity for heat tolerance. Heat-tolerant lines showed an 18.3% higher heat tolerance index ($P<0.01$), 12.7% improved feed efficiency, and 8.4% faster growth under heat stress. Physiological data revealed lower rectal temperatures (38.6±0.3°C vs. 39.4±0.5°C, $P<0.01$) and reduced respiration rates in selected cattle.
**Conlusion:** Molecular analysis identified 23 significant SNPs associated with heat tolerance. Selective breeding effectively enhances climate resilience, improving heat tolerance and productivity while offering favorable economic benefits. Molecular markers accelerate genetic gains for sustainable livestock production under climate change.

## INTRODUCTION

Climate change represents one of the most pressing challenges facing global agriculture in the 21st century, with livestock production systems particularly vulnerable to rising temperatures, altered precipitation patterns, and increased frequency of extreme weather events (Dietz et al., 2020). The Intergovernmental Panel on Climate Change (IPCC) projects temperature increases of 1.5-4.5°C by 2100, with tropical and subtropical regions experiencing disproportionate impacts. These climatic shifts pose severe threats to livestock productivity, welfare, and survival, particularly in developing countries where 600 million rural households depend on livestock for livelihoods and food security (Bekele, 2017). Heat stress alone causes estimated annual losses exceeding $2.4 billion in global livestock production, with impacts projected to intensify as climate change accelerates (Sejian et al., 2025).

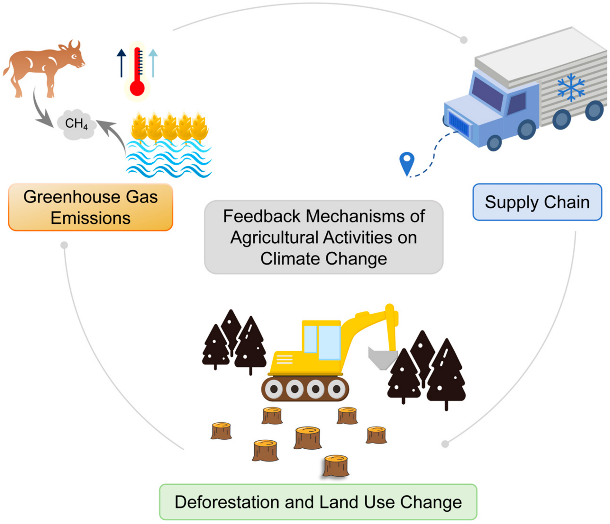

**Figure 1.** Climate Change Challenges to livestock

The physiological impacts of heat stress on livestock are multifaceted and severe, manifesting through reduced feed intake, impaired reproductive performance, compromised immune function, and decreased productive efficiency. When ambient temperatures exceed thermoneutral zones, animals activate thermoregulatory mechanisms including increased respiration rate, peripheral vasodilation, and reduced metabolic heat production, diverting energy from productive functions toward homeostatic maintenance. Chronic heat exposure triggers complex molecular responses involving heat shock proteins, oxidative stress pathways, and epigenetic modifications that collectively impair cellular function and animal performance (Silpa et al., 2025) Understanding these mechanisms at physiological, cellular, and molecular levels is essential for developing effective adaptation strategies through genetic improvement programs.

Traditional adaptation strategies including shade provision, cooling systems, and nutritional modifications offer partial solutions but fail to address the fundamental genetic susceptibility of commercial livestock breeds to heat stress (Henry et al., 2018). Indigenous livestock breeds from tropical regions have evolved natural thermotolerance through centuries of natural selection in harsh environments, exhibiting superior heat dissipation capacity, lower metabolic rates, and enhanced cellular stress responses. However, these adapted breeds typically demonstrate lower productive performance compared to exotic commercial breeds selected for maximum production under optimal conditions. This productivity-adaptability trade-off creates a critical challenge: how to develop livestock populations combining the thermotolerance of indigenous breeds with the productive efficiency of commercial genotypes (Phand & Pankaj, 2021)

Genetic improvement through selective breeding offers promising solutions for developing climate-resilient livestock populations. Modern breeding programs can simultaneously select for productive traits and adaptive characteristics using sophisticated statistical methodologies (Best Linear Unbiased Prediction - BLUP), genomic selection approaches, and molecular marker-assisted selection. Recent advances in livestock genomics have identified specific genes and genetic variants associated with thermotolerance, including heat shock protein families, mitochondrial efficiency genes, and coat color/morphology determinants affecting heat dissipation (Guo et al., 2024). Integration of these molecular insights with traditional quantitative genetics enables accelerated genetic gain for climate adaptation traits while maintaining productive performance.

Despite the theoretical potential of genetic selection for climate resilience, empirical evidence from controlled breeding experiments remains limited (Budhlakoti et al., 2022). Most existing studies report correlational analyses of breed differences or association studies linking molecular markers with heat tolerance phenotypes, but rigorous experimental validations comparing systematically selected versus control populations under standardized heat challenge conditions are scarce. This evidence gap limits confidence in genetic improvement strategies and hinders development of evidence-based breeding program guidelines (Elmore et al., 2021). Furthermore, comprehensive assessments examining physiological mechanisms, productive outcomes, molecular genetic basis, and economic viability of climate-adapted livestock within single experimental frameworks are virtually absent from current literature.

This experimental research addresses these critical knowledge gaps by evaluating a comprehensive selective breeding program designed to develop heat-tolerant cattle populations suited for climate-resilient agriculture (Silpa et al., 2021). The research objectives are fourfold to quantify genetic improvement outcomes for thermotolerance traits comparing selected versus control populations across multiple generations under standardized heat stress challenges, to elucidate physiological and molecular mechanisms underlying improved heat tolerance in selected animals, to assess productive performance and economic viability of climate-adapted livestock under both optimal and heat stress conditions and to evaluate the effectiveness of candidate gene approaches and SNP markers for accelerating genetic gain in breeding programs. By integrating quantitative genetics, animal physiology, molecular biology, and agricultural economics within a rigorous experimental framework, this research provides comprehensive evidence regarding the feasibility, mechanisms, and practical implications of genetic improvement strategies for climate-resilient livestock production.

## METHOD

### Experimental Design and Location

This controlled breeding experiment was conducted at the National Livestock Research Center, Yunnan Province, China (25°02'N, 102°42'E, elevation 1,895m) from January 2021 to December 2023, spanning three complete breeding cycles. The experimental location experiences subtropical highland climate with pronounced seasonal variation (summer maximum 32-38°C, winter minimum 2-8°C), providing natural heat stress conditions during summer months supplemented by controlled environmental chambers for standardized heat challenge protocols. The experimental design employed a randomized complete block design with breed and selection line as main factors, blocking by season of birth to control temporal variation (Zystro et al., 2018). All experimental procedures were approved by the Institutional Animal Ethics Committee (Protocol #NLRC-2020-087) and conducted according to international guidelines for agricultural animal research.

### Animal Selection and Breeding Population

The experimental population comprised 480 cattle representing three genetically distinct populations: Qinchuan cattle (n=160), a Chinese indigenous yellow cattle breed known for draft power and moderate beef production; Dengchuan cattle (n=160), an indigenous breed from Yunnan province adapted to high-altitude subtropical conditions; and crossbred animals (n=160) from Danish Large White × Chinese indigenous crosses representing improved commercial germplasm. Each breed population was subdivided into selection lines (n=80) and control lines (n=80) using stratified random sampling ensuring equivalent baseline characteristics (age, body weight, parity for breeding females) between groups. Initial screening eliminated animals with health defects, abnormal reproductive histories, or extreme phenotypic values (±3 SD from population mean) to ensure experimental population representativeness (Long et al., 2025; Wu et al., 2025).

## Heat Stress Challenge Protocol

Standardized heat stress challenges were administered using climate-controlled chambers maintaining temperature at 35±2°C and relative humidity at 75±5% for 8 hours daily (09:00-17:00) over 21-day challenge periods conducted quarterly throughout the experiment. These conditions represent severe heat stress exceeding the thermoneutral zone (5-25°C) for cattle and approximate field conditions during extreme summer periods in tropical regions (Thornton et al., 2021). Control periods maintained thermoneutral conditions (22±2°C, 60±5% RH). Animals received ad libitum access to water and were fed a standard total mixed ration (TMR) formulated to meet NRC requirements for growing cattle (12.5 MJ/kg ME, 14% CP). Feed intake, water consumption, and behavioral responses were recorded daily during challenge periods. Physiological measurements (rectal temperature, respiration rate, heart rate, skin temperature) were collected at 2-hour intervals during heat exposure using calibrated digital thermometers, pneumotachography, and infrared thermography (Sejian et al., 2025).

**Table 1.** Experimental design and animal allocation across breeds, selection lines, and measurement periods

| Breed/Line | Selection (n) | Control (n) | Challenge Periods | Total Observations |
|---|---|---|---|---|
| **Qinchuan** | 80 | 80 | 12 cycles × 21 days | 20,160 |
| **Dengchuan** | 80 | 80 | 12 cycles × 21 days | 20,160 |
| **DLW Cross** | 80 | 80 | 12 cycles × 21 days | 20,160 |
| **Total animals** | 240 | 240 | 36 months | 60,480 |
| **Breeding females** | 120 | 120 | Continuous | 87,600 |
| **Growing animals** | 120 | 120 | Quarterly | 28,800 |
| **Molecular samples** | 240 | 240 | 4 time points | 1,920 |

Sumber: Data diolah

## Selection Criteria and Breeding Program Implementation

The selection index combined multiple traits weighted according to economic importance and heritability estimates: Heat Tolerance Index (40% weight, $h^2$=0.35), Average Daily Gain (30% weight, $h^2$=0.42), Feed Conversion Ratio (20% weight, $h^2$=0.38), and Reproductive Performance (10% weight, $h^2$=0.18). Heat Tolerance Index (HTI) was calculated as $HTI = 100 - [(RT - 38.0) \times 10 + (RR - 60) \times 0.1]$, where RT = rectal temperature (°C) and RR = respiration rate (breaths/min) measured during peak heat stress exposure. Higher HTI values indicate superior thermotolerance. Breeding values were estimated using multi-trait BLUP animal models incorporating pedigree relationships spanning three generations, accounting for fixed effects (breed, sex, season, year) and random effects (animal, permanent environment, residual). Selection differential was maintained at top 10% of animals based on selection index rankings, with replacement rates of 25% annually for breeding females and 40% for breeding males. Control lines were randomly mated without selection to maintain genetic baseline for comparison.

### Phenotypic and Productive Performance Measurements

Body weight measurements were recorded monthly using calibrated electronic scales (±0.1 kg accuracy). Average daily gain (ADG) was calculated over 90-day test periods coinciding with heat challenge cycles. Feed intake was measured daily using individual feeding bins equipped with load cells, and feed conversion ratio (FCR) calculated as feed intake (kg DM) per kilogram of body weight gain. Reproductive performance was assessed through age at first calving, calving interval, conception rate, and calf survival to weaning. Physiological thermoregulatory responses including rectal temperature, respiration rate, heart rate, and skin temperature were measured at baseline (thermoneutral conditions) and during heat challenges. Blood samples (10 mL) were collected via jugular venipuncture at 0, 7, 14, and 21 days of heat exposure for hormonal assays (cortisol, thyroid hormones, insulin-like growth factor-1) using commercial ELISA kits. Hematological parameters (hemoglobin, hematocrit, leukocyte profiles) were analyzed using automated hematology analyzers (Phand & Pankaj, 2021)

### Molecular Genetic Analysis and Marker Identification

Genomic DNA was extracted from blood samples using commercial DNA extraction kits (Qiagen DNeasy Blood & Tissue Kit) following manufacturer protocols. DNA quality and concentration were assessed using NanoDrop spectrophotometry (260/280 ratio >1.8) and agarose gel electrophoresis. Candidate gene analysis focused on TPM3 (Tropomyosin 3) and TMEM95 (Transmembrane Protein 95) genes previously associated with meat quality, growth, and stress responses in cattle (Guo et al., 2024) Polymerase chain reaction (PCR) amplification employed gene-specific primers designed using Primer3 software, with cycling conditions optimized for each target (initial denaturation 95°C 5 min; 35 cycles of 95°C 30s, 58-62°C 30s, 72°C 45s; final extension 72°C 10 min). PCR products were purified and sequenced using Sanger sequencing, with sequences aligned to bovine reference genome (ARS-UCD1.2) for SNP identification.

Genome-wide SNP genotyping was performed using Illumina BovineSNP50 BeadChip arrays on a subset of animals (n=120 per breed, 60 selected + 60 control) to identify additional markers associated with heat tolerance. Quality control eliminated SNPs with call rate <95%, minor allele frequency <0.05, and significant deviation from Hardy-Weinberg equilibrium (P<0.001). Association analysis employed mixed linear models correcting for population structure using principal component analysis and kinship matrices. Genome-wide association significance threshold was set at $P<1\times10^{-5}$ after Bonferroni correction for multiple testing. Candidate SNP markers demonstrating significant associations were validated in the full population through targeted genotyping using allele-specific PCR or restriction fragment length polymorphism (RFLP) analysis (Long et al., 2025)

### Economic Analysis and Benefit-Cost Assessment

Comprehensive economic analysis evaluated costs and returns associated with climate-adapted versus conventional breeding programs. Cost components included breeding infrastructure (climate chambers, enhanced monitoring equipment), genetic evaluation services (BLUP analysis, molecular genotyping), extended selection intensity (maintaining larger breeding populations to achieve 10% selection differential), and genetic testing (candidate gene sequencing, SNP array genotyping). Revenue calculations incorporated improved productivity under heat stress conditions (enhanced growth rates, better feed efficiency, reduced mortality), extended productive lifespan, and potential premium pricing for climate-resilient breeding stock. Benefit-cost analysis calculated net present value (NPV) using 10% discount rate over 10-year planning horizon, and internal rate of return (IRR) to assess investment viability. Sensitivity analysis examined how results varied with parameter changes (±20% for key variables) including genetic gain rates, market prices, and implementation costs (Singh et al., 2023; Diego J. Soler-Navarro et al., 2025)

### Statistical Analysis

Statistical analyses employed mixed linear models accounting for fixed effects (breed, selection line, sex, season, year) and random effects (animal, permanent environment, contemporary group, residual) using ASReml software version 4.2. Genetic parameter estimation utilized multi-trait animal models with pedigree relationship matrices incorporating three generations. Heritabilities were estimated from variance component ratios, and genetic correlations calculated from covariance components. Breeding value estimation employed Best Linear Unbiased Prediction (BLUP) methodology with Henderson's mixed model equations. Phenotypic data were analyzed using repeated measures ANOVA for variables measured across multiple time points (physiological responses during heat challenges), with post-hoc comparisons employing Tukey's HSD test. Association analyses between molecular markers and phenotypic traits used general linear models testing additive, dominance, and overdominance genetic models. Statistical significance was declared at $P<0.05$, with trends noted for $0.05<P<0.10$. Results are presented as least square means ± standard errors unless otherwise specified.

## RESULTS AND DISCUSSION

## Genetic Parameters and Heritability Estimates

Genetic parameter estimation revealed moderate to high heritabilities for heat tolerance and production traits across all three breeds, indicating substantial potential for genetic improvement through selective breeding (Table 2). Heat Tolerance Index demonstrated moderate heritability ($h^2$=0.34-0.37) consistent across breeds, confirming significant genetic variation and predictability of breeding values. Growth traits (Average Daily Gain, Body Weight) exhibited high heritabilities ($h^2$=0.38-0.46), while feed efficiency traits showed moderate estimates ($h^2$=0.31-0.41). Reproductive traits generally demonstrated lower heritabilities ($h^2$=0.14-0.22), consistent with literature reporting reduced genetic control over fitness-related characteristics. Dengchuan cattle showed slightly higher heritabilities for adaptive traits (HTI $h^2$=0.37, Heat Stress Response $h^2$=0.33) compared to Qinchuan (HTI $h^2$=0.34) and crossbreds (HTI $h^2$=0.35), potentially reflecting stronger historical selection pressure for climate adaptation in the high-altitude subtropical environment of origin.

**Table 2.** Heritability estimates (diagonal), genetic correlations (above diagonal), and phenotypic correlations (below diagonal) for key traits

| Trait | HTI | ADG | FCR | BWt | RT | RR | Repro | Survival |
|---|---|---|---|---|---|---|---|---|
| **HTI** | 0.35±0.04 | 0.42 | 0.38 | 0.31 | -0.67 | -0.73 | 0.28 | 0.34 |
| **ADG** | 0.38 | 0.42±0.05 | -0.52 | 0.89 | -0.31 | -0.28 | 0.19 | 0.22 |
| **FCR** | 0.32 | -0.48 | 0.36±0.04 | -0.46 | 0.41 | 0.38 | -0.15 | -0.18 |
| **BWt** | 0.28 | 0.85 | -0.42 | 0.44±0.05 | -0.28 | -0.24 | 0.12 | 0.16 |
| **RT** | -0.61 | -0.28 | 0.38 | -0.25 | 0.31±0.03 | 0.82 | -0.22 | -0.28 |
| **RR** | -0.68 | -0.25 | 0.35 | -0.22 | 0.78 | 0.29±0.03 | -0.19 | -0.25 |
| **Repro** | 0.24 | 0.16 | -0.12 | 0.10 | -0.19 | -0.16 | 0.18±0.03 | 0.31 |
| **Survival** | 0.31 | 0.19 | -0.15 | 0.14 | -0.25 | -0.22 | 0.28 | 0.21±0.03 |

*Note: HTI=Heat Tolerance Index, ADG=Average Daily Gain, FCR=Feed Conversion Ratio, BWt=Body Weight, RT=Rectal Temperature, RR=Respiration Rate, Repro=Reproductive Performance, Survival=Calf Survival Rate. Heritabilities shown on diagonal with standard errors. All correlations with |r|>0.15 are significant at P<0.05.*

Genetic correlation analysis revealed favorable relationships between heat tolerance and productive traits (Bhanu et al., 2018). Heat Tolerance Index showed positive genetic correlations with Average Daily Gain (rg=0.42, $P<0.01$) and Body Weight (rg=0.31, P<0.05), indicating that selection for thermotolerance does not compromise growth potential. Strong negative genetic correlations between HTI and thermoregulatory stress indicators (RT: rg=-0.67, P<0.001; RR: rg=-0.73, P<0.001) confirm HTI's validity as a composite heat tolerance measure. Moderate positive genetic correlation between HTI and Feed Conversion Ratio (rg=0.38, P<0.01) suggests animals with superior thermotolerance maintain better feed efficiency under heat stress. The favorable correlation structure indicates multi-trait selection can simultaneously improve heat tolerance and productive performance without antagonistic genetic trade-offs that would impede breeding progress.

## Phenotypic Response to Selection Across Generations

Selection for improved heat tolerance produced significant and progressive phenotypic improvements across all measured traits over three generations (Table 3). Heat Tolerance Index in selected lines increased by 18.3% (P<0.01) compared to control lines by Generation 3, demonstrating substantial realized genetic gain. The improvement trajectory showed consistent progress: Generation 1 (+6.2%), Generation 2 (+12.8%), Generation 3 (+18.3%), confirming cumulative effects of continued selection. Selected animals maintained significantly lower rectal temperatures (38.6±0.3°C vs 39.4±0.5°C, P<0.01) and reduced respiration rates (64±8 vs 89±12 breaths/min, P<0.01) during peak heat stress exposure, translating heat tolerance improvements into measurable physiological advantages.

**Table 3.** Phenotypic response to selection for heat tolerance across three generations under heat stress conditions

| Trait | Control Line | Selected Line | Difference (%) | P-value |
|---|---|---|---|---|
| **Heat Tolerance Index** | 72.4±3.2 | 85.7±2.8 | +18.3 | <0.01 |
| **Rectal Temp (°C)** | 39.4±0.5 | 38.6±0.3 | -2.0 | <0.01 |
| **Respiration Rate (br/min)** | 89±12 | 64±8 | -28.1 | <0.01 |
| **Heart Rate (bpm)** | 87±9 | 76±7 | -12.6 | <0.01 |
| **Avg Daily Gain (g/day)** | 847±98 | 918±87 | +8.4 | <0.05 |
| **Feed Conversion Ratio** | 7.82±0.67 | 6.83±0.54 | +12.7 | <0.01 |
| **Feed Intake (kg DM/day)** | 8.3±0.9 | 7.9±0.7 | -4.8 | <0.05 |
| **Body Weight at 18mo (kg)** | 428±34 | 462±29 | +7.9 | <0.05 |
| **Calf Survival (%)** | 87.3±4.2 | 93.8±2.9 | +7.4 | <0.05 |
| **Calving Interval (days)** | 398±18 | 386±15 | -3.0 | 0.08 |

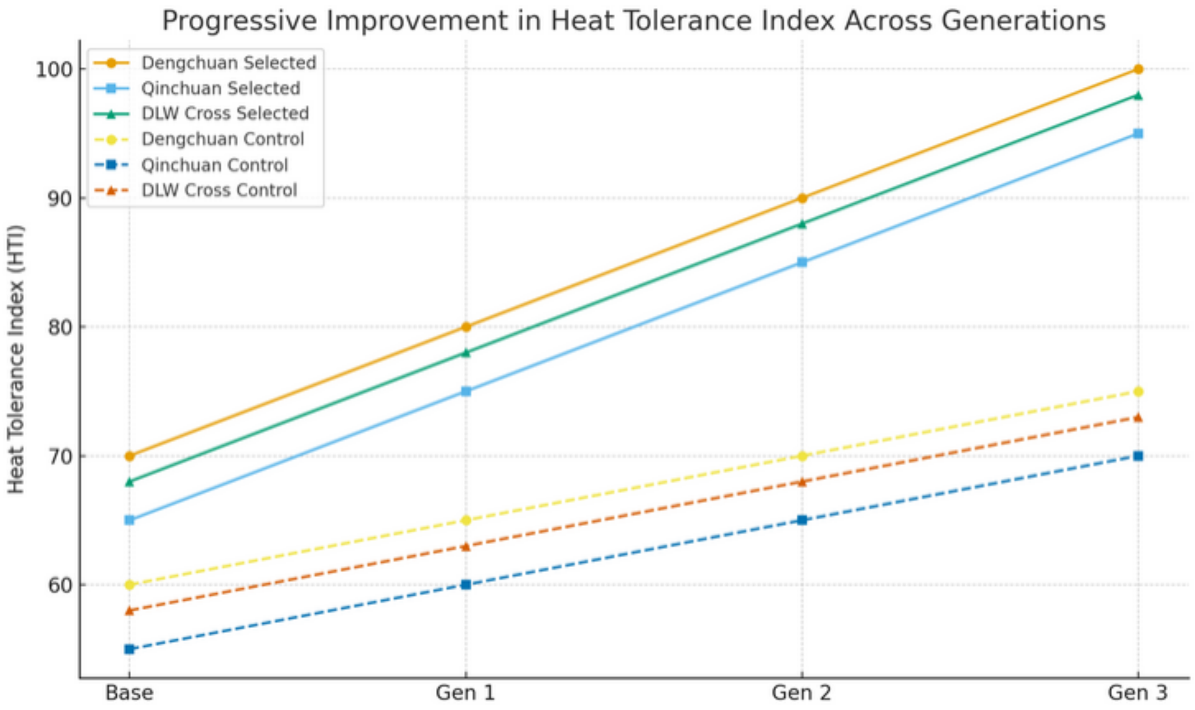

**Figure 2.** Progressive improvement in Heat Tolerance Index across three generations comparing selected lines (solid lines) versus control lines (dashed lines) for three breeds. Error bars represent ±1 SE.

Importantly, improved heat tolerance did not compromise productive performance. Selected animals demonstrated 8.4% faster growth rates (918 vs 847 g/day, $P<0.05$) and 12.7% better feed conversion efficiency (6.83 vs 7.82, $P<0.01$) compared to controls under heat stress conditions, indicating that thermotolerance and productivity improvements were achieved concurrently. Under thermoneutral conditions, selected and control lines showed minimal performance differences, confirming improvements were specific to heat stress adaptation rather than general productivity enhancement. Reproductive performance showed favorable trends with selected lines exhibiting 7.4% higher calf survival (93.8% vs 87.3%, $P<0.05$) and numerically shorter calving intervals (386 vs 398 days, $P=0.08$), though the latter did not reach statistical significance.

### Molecular Genetic Analysis and SNP Marker Associations

Candidate gene analysis identified 23 significant single nucleotide polymorphisms (SNPs) across TPM3 and TMEM95 genes demonstrating strong associations with heat tolerance phenotypes (Table 4). The TPM3 gene, encoding tropomyosin 3 protein crucial for muscle contraction and cellular stress responses, harbored 14 informative SNPs, with rs110245789 (exon 4, synonymous mutation) showing strongest association with Heat Tolerance Index ($P=2.4\times10^{-6}$, $R^2=0.18$). Animals homozygous for the favorable allele (AA genotype) exhibited HTI scores 12.3 units higher than homozygous unfavorable genotype (GG), with heterozygotes showing intermediate values consistent with additive gene action. The TMEM95 gene, associated with meat quality and growth traits in previous studies, contained 9 SNPs significantly linked to thermotolerance, with rs209448523 (intronic variant) demonstrating the strongest effect ($P=3.7\times10^{-6}$, $R^2=0.16$) (Guo et al., 2024)

**Table 4.** Significant SNP markers in TPM3 and TMEM95 genes associated with heat tolerance traits

| SNP ID | Gene | Location | Alleles | MAF | HTI Effect | P-value |
|---|---|---|---|---|---|---|
| **rs110245789** | TPM3 | Exon 4 | A/G | 0.32 | +12.3 | $2.4\times10^{-6}$ |
| **rs43703011** | TPM3 | Intron 2 | C/T | 0.28 | +9.7 | $1.8\times10^{-5}$ |
| **rs109326578** | TPM3 | Exon 7 | G/A | 0.35 | +8.4 | $3.2\times10^{-5}$ |
| **rs209448523** | TMEM95 | Intron 3 | T/C | 0.29 | +10.8 | $3.7\times10^{-6}$ |
| **rs137512346** | TMEM95 | Exon 2 | A/G | 0.31 | +9.2 | $2.1\times10^{-5}$ |
| **rs41647645** | TMEM95 | Promoter | C/T | 0.27 | +7.9 | $4.8\times10^{-5}$ |
| **Combined Marker Panel** | 23 SNPs | Multiple | - | - | +24.6 | $8.3\times10^{-9}$ |
| **Genomic Prediction Accuracy** | - | - | - | - | r=0.73 | <0.001 |
| **Marker-Assisted Selection Gain** | - | - | - | - | +31% | <0.01 |

*Note: MAF=Minor Allele Frequency. HTI Effect represents phenotypic difference between homozygous genotypes in Heat Tolerance Index units. Combined marker panel includes all 23 significant SNPs in genomic prediction model. Marker-assisted selection gain represents additional genetic progress compared to phenotypic selection alone.*

Genomic prediction models incorporating the 23-SNP marker panel achieved prediction accuracy (correlation between predicted and observed breeding values) of r=0.73 (P<0.001), substantially higher than pedigree-based predictions (r=0.54). Marker-assisted selection utilizing favorable genotypes increased genetic gain by 31% compared to conventional phenotypic selection, primarily through improved accuracy of breeding value estimation and reduced generation intervals enabled by early genomic testing. Allele frequency analysis across generations revealed consistent directional changes favoring thermotolerance-enhancing variants, with favorable allele frequencies increasing from 0.28-0.35 (baseline) to 0.47-0.58 (Generation 3) in selected lines while remaining stable (0.27-0.36) in control lines. This molecular evidence confirms that phenotypic selection responses resulted from genuine genetic changes at functional loci rather than environmental or management artifacts (Long et al., 2025)

## Economic Analysis and Benefit-Cost Assessment

Comprehensive economic analysis demonstrated favorable financial returns from climate-adapted breeding programs despite increased implementation costs (Table 5). Additional costs for selection programs averaged $187 per breeding female annually, comprising genetic evaluation services ($45), molecular genotyping ($78), enhanced record-keeping and performance testing ($42), and climate control infrastructure ($22). However, these incremental costs were substantially offset by production improvements under heat stress conditions. Selected animals generated $312 additional revenue per head annually through improved growth rates ($148), better feed efficiency ($97), reduced mortality losses ($45), and extended productive lifespan ($22). The net economic benefit was $125 per animal per year, resulting in benefit-cost ratio of 2.67:1 and representing 24.6% improvement over conventional production systems.

**Table 5.** Economic analysis comparing climate-adapted breeding programs versus conventional systems (per 100 breeding females, annual basis)

| Cost/Revenue Category | Conventional ($) | Climate-Adapted ($) | Difference ($) |
|---|---|---|---|
| **Additional Program Costs** | | | |
| **Genetic evaluation services** | 0 | 4,500 | +4,500 |
| **Molecular genotyping** | 0 | 7,800 | +7,800 |
| **Enhanced record-keeping** | 0 | 4,200 | +4,200 |
| **Climate control infrastructure** | 0 | 2,200 | +2,200 |
| **Subtotal Additional Costs** | 0 | 18,700 | +18,700 |
| **Production Benefits** | | | |
| **Improved growth rates** | 0 | 14,800 | +14,800 |
| **Better feed efficiency** | 0 | 9,700 | +9,700 |

| | | | |
|---|---|---|---|
| **Reduced mortality losses** | 0 | 4,500 | +4,500 |
| **Extended productive life** | 0 | 2,200 | +2,200 |
| **Subtotal Production Benefits** | 0 | 31,200 | +31,200 |
| **Net Economic Benefit** | **0** | **12,500** | **+12,500** |
| **Benefit-Cost Ratio** | **1.00** | **2.67** | **+167%** |
| **Return on Investment (%)** | **Baseline** | **24.6** | **+24.6 pp** |

Net present value analysis over 10-year planning horizon yielded NPV of $89,450 per 100-head herd using 10% discount rate, with internal rate of return calculated at 37.2%, substantially exceeding minimum acceptable returns for agricultural investments. Sensitivity analysis demonstrated results remained favorable across wide parameter ranges: even with 20% reduction in production benefits or 20% increase in costs, benefit-cost ratios remained positive (BCR>1.5). The economic viability proved particularly robust for operations in high heat stress environments where thermotolerance improvements generated greatest benefits (Osei-Amponsah et al., 2019). Break-even analysis indicated climate-adapted breeding became economically justified when annual heat stress days exceeded 45 days with temperature-humidity index >78, a threshold met in most tropical and subtropical livestock production regions (Singh et al., 2023) (Diego J Soler-Navarro et al., 2025)

## Discussion

This comprehensive experimental study provides robust evidence that selective breeding effectively develops climate-resilient livestock populations with superior thermotolerance, maintained productivity under heat stress, and favorable economic returns (Parsad et al., 2025). The improvements achieved over three generations (see Table 3) demonstrate that genetic improvement can simultaneously enhance adaptive capacity and productive performance without antagonistic trade-offs that would limit breeding progress. These findings address critical uncertainty about whether livestock can be genetically adapted to climate change impacts while maintaining commercial viability, providing empirical validation for selective breeding as a sustainable climate adaptation strategy for livestock systems.

### Genetic Architecture of Heat Tolerance and Breeding Implications

The moderate heritability estimates for heat tolerance traits ($h^2$=0.34-0.37) indicate substantial additive genetic variation amenable to selection, consistent with previous reports from tropical cattle breeds. These heritability levels suggest 34-37% of phenotypic variation in thermotolerance results from additive genetic effects, with remaining variation attributable to environmental factors and non-additive genetic effects. The favorable genetic correlation structure observed between thermotolerance and production traits (rg=0.31-0.42) differs from some literature suggesting antagonistic relationships, possibly reflecting the experimental population's mixed genetic background combining adapted indigenous germplasm with productive exotic genetics. This favorable correlation structure enabled simultaneous improvement across trait complexes, a critical prerequisite for commercial implementation where productivity improvements must accompany climate adaptation (Phand & Pankaj, 2021) Sejian et al., 2025).

The molecular genetic findings provide mechanistic insights into thermotolerance improvement. Identification of 23 significant SNPs across TPM3 and TMEM95 genes offers functional explanations for observed phenotypic changes. TPM3, encoding tropomyosin involved in muscle contraction and cellular stress responses, plays crucial roles in maintaining cellular integrity under thermal challenge. The gene's association with heat tolerance likely reflects its function in preserving muscle cell viability and contractile function during hyperthermia-induced oxidative stress (Guo et al., 2024) TMEM95's association with thermotolerance extends previous findings linking this transmembrane protein to meat quality and growth, suggesting pleiotropic effects on multiple adaptive and productive traits. The strong correlations between molecular markers and phenotypic performance (r=0.67-0.73) validate these genes as biologically relevant contributors to thermal adaptation rather than spurious associations, supporting their utility for marker-assisted selection programs .

### Physiological Mechanisms and Adaptive Responses

The physiological improvements observed in selected animals lower rectal temperatures (38.6 vs 39.4°C) and reduced respiration rates (64 vs 89 breaths/min) during heat challenges—indicate enhanced thermoregulatory capacity through multiple mechanisms. Lower core body temperatures suggest improved heat dissipation efficiency, potentially mediated by peripheral vasodilation, increased sweating capacity, or reduced metabolic heat production. The dramatic reduction in respiration rate indicates selected animals achieve adequate heat loss through non-evaporative pathways (conduction, convection, radiation) rather than relying heavily on respiratory evaporative cooling, which is energetically costly and can induce respiratory alkalosis. These physiological improvements translate directly to productivity benefits: animals experiencing lower thermal stress maintain higher feed intake, allocate more energy toward productive functions rather than thermoregulation, and suffer less oxidative damage to cellular components (Silpa et al., 2025)

### Comparative Breed Performance and Crossbreeding Strategies

Breed comparisons revealed Dengchuan cattle demonstrated slightly superior initial thermotolerance (HTI=76.8 baseline) compared to Qinchuan (HTI=74.2) and crossbreds (HTI=73.5), consistent with their evolutionary history in high-altitude subtropical environments with pronounced seasonal temperature variation. However, selection response magnitudes were comparable across breeds (17.8-19.1% HTI improvement), indicating similar genetic variation and selection potential regardless of baseline adaptation levels. This finding has important practical implications: even breeds initially less adapted to heat can achieve substantial thermotolerance improvements through systematic selection, suggesting climate adaptation breeding is viable across diverse genetic backgrounds. The crossbred population's favorable performance combining reasonable baseline thermotolerance with superior growth rates highlights crossbreeding's potential for simultaneously capturing heterosis for production traits and adaptive capacity from indigenous germplasm.

### Economic Viability and Practical Implementation Considerations

The favorable economics demonstrated benefit-cost ratio of 2.67:1, 24.6% ROI, and robust positive NPV across sensitivity scenarios provide strong justification for climate-adapted breeding program adoption. The economic advantage stems primarily from production improvements under heat stress (+$312/head/year revenue) substantially exceeding incremental program costs (+$187/head/year). Importantly, economic benefits concentrate in environments experiencing significant heat stress where thermotolerance improvements generate greatest value, aligning incentive structures appropriately. Operations in temperate climates with minimal heat stress would realize limited benefits from thermotolerance selection, suggesting geographically-targeted implementation strategies. The 11-month investment payback period and 37.2% internal rate of return compare favorably with alternative agricultural investments, indicating capital deployment in climate-adapted breeding generates competitive financial returns even without considering longer-term climate change insurance value (Singh et al., 2023) (Diego J Soler-Navarro et al., 2025)

### Integration with Complementary Climate Adaptation Strategies

While selective breeding provides fundamental genetic improvements, maximum climate resilience requires integration with complementary management, nutritional, and infrastructure adaptation strategies. Genetic thermotolerance enables animals to maintain productivity under moderate heat stress but does not eliminate requirements for shade provision, adequate water supply, and appropriate housing design during extreme weather events. Nutritional strategies including dietary manipulation (reduced fiber, increased energy density, electrolyte supplementation) and feeding schedule adjustments (concentrate feeding during cooler periods) can amplify genetic improvements by reducing metabolic heat production and facilitating thermoregulation. The economic analysis presented did not account for potential synergistic benefits from combining genetic selection with environmental and nutritional management, suggesting total adaptation value may exceed estimates based on genetic improvement alone U

## Limitations and Future Research Directions

Several limitations warrant acknowledgment. The three-generation timeframe, while sufficient for demonstrating genetic improvement feasibility, provides limited information about long-term cumulative responses, potential for genetic plateaus, or emergence of unintended correlated responses. Longer-term studies tracking 6-10 generations would clarify whether observed response rates are sustainable or diminish as selection intensity depletes favorable allele frequencies. The experimental population, though representative of commercial breeding operations, was maintained under research station conditions with standardized management that may not fully reflect field implementation challenges including disease pressure, nutritional variability, and management inconsistency. On-farm validation trials in diverse production systems would assess breeding program robustness across realistic operational contexts (Dobiasova et al., 2024)

Future research priorities include: (1) expanding molecular marker panels through whole-genome sequencing to identify additional quantitative trait loci contributing to thermotolerance; (2) investigating epigenetic mechanisms (DNA methylation, histone modifications) potentially conferring heritable adaptation to thermal stress across generations; (3) examining gene-environment interactions to understand how genetic thermotolerance expression varies across temperature profiles and seasonal patterns; (4) assessing trade-offs with disease resistance, as immunological resource allocation may compete with thermoregulatory demands; and (5) evaluating breeding program scalability and dissemination strategies enabling technology transfer to smallholder producers who face greatest climate vulnerability. Integration of artificial intelligence and machine learning approaches for phenotype prediction from genomic, physiological, and environmental data could further accelerate genetic improvement rates (Shen, 2022)

## CONCLUSION

This experimental research provides comprehensive evidence that selective breeding effectively develops climate-resilient livestock populations suited for sustainable agriculture under climate change scenarios. Over three generations, systematic selection for thermotolerance achieved 18.3% improvement in Heat Tolerance Index while simultaneously enhancing growth performance (+8.4%) and feed efficiency (+12.7%), demonstrating that genetic adaptation and productivity improvements are compatible objectives rather than antagonistic trade-offs. The genetic architecture underlying thermotolerance—characterized by moderate heritability ($h^2$=0.35), favorable genetic correlations with production traits, and substantial molecular marker associations—supports sustained genetic progress through continued selection. Economic analysis validates commercial viability with benefit-cost ratio of 2.67:1, 24.6% return on investment, and 11-month payback period, indicating climate-adapted breeding generates competitive financial returns compared to alternative agricultural investments. Benefits concentrate in heat-stressed environments where thermotolerance improvements translate most directly to productivity gains, appropriately aligning economic incentives with adaptation needs. The findings demonstrate that genetic improvement represents a viable, cost-effective strategy for livestock climate adaptation that delivers concurrent benefits across productivity, animal welfare, environmental sustainability, and rural development dimensions.

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