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GENETIC IMPROVEMENT AND HYBRID BREEDING OF BLACK SOLDIER FLY (*HERMETIA ILLUCENS*) FOR SUSTAINABLE FEED PRODUCTION AND ORGANIC WASTE VALORIZATION: ADVANCES, CHALLENGES AND FUTURE PROSPECTS

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***Abstract*—**Black soldier fly (BSF; *Hermetia illucens*) production is expanding as a route to insect protein and the recovery of nutrients from suitable organic side-streams. Yet variable larval performance, uncertain genetic merit, inbreeding, substrate-dependent responses and feed-safety constraints complicate industrial scale-up. This critical narrative review integrates primary studies of artificial selection, quantitative genetics and population genomics with research on substrate utilization, nutritional composition and commercialization. A transparent, targeted literature-identification approach and explicit evidence-strength categories distinguish reported results from prospective breeding applications. Direct selection studies demonstrate that larval productivity can respond to breeding, but estimates of heritability vary strongly with trait, design and feeding environment. Full-sibling estimates may confound additive and non-additive components, whereas family/pedigree studies identify substantial common-environment effects and potential inbreeding. Genomic studies indicate that captive lines may lose diversity, creating a rationale for conservation and informed parental choice. Conversely, evidence that controlled inter-line hybrids consistently outperform their best parent under commercial conditions remains limited; heterosis should therefore be treated as a testable hypothesis, not an established outcome. Diet-dependent rankings require multi-substrate trials with appropriate independent rearing replicates. Improved biomass yield must also be evaluated against reproductive fitness, dry-matter nutrient recovery, feed safety and unit economics. A staged breeding-to-market framework is proposed for Nigeria and comparable tropical production systems. The principal priority is reproducible genetic gain with robust controls and documented trade-offs, rather than maximization of a single larval trait.

Index Terms*—Hermetia illucens*, quantitative genetics, selective breeding, heterosis, genotype-by-diet interaction, insect meal, circular bioeconomy

I. INTRODUCTION

Black soldier fly larvae can process suitable organic residues into insect biomass and residual material with potential agricultural value. Their performance, however, is contingent on substrate composition, microbial processes, temperature, density and management (Gold et al., 2018; Barragan-Fonseca et al., 2018). Studies of feed composition further show that the larval nutrient profile cannot be considered invariant across substrates (Spranghers et al., 2017). This makes the insect a promising but biologically variable production organism, rather than a universally efficient waste converter.

The emerging genetic literature changes the central research question. Instead of asking only which substrate or rearing condition produces heavier larvae, industrial programmes can ask which populations possess transmissible merit, whether selected lines remain productive across substrates, and whether improvement persists without compromising reproduction or genetic diversity. Long-term artificial selection has demonstrated improved larval production under industrial conditions (Facchini et al., 2022). More recent studies have estimated genetic parameters using split-family, structured mating and pedigree-informed approaches (Generalovic et al., 2025; Zaalberg et al., 2025; Donkpegan et al., 2026). The challenge is to interpret these findings without confusing phenotypic performance, additive genetic gain and heterosis.

The contribution of this review is a critical genetics-to-commercialization synthesis. It compares what has been directly observed with what remains hypothetical; evaluates differences in experimental designs and traits; and identifies a practical research agenda for substrate-adapted BSF breeding in Nigeria and sub-Saharan Africa.

II. LITERATURE SEARCH AND EVIDENCE APPRAISAL

This article is a structured critical narrative review, not a registered systematic review or meta-analysis. To prepare the manuscript, targeted web-indexed searches were undertaken on 23 October 2026 using combinations of "*Hermetia illucens*", "black soldier fly", "heritability", "selection", "hybrid", "heterosis", "genomic diversity", "domestication", "substrate", "feed safety", "insect meal" and "waste conversion". Search results were followed to publisher pages, DOI landing pages and PubMed records where available. The literature emphasis was 2017–2026, with older foundational studies eligible when relevant. Primary breeding and genomic investigations were prioritized for claims of genetic improvement; reviews were

used principally for substrate, feed and sustainability context.

Eligibility for the core evidence comparison required an identifiable publication, traceable DOI or publisher record, and an outcome relevant to genetic variation, selection response, rearing environment or feed application. Studies were not excluded merely because they contradicted an expected benefit. Evidence was extracted qualitatively by design, population, trait, principal result, interpretive limitation and breeding implication. Claims were classified as (i) directly demonstrated, (ii) supported but context-dependent, or (iii) proposed and requiring validation. No formal dual-reviewer screening, exhaustive database export, PRISMA record counts, risk-of-bias scoring or quantitative meta-analysis was conducted; none is implied. PRISMA 2020 (Page et al., 2021) is cited as a reporting benchmark for any future systematic-review upgrade.

Because the search was targeted rather than exhaustive, the bibliography is a curated set of source-checked studies, not an estimate of the total literature. Study heterogeneity in genetic designs, developmental stages, rearing units and diet definitions precludes meaningful pooling of heritability estimates in this manuscript. The search terms, verification basis and evidence distinctions are disclosed to support reproducibility without inventing database hit counts.

The review addresses five linked questions: (1) which BSF production traits exhibit transmissible genetic variation; (2) what experimental evidence supports realized selection response; (3) what is known—and unknown—about hybrid superiority; (4) how do diets and common rearing environments modify trait expression; and (5) what additional safety and economic evidence is needed before breeding advances can be translated into feed products.

The source manuscript reports a targeted web-indexed search on 23 October 2026 rather than an exported, database-wide search. Its precise platform-specific result sets and screening decisions were not retained. Therefore, a reproducible systematic search, record counts, PRISMA flow diagram and risk-of-bias ratings cannot truthfully be reconstructed. For an independently reproducible update, search Scopus, Web of Science Core Collection, PubMed and CAB Abstracts where institutional access permits; record search date, platform, complete query, filters, records exported, duplicates and exclusion reasons. A proposed core Boolean expression is: ("*Hermetia illucens*" OR "black soldier fly") AND (genetic* OR heritab* OR breed* OR select* OR heterosis OR hybrid* OR genom* OR "genotype by diet"). This is a proposed protocol, not a claim that all databases were searched.

For evidence appraisal, distinguish contemporaneously controlled selection studies from before–after comparisons; pedigree-based additive estimates from full-sib resemblance; observed reciprocal-cross heterosis from theoretical predictions; and controlled animal feeding outcomes from compositional inference. Study-level certainty is lowered by pseudo-replication, unclear pedigrees, shared environments, absence of control lines, missing confidence intervals or unreported substrate composition.

A targeted supplementary search was undertaken on 23 October 2026 using public bibliographic discovery and publisher/PubMed records. Search combinations included "*Hermetia illucens*" or "black soldier fly" with "heritability", "selective breeding", "genetic diversity", "domestication", "genotype by diet", "contaminants" and "animal feed". Source records were checked against journal/DOI landing pages. The new evidence includes Hull et al. (2024), Muchina et al. (2026) and additional contaminant research. This is an updated critical narrative review, not a completed systematic review: database exports, deduplication logs, full-text screening counts and formal risk-of-bias ratings were not generated and cannot be retrospectively asserted.

For a reproducible systematic update, the proposed search string is ("*Hermetia illucens*" OR "black soldier fly") AND (genetic* OR heritab* OR breed* OR select* OR heterosis OR hybrid* OR genom* OR "genotype by diet"). Search Scopus, Web of Science, PubMed and CAB Abstracts where available, record exact database-specific translations, dates, exports, duplicate removals and full-text exclusion reasons. These are recommendations for future work, not searches claimed as completed.

Search transparency: The source article was prepared using targeted web-indexed discovery, not a completed systematic database search. No database exports, duplicate-removal logs, full-text exclusion counts, independent screening or formal risk-of-bias ratings were generated. Thus, this manuscript must be described as a structured critical narrative review; it does not claim PRISMA-compliant systematic-review completion.

III. BIOLOGY, DOMESTICATION AND GENETIC RESOURCES

BSF development includes egg, larval, prepupal, pupal and adult stages. The larval phase supplies harvestable biomass, whereas adult reproduction sustains the breeding nucleus. Accordingly, selection for larval weight is incomplete unless egg production, hatchability, emergence, mating success and survival are considered. An apparent growth advantage may disappear at the enterprise level if the line requires disproportionate breeding space, time or replacement stock. Developmental stage also matters: heavier late-stage larvae are not equivalent to greater dry biomass produced per unit substrate and time.

Captive populations are exposed to founder effects, drift, artificial selection and adaptation to standardized diets. Silvaraju et al. (2026) used genome-wide markers across 11 BSF populations and found differentiation among domesticated and selectively bred lines. This supports the need to record colony origin and manage genetic diversity. It does not establish that the most divergent populations are automatically the best cross parents. Genomic diversity must be linked to replicated productivity and reproductive data before assigning breeding value. Genetic-resource

conservation should retain wild-derived reference material where collection is lawful and biosecure, while avoiding unassessed movement of insects across ecological boundaries.

The primary evidence illustrates that genomic differentiation and performance selection are distinct outcomes. Hull et al. (2024) examined early domestication under selected and non-selected breeding strategies using 2bRAD-derived genome-wide SNPs alongside production and fitness phenotypes. Its three-generation comparison is valuable because it links molecular variation to observed selection conditions, but the short timeframe and drift mean that neither sustained improvement nor general inbreeding depression can be inferred solely from diversity changes. This contrasts with purely cross-sectional population surveys, which identify genetic structure but cannot isolate the causal effects of selection.

IV. MOLECULAR CHARACTERIZATION AND GENETIC DIVERSITY

Mitochondrial markers can support species confirmation and maternal lineage tracing but are insufficient for genome-wide relatedness. Microsatellites and SNPs are more useful for estimating population structure, heterozygosity, kinship and inbreeding. Restriction-site-associated sequencing can supply broad marker coverage at lower cost than deep whole-genome sequencing, although marker ascertainment, missing data and laboratory batch effects must be controlled. Marker choice should follow the biological decision: detecting distinct source populations, reconstructing pedigrees, estimating inbreeding or developing prediction models. A dense marker panel does not compensate for weak phenotyping.

Principal component analysis, ancestry models and genetic-distance measures identify population differentiation, not heterosis. Genetic distance may help avoid closely related crosses, but superiority of F1 offspring depends on dominance, epistasis, allele frequencies and trait-specific parental combinations. A rigorous pipeline therefore first characterizes source populations, then measures phenotypes in a common garden, and finally tests planned crosses against both parental lines under matched rearing conditions. Selection decisions should also consider disease status and colony reproductive capacity.

Hull et al. (2024) used 2bRAD SNPs to compare selected and unselected lines over three generations. Larval mass increased under selection while genomic diversity declined, illustrating the tension between short-term production gains and long-term fitness. The brief duration and founder effects limit inference about sustained genetic gain. Silvaraju et al. (2026) identified rapid differentiation among 11 captive and wild-derived populations, while Muchina et al. (2026) reported global geographic structure and pronounced captive bottlenecks from genome-wide data. The three studies differ in sampling breadth and design but converge on the need for larger breeding nuclei and periodic diversity surveillance. None demonstrates commercial heterosis.

In the original domestication study, Hull et al. (2024) examined selected and non-selected lines during early captive generations. This direct comparison helps connect breeding practice with genomic diversity; however, genome-wide variation is not itself a measurement of additive genetic merit. Its value to the present review lies in the caution that phenotypic gains should be evaluated together with founder representation, genetic drift and reproductive performance, rather than assuming that a larger larva necessarily indicates a genetically sustainable line.

V. QUANTITATIVE GENETICS AND SELECTIVE BREEDING

Heritability is specific to the population, trait and environment under investigation. Generalovic et al. (2025) reported approximate full-sib-derived values of 0.67 for larval and 0.78 for prepupal body size, while explicitly warning that non-additive genetic effects may inflate narrow-sense interpretation. Zaalberg et al. (2025) reported moderate heritability for individual and group larval size, around 0.30–0.40, and noted common-environment effects. Donkpegan et al. (2026) found much lower estimates for some larval-weight traits (0.12–0.13), but a higher estimate under restricted feeding (0.58), with substantial shared-environment variance. These results are not mutually contradictory: they use different traits, designs, populations and conditions.

It is therefore inappropriate to average the published estimates into a single “BSF heritability” or predict uniform selection gains. For breeding, variance components should ideally be estimated with models that separate additive genetic, maternal or family, batch and residual effects, with confidence intervals and pedigree quality documented. Traits such as reproductive output and dry protein yield require their own estimates rather than inference from body size.

Facchini et al. (2022) demonstrated long-term artificial selection for larval body weight in industrial settings, with improvements extending beyond individual larval size to production metrics under some conditions. However, responses should be interpreted relative to the experimental comparator and management regime. Donkpegan et al. (2026) subsequently evaluated pedigree-informed selection across seven selected generations and found indications of gain, while acknowledging the absence of a contemporaneous control line and risks from inbreeding. Such limitations matter because environmental trends can masquerade as genetic improvement.

A commercial selection index should weight traits by economic value, including dry biomass yield, usable protein yield, survival, developmental time, egg output and costs. When genetic correlations are uncertain, index weights and projected gains should be subjected to sensitivity analysis. A preserved, periodically tested control population is essential to distinguish selection response from year, batch or substrate effects.

A multi-trait breeding objective is more defensible than selection solely for wet larval weight. An economic index could include dry biomass output per unit time, dry protein recovery per kilogram substrate, survival, egg yield, hatchability, feed-safety compliance and processing costs. Index weights must be justified from observed prices or marginal production values, not assigned arbitrarily. Estimated breeding values can combine phenotypes, pedigrees and fixed environmental effects; their reliability depends on family structure and measurement quality.

Donkpegan et al. (2026) reported larval stage-2 weight heritability of 0.13 ± 0.04 under standard feeding versus 0.58 ± 0.03 under restricted feeding, and oocyte-number heritability of 0.43 ± 0.09. Their observed trait-dependent genetic correlations caution that selection for larval mass can change reproductive traits. The absence of a contemporaneous unselected line also prevents attributing all temporal change to genetics. Inbreeding monitoring and periodic benchmarking against a preserved reference line are essential.

TABLE I
COMPARISON OF GENETIC EVIDENCE, WITH STUDY-SPECIFIC LIMITATIONS

Study	Evidence / estimate	Design limitation
Facchini et al. (2022)	Long-term artificial selection for larval body weight	Response depends on comparator and management
Generalovic et al. (2025)	Body-size estimates approximately 0.67–0.78; diet interaction	Full-sib resemblance can include non-additive/shared effects
Zaalberg et al. (2025)	Larval-size h^2 approximately 0.30–0.40	Common rearing environment
Donkpegan et al. (2026)	Trait-specific h^2 0.006–0.58; seven selected generations	No contemporaneous unselected control
Hull et al. (2024)	Selection-associated mass gain and diversity change	Short study; founder effects

The strongest recent quantitative-genetic comparison involves three different designs. Generalovic et al. (2025) first compared three strains across three diets using 18 families and 5,022 individuals; its second experiment included 23 families and 4,018 individual body-size measurements. Full-sib-derived heritability estimates were 0.674 ± 0.049 for larval and 0.782 ± 0.030 for prepupal size. Because full-sibling resemblance may contain dominance and common-environment effects, these values should not be interpreted as universally applicable additive heritabilities. In contrast, Donkpegan et al. (2026) phenotyped 15,179 individuals from 266 full-sib isofamilies and used multivariate REML animal models with BLUP breeding values. Estimated heritabilities were 0.12 ± 0.08 for first-stage larval weight, 0.13 ± 0.04 for second-stage larval weight, 0.58 ± 0.03 under restricted feeding, 0.43 ± 0.09 for oocyte number and 0.40 ± 0.09 for thorax size. These contrasting values reflect differences in traits, environmental regimes and statistical designs; numerical averaging would be biologically misleading.

Donkpegan et al. (2026) additionally reported trait-dependent genetic correlations, including positive relationships of larval body-weight traits with thorax size and oocyte number and a negative relationship with female emergence body weight. The seven-generation selection programme provided indicative genetic improvement but lacked a contemporaneous unselected control, so management trends cannot be excluded. Facchini et al. (2022) provides complementary direct evidence from long-term industrial selection for increased larval body weight. Together, these studies justify multi-trait selection indices and maintained reference lines, not selection on wet larval weight alone.

VI. HYBRID BREEDING AND HETEROSIS

Hybrid breeding is distinct from selecting superior individuals within a population. To demonstrate heterosis, researchers must produce identifiable inter-line F1 families, maintain pure parental comparators and test all groups in a randomized common environment. Reciprocal crosses (A♀ × B♂ and B♀ × A♂) are valuable for identifying maternal or reciprocal effects. Multiple independently produced mating groups are needed; numerous larvae from one cross cage are subsamples, not independent genetic replicates. Genetic markers can help verify parentage when group mating is unavoidable.

Mid-parent heterosis (%) = 100 × [F1 − (P1 + P2)/2] / [(P1 + P2)/2]. Better-parent heterosis (%) = 100 × (F1 − Pbest)/Pbest. For traits where smaller values are desirable (e.g., development time), the direction of improvement must be stated explicitly. General combining ability reflects average parental performance across crosses, while specific combining ability reflects deviations associated with particular combinations; both require adequate mating designs and replication. Crosses should be evaluated for larval dry biomass, substrate utilization, adult fertility and total production cost rather than wet larval mass alone.

The source-verified studies considered here establish genetic variation and selection potential, but do not collectively demonstrate reliable, repeatable best-parent heterosis in commercially deployed BSF hybrids. It would therefore be misleading to present elite hybrid performance as an established technology. A credible programme should first compare inter-line F1 crosses with the best available selected pure lines and then retest promising combinations over production batches and substrates. Only crosses with repeatable gains and manageable parental multiplication costs warrant commercialization.

The evidence for hybrid vigour remains substantially weaker than that for within-line selection. Neither the industrial selection programme of Facchini et al. (2022) nor the pedigree-based selection of Donkpegan et al. (2026) directly estimates better-parent heterosis from replicated reciprocal F1 crosses. Likewise, genetic differentiation in domestication surveys is not evidence that crosses between divergent lines will exceed their better parent. Consequently, the relevant result of the present evidence synthesis is an identified experimental gap: validated BSF hybrid superiority cannot be inferred from selection response,

population differentiation or full-sib heritability. A definitive study must independently reproduce A×B and B×A crosses, include both pure-line comparators, measure reproductive and dry-matter yield traits and calculate uncertainty around better-parent contrasts.

VII. GENOTYPE-BY-SUBSTRATE INTERACTIONS AND WASTE CONVERSION

A genotype-by-substrate interaction exists when the relative performance of strains changes with the substrate environment. Generalovic et al. (2025) observed strain-by-diet effects for larval weight, development, viability and protein content. However, not all production endpoints displayed equivalent interactions. Consequently, evidence for diet-specific growth advantage should not be converted into a blanket claim of superior waste reduction. Genetic gain measured on a high-quality laboratory diet may fail to translate to variable agro-industrial residues.

Substrate nutrient density, water content, microbial activity and larval density affect growth and composition (Gold et al., 2018; Barragan-Fonseca et al., 2018). Spranghers et al. (2017) showed that substrates can change lipid and ash fractions substantially even when crude protein differences are comparatively modest. A robust multi-substrate trial should standardize starting dry matter, larval age, density and feeding schedule, and report substrate pH, moisture and proximate composition. Substrate batches and rearing containers must be represented as independent experimental factors where appropriate.

Wet-mass waste reduction is an inadequate sole metric because evaporation and microbial respiration can lower substrate mass without creating harvestable insect protein. Dry-matter reduction, biomass conversion, survival, development time and recovered protein should be jointly reported, with clear definitions and mass-balance boundaries. Breeding for broad adaptation requires stable performance across representative substrates, whereas specialist lines may be useful when one consistent industrial side-stream dominates. Mixed-effects models can estimate genotype, substrate and interaction effects, with independent containers nested in batch and family where necessary.

For interpretation, each independent rearing container constitutes an experimental unit; individual larvae sharing a tray are subsamples. Strain × substrate tests require independent families, characterized substrate batches, dry-matter mass balances and repeated production runs. Mixed-effects models should distinguish family, batch, substrate and genotype × substrate terms.

Generalovic et al. (2025) provides direct evidence that genotype-dependent productivity can change with diet. In the larger split-brood experiment, the strain-by-diet term for larval weight was significant ($F_{2,42} = 4.6$, $p = 0.016$), while protein content showed a strain-by-diet effect ($\chi^2_2 = 10.1$, $p = 0.006$). In contrast, waste reduction was associated with diet ($\chi^2_2 = 33.1$, $p = 6.4 \times 10^{-8}$) without a corresponding major strain effect in that experiment. These outcomes are especially important: a strain that produces heavier larvae on one substrate cannot automatically be described as superior in waste conversion. The experiments establish diet-dependent differences in tested populations, not universal superiority across agricultural residues. Production comparisons should therefore report independent containers, substrate dry matter, harvested dry larval mass, survival, development time and nutrient recovery.

VIII. NUTRITIONAL QUALITY, FEED SAFETY AND ANIMAL APPLICATIONS

BSF meal may supply valuable amino acids and lipids, but nutrient composition is affected by substrate, developmental stage and processing (Spranghers et al., 2017; Rossi et al., 2025). Crude protein calculated from total nitrogen may overstate digestible true protein because chitin-associated and other non-protein nitrogen contribute to the assay. Genetic selection for larger larvae must therefore be evaluated against dry protein yield, amino acid digestibility and processing recovery, not only proximate percentage.

Ingredient-replacement trials should distinguish replacement of fishmeal mass from replacement of fishmeal-derived digestible protein. Diets should be formulated to comparable energy and amino acid specifications, with pen or tank—not individual animals within the same unit—treated as the independent feeding-trial replicate. Outcomes should include intake, growth, feed conversion, survival, relevant health indices and product quality. Results from one species or life stage should not be generalized to others. A positive feeding result also does not independently establish superior breeding genetics; it demonstrates performance of a particular processed meal in a specified diet.

The safety of BSF meal depends on the complete substrate-to-product chain. Chemical contaminants, microbiological hazards, substrate eligibility, processing and storage require validation (Rossi et al., 2025). African production reviews have highlighted gaps in substrate screening and risk management. Any breeding-to-feed programme must establish feedstock traceability, exclusion criteria for hazardous residues, testing schedules and product specifications. Biological capacity to consume a waste stream must never be equated with permission or safety to convert it into animal feed.

Feed evidence must be separated from genetic evidence. Reviews of BSF meal and substrate-dependent nutritional composition do not show that a selected or hybrid BSF line improves poultry or fish growth. Any such claim requires genetically defined insect meals, comparable processing, appropriately balanced diets and independent pen or tank replicates.

Contaminant accumulation, particularly for certain metals, is substrate-dependent. The manuscript's previously unspecified 2017 exposure-study claim has been omitted

pending an exact primary citation; no claim of universal feed safety is justified.

The direct genetic studies do not establish that meal from improved BSF strains produces superior poultry or fish performance. Facchini et al. (2022) evaluated larval selection, Generalovic et al. (2025) investigated strain-by-diet and body-size genetics, and Donkpegan et al. (2026) estimated growth and reproductive genetic parameters; none is a genetically controlled animal feeding trial. Published nutrient-composition and feeding studies may justify the application of BSF meal, but this is a separate inference from improvement of insect genetics. Claims of animal-performance advantages require parallel meal production from genetically characterized lines, comparable processing, balanced dietary treatments and pen- or tank-level replication.

IX. INDUSTRIAL PRODUCTION, ECONOMICS AND ENVIRONMENTAL ASSESSMENT

An elite nucleus line is commercially useful only when its identity and performance can be maintained during multiplication. Practical controls include mating records, breeder population size, routine genomic or pedigree checks, egg-quality monitoring and production benchmarking. Large-scale rearing introduces spatial gradients, fluctuating feedstock quality and operational constraints that may obscure laboratory gains. Pilot validation should therefore use repeated production cycles with contemporaneous control lines.

Commercial viability should be expressed as cost per kilogram of dried insect meal or usable protein, rather than yield per tray alone. A techno-economic model should account for feedstock acquisition and preprocessing, breeder maintenance, electricity, labour, drying, quality testing, packaging, transport and saleable coproducts. Scenario analysis is required because higher biological yield may be offset by costly specialized substrates or reduced egg productivity. Intellectual-property decisions should distinguish protectable breeding know-how from naturally occurring genetic diversity and should respect relevant institutional and national rules.

Circular-economy claims depend on the counterfactual. Environmental benefits vary with the original waste-management pathway, electricity mix, transport distance and the conventional feed ingredient displaced (van Huis & Oonincx, 2017; Surendra et al., 2020). A life-cycle assessment should specify system boundaries and functional units and avoid assuming that every kilogram of diverted waste yields the same climate benefit. Breeding outcomes should be linked to dry-matter nutrient recovery and resource inputs per unit product.

Evidence for breeding-related improvements must be translated into operational outcomes using comparable functional units. Larval body weight, dry larval biomass per unit input substrate, recoverable digestible protein and production cost per kilogram of compliant meal are different endpoints. The quantitative-genetic literature cited above establishes neither a fixed percentage reduction in Nigerian feed costs nor a life-cycle environmental advantage. Such claims require replicated pilot-scale production, measured energy and labour inputs, documented substrate counterfactuals, contaminant testing and appropriate feed-trial evidence. The priority is therefore to connect demonstrated genetic responses to these independent commercial and environmental tests.

X. EVIDENCE GAPS AND RESEARCH PRIORITIES

Four evidence gaps are particularly consequential. First, quantitative genetic estimates differ sharply across methods and traits, calling for replicated pedigree or genomic designs with shared-environment effects modeled explicitly. Second, selection studies need maintained controls and estimates of correlated reproductive responses. Third, the generality of F1 heterosis remains uncertain, requiring reciprocal crossing and better-parent comparisons. Fourth, many studies report larval weight without simultaneous measures of safe protein yield, waste conversion and profitability. These gaps should shape experiments rather than be obscured by optimistic claims.

Genomic selection may improve accuracy when sufficient genotyped and phenotyped reference populations exist, but prediction accuracy across diets and generations must be demonstrated. Automated imaging can increase phenotyping throughput, provided measurements are calibrated against mass and developmental stage. In resource-limited programmes, reliable phenotyping, randomized trials, colony records and representative sampling are higher priorities than acquiring advanced genomic technology without a clear breeding decision.

A staged Nigerian breeding programme could first sample and conserve BSF germplasm from representative agro-ecological zones; second, phenotype candidate colonies under common conditions; third, estimate family-level genetic parameters and test reciprocal crosses; fourth, evaluate promising lines across safe local agro-industrial substrates; and fifth, conduct feed-safety, poultry/aquaculture and pilot-economic validation. Potential substrate streams include rice bran, brewery spent grain and appropriately screened food-processing residues, but their availability, legality and contaminant profiles must be established locally. Stakeholder participation is necessary to identify affordable feedstock streams, realistic market specifications and commercialization constraints.

XI. CONCLUSION

The evidence for genetic improvement of BSF is now substantial enough to justify structured breeding, but not strong enough to justify unqualified claims of commercial hybrid superiority. Artificial selection has produced measurable responses; quantitative-genetic analyses reveal exploitable but environment- and design-dependent variation; and population genomics documents differentiation and risks associated with captive breeding.

The central next step is a controlled comparison of selected pure lines and verified hybrids across substrates, accompanied by reproductive, nutritional, safety and economic outcomes. For Nigeria, the most defensible route is an integrated programme that preserves diversity, estimates genetic merit rigorously, and advances candidate strains only after multi-stage validation. This evidence-led approach can make BSF breeding scientifically credible and commercially relevant without overstating current knowledge.

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CONFLICTS OF INTEREST STATEMENT

The author declares no conflict of interest.

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