

INTEGRATING GENOMIC SELECTION, GENE EDITING AND AI FOR NEXT-GENERATION INSECT-RESISTANT CROP BREEDING: A REVIEW

Dr. Ranveer M. Pawar^{1*}, Dr. Sakshi Bajaj², Dr. Padmini Das³, M.Devendran⁴, Dr. Vandana Shukla⁵, Dr. B. Rama Devi⁶, Dr. Rajumari⁷, Dr. Ajeet Pratap Singh⁸, Dr. Nishikanta K⁹, Dr. Biju Sidharthan¹⁰

¹Vice Principal (Academics), Department of Agricultural Botany, Bharati Vidyapeeth's Loknete Mohanrao Kadam College of Agriculture, Kadegaon, Maharashtra, India.

²Assistant Professor, Department of Agronomy, RSVARS, Bemeta IGKV, Raipur Chhattisgarh, India.

³Scientist, Department of Plant Breeding and Genetics, AAU-ZRS, Shillongani, Nagaon, Assam, India.

⁴Assistant Professor, Department of Artificial Intelligence and Data Science, Hindustan Institute of Technology, Coimbatore, India.

⁵Assistant Professor, Department of Plant Pathology, Ramprasad Potai College of Agriculture and Research Station, Singarbhat, Kanker, IGKV, Chhattisgarh, India.

⁶Assistant Professor, Department of Agronomy, College of Agriculture, Koneru Lakshmaiah Education Foundation, KL University, Vadheswaram, Guntur, Andhra Pradesh, India.

⁷Guest Lecturer, Department of Entomology, Mahatma Gandhi Udyanik Evam Vanik Vishwavidyalaya, Durg, Chhattisgarh, India.

⁸Assistant Professor, Department of Genetics and Plant Breeding, Shri Durga PG College Chandeshwar Azamgarh Uttar Pradesh affiliated MSDU Azamgarh, India.

⁹Assistant Professor, Department of Zoology, Dhanamanjuri University, Imphal West, Manipur, India.

¹⁰Scientist, Department of Plant Breeding and Genetics, College of Agriculture, Vellanikkara, Thrissur 680656, Kerala Agricultural University, Kerala, India.

*Corresponding Author: Dr. Ranveer M. Pawar E-mail: ranveerpawar1972@gmail.com

ABSTRACT

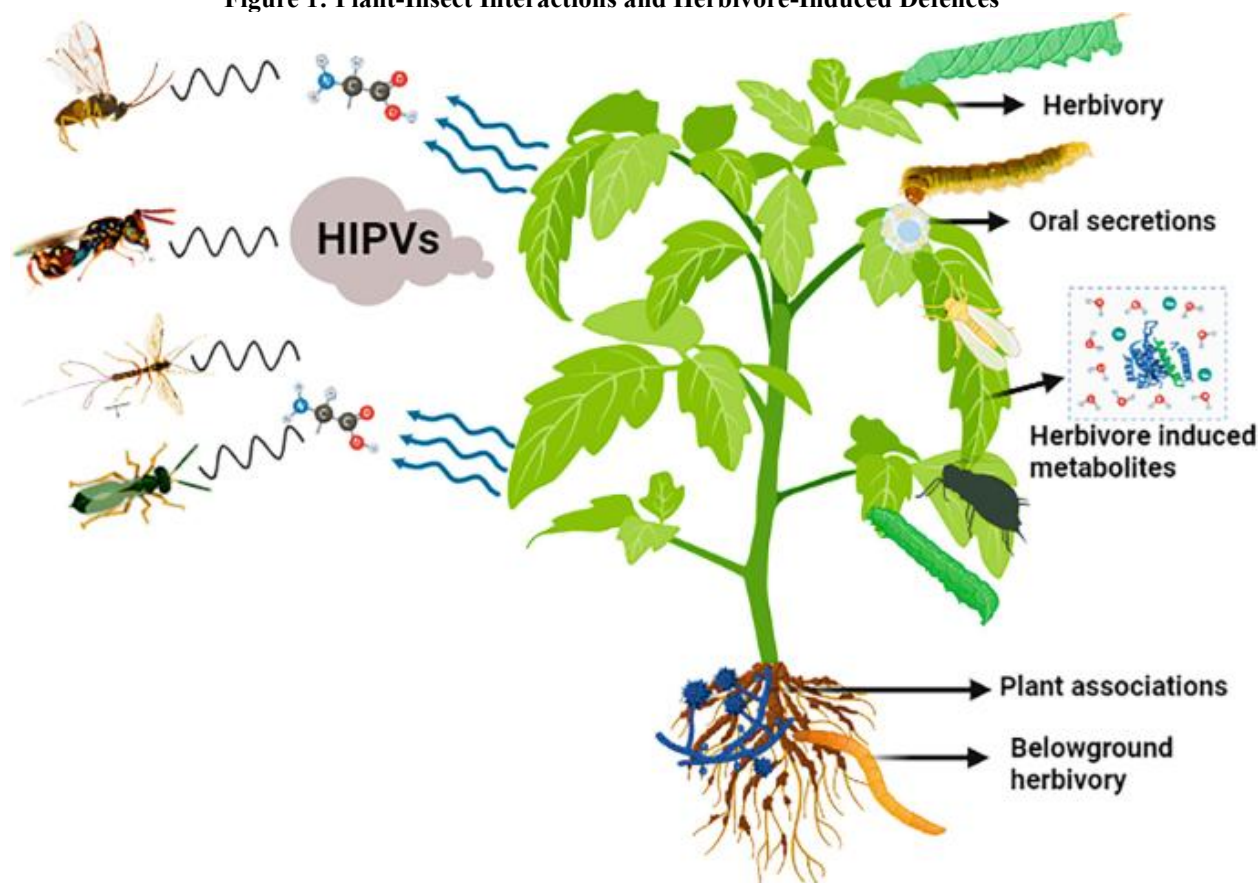
Insect pests continue to be a significant factor limiting agricultural production, its profitability and world food security, and these are becoming more difficult to manage with climate change, increasing international trade and resistance to pesticides. Conventional resistance breeding has produced valuable cultivars, but its success is frequently limited by long breeding cycles, challenging phenotyping, polygenic inheritance, linkage drag and rapid evolution in insect populations. The integration of genomic selection, gene editing, and artificial intelligence offers a comprehensive approach to produce insect-resistant crops faster, with higher precision, and ensuring durability. Genomic selection can estimate the genetic value for untested individuals based on genome-wide markers, gene editing can target resistance or susceptibility genes directly, and artificial intelligence can identify relevant information within genomic, phenomic, environmental, and entomological data. Combined, these techniques may enhance parent selection, cross design, editing-target identification, resistance phenotyping, and prediction by environment. Nevertheless, the effective implementation depends on having representative training populations, on efficient transformation systems, on robust field validation, on responsible data governance and on biosafety assessment and on accurate resistance stewardship. Here we review the basic concepts, current applications, constraints and future opportunities of the combined technology in the breeding of next-generation insect-resistant crops.

KEYWORDS: Artificial intelligence, crop improvement, genomic prediction, host-plant resistance, insect pests, machine learning, precision breeding

1. INTRODUCTION

Insect pests cause crop damage by direct feeding, sap extraction, tissue mining, gall formation, contamination and transmission of plant pathogens. This can result in more than just visible yield reduction; infestation can also reduce the quality of the product, seed viability, market value and storage life. For many years, farmers have depended on synthetic insecticides, but repeated use can increase production costs and can select for insect populations that are resistant, can kill beneficial organisms, can pollute the ecosystem and can put agricultural workers at risk (Stout *et al.*, 2024). Host-plant resistance is a more prophylactic and cost-effective form of crop protection as the defensive trait is intrinsic to the plant. However, it is challenging to breed for durable resistance as insects are genetically diverse, highly motile and rapidly evolving organisms, which can quickly overcome plant defences (Kumari *et al.*, 2022). Expression of resistance may also be influenced by stage of host development, pest biotype, temperature, nutrition, water stress and interaction with other beneficial organisms. Therefore, the next-generation resistant cultivars have to be developed as a dynamic defensive system instead of the reliance on a single resistance gene (Li *et al.*, 2024).

Figure 1: Plant-Insect Interactions and Herbivore-Induced Defences



Source- Kumaraswamy *et al.*, 2024

Traditional breeding has detected valuable resistance sources in landraces, wild relatives and adapted germplasm, however, the introgression of the traits into elite cultivars may take the form of many generations of crossing and selection. High-impact resistance genes can occasionally be manipulated efficiently by marker-assisted selection, but similarly to classical breeding approaches, enhancing quantitative resistance governed by many minor-effect loci by means of a few markers is challenging (Parveen *et al.*, 2023). Genomic selection overcomes this limitation by estimating overall genetic merits based on genome-wide marker information (Kumar and Furlong, 2024). Other advantage-level of precision is due to the fact gene editing allows breeders to knock-out susceptibility genes, alter regulatory regions, mimic beneficial alleles or make precise edits to elite germplasm. Artificial intelligence connects all these possibilities by processing large and disparate datasets, and reveals connections that can be missed by formalized methods. Their convergence offers a prospect to shift from a reactive breeding, where plants are selected post significant insect damage, to a predictive breeding, where genotypes, crosses and molecular interventions are chosen based on expected pest threats and future production environments (Tuncel *et al.*, 2025).

2. The Biological Complexity of Insect Resistance

2.1 Mechanisms of Host-Plant Resistance

Plant resistance to insect pests is generally expressed as antixenosis, antibiosis and tolerance, and these mechanisms often interact within the same plant genotype. Antixenosis is where the plant deters insect colonization, feeding or oviposition through its physical attributes, such as surface characteristics, colours, odours, waxes, trichomes or chemical profile (Gebretsadik *et al.*, 2025). Antibiosis reduces insect survival, growth, development or reproduction once the pest starts feeding. This can be due to toxic secondary metabolites, proteinase inhibitors, lectins, defensive proteins, induced enzymes or nutritional imbalances (Leybourne and Aradottir, 2022). Tolerance is when the plant is able to sustain acceptable growth and yield levels in the presence of insect damage by compensating through tillering, branching, photosynthetic regulation, resource remobilization or rapid tissue regeneration. Genes and signalling pathways interact to mediate these mechanisms, which do not function in isolation. A resistant plant may sense insect-derived molecules, produce calcium and reactive-oxygen signals, activate jasmonate or salicylate-associated pathways and finally produce defensive compounds. Thus, the final phenotype is a consequence of the integration of many processes, from pest recognition to cellular signalling, metabolism, tissue architecture and whole-plant recovery (Wang *et al.*, 2023).

2.2 Influence of Insect Biology and Feeding Behaviour

Resistance expression is highly dependent on the physiology and feeding habits of the target insect. Chewing caterpillars, beetles, and grasshoppers produce significant mechanical injury and introduce oral secretions to the

injured plant tissues, while aphids, whiteflies, planthoppers and other piercing-sucking insects extract phloem or xylem sap and manipulate living cells (Kallure *et al.*, 2022). Stem borers, fruit borers, leaf miners, and gall formers feed at sites that provide some protection from insecticides and natural enemies. Some insects inject effectors that suppress plant immunity or alter nutrient allocation, while others bear microorganisms that alter plant responses or aid digestion (Pirttilä *et al.*, 2023). Resistance effective for one type of feeding guild could be irrelevant for another, and boosting one defensive pathway can, in some cases, increase susceptibility in another. Breeding decisions have to take pollinators, parasitoids, predators, and non-target herbivores along the way. A cultivar that is active against a major pest and conserves beneficials is ecologically more useful than one exhibiting broad spectrum biological toxicosis without adequate selectivity (Blanchard and Holeski, 2024).

3. Why Conventional and Marker-Assisted Breeding Are Not Enough

Conventional breeding is still required as it generates recombination, assesses whole-plant performance and produces cultivars adapted to farmers environments. These have the potential to be limiting, especially for traits that are polygenic, recessive, developmentally regulated or strongly influenced by the environment (Mohanavel *et al.*, 2024). For accurate insect screening, a well-synchronized pest colony, controlled infestation, replicated field nurseries and measurement of both plant damage and insect performance (Wani *et al.*, 2022) may be needed. Escape from infestation can be mistaken for genetic resistance, while high pest pressure can hide moderate but agriculturally relevant variation. Introgressing genes from wild relatives can bring undesirable traits such as reduced yield, poor quality, late maturity or plant architecture. Recombination is then needed to break the linkage between resistance alleles and negative traits, adding time to the breeding programme. The time taken to combine resistance with commercially acceptable productivity and quality can be a particularly limiting factor in perennial crops, clonally propagated species and crops with long generation intervals (Bohra *et al.*, 2022).

Marker-assisted selection enhanced the efficiency of breeding by allowing plants to be chosen based on markers associated with major resistance genes or quantitative trait loci. It is still very effective for foreground selection, gene pyramiding and removing unwanted donor chromosome segments (Sowmiya *et al.*, 2024). But a few markers only explain a small fraction of the variation of complex quantitative resistance. Genes for resistance identified in one population may have a lower effect in another genetic background or against a different pest population (Alemu *et al.*, 2024). The mapping resolution may also be too low to distinguish a causal gene from its neighbouring genes. Since insect resistance is often controlled by many small-effect alleles, epistasis and genotype-by-environment interaction, selection of only significant markers can result in loss of important genome-wide information. Genomic selection, high-throughput phenotyping and gene editing do not replace marker-assisted breeding; rather, they augment it by including polygenic traits, increasing the resolution of traits and adding the ability to precisely manipulate the traits once beneficial resistance mechanisms have been identified (Mascher *et al.*, 2024).

4. Genomic Selection for Quantitative Insect Resistance

4.1 Training Populations and Resistance Phenotyping

Genomic selection estimates genomic breeding values by modeling genome-wide marker effects joint in a training population with both genotype and phenotype information. After training the prediction model, selection candidates may be ranked on the basis of marker data without having to expose each one to insects in each breeding round (Gesteiro *et al.*, 2023). This is especially useful if resistance testing is destructive, costly, seasonal or difficult to standardize (Chen *et al.*, 2024). Damage scores, pest survival, larval weight, number of adult, fecundity, feeding behaviour and crop yield under infestation can be considered in prediction models. Rather than only breeding for less injury visible, farmers can calculate resistance indices that include pest suppression, crop tolerance, yield stability, and agronomic quality. Genomic selection thus enables the development of complex resistance and multi-trait improvement, including maturity, product quality and environmental adaptation. The main benefit lies in increasing the accuracy and intensity of selection in the early generations and at the same time shortening the cycle duration in breeding (Joukhadar *et al.*, 2024).

Prediction accuracy is a function of the size and the quality and relatedness of the training population. The training set should capture the genetic diversity, population structure, pest biotypes, and environmental factors that one expects to see in future candidates for selection. Prediction and training populations that are more closely related will likely result in greater accuracy due to more stable marker-trait associations (Beaulieu *et al.*, 2024). Nevertheless, models developed for a specific lineage may have limited predictive power when used to assess very different germplasm or advancing generations (Chiaravallotti *et al.*, 2024). Updated training populations should thus be selected strategically to incorporate individuals that increase the genetic, phenotypic, or environmental space. Historical breeding data could be used to offer a cost-effective starting point, but scoring systems that are inconsistent, shifting pest pressure and experimental records that are incomplete will need to be addressed. Advanced experimental designs, replicate checks and spatial adjustment enhance the quality of phenotypes. Genotyping costs may be reduced with the use of low pass sequencing, genotype imputation, and judiciously chosen marker panels, if marker density is sufficient to capture linkage disequilibrium as well as any major resistance alleles (Yeon *et al.*, 2024).

4.2 Prediction Models for Complex Resistance

Genomic prediction methods exhibit certain advantages and disadvantages for breeding insect resistance. Genomic best linear unbiased prediction provides a strong baseline when many causal loci have small additive effects, and Bayesian methods can handle mixtures of large and small marker effects (Meher *et al.*, 2022). Kernel methods can model nonlinear genomic relationships, and machine-learning methods can model higher-order interactions if sufficient training data are acquired. Multi-trait models improve accuracy by borrowing information from correlated characteristics such as trichome density, lignin content, defensive metabolites, insect growth rate or canopy recovery (Lee *et al.*, 2024). Multi-environment models also distinguish between generally stable resistance and location, season, or pest population-specific responses. Known resistance genes can be treated as fixed effects, while the rest of the polygenic background is predicted with genome-wide markers. This combined approach is necessary because major genes may confer a strong defense, but minor alleles may modify their expression, agricultural cost and longevity. Genomic selection can thus bring together a supportive genetic background for big resistance factors instead of viewing individual genes as the entire solution (Piepho and Williams, 2024).

5. Building Durable Resistance Through Genomic Prediction

Durability should be considered a quantifiable breeding goal, not a characteristic by default of a resistant genotype. The use of a single recognition gene/t oxin can result in intense selection for pest populations to evade that defence (Tabashnik *et al.*, 2023). Genomic-selection programs can mitigate this risk, by pyramiding mechanisms with different mode of actions (Kennedy *et al.*, 2023). For instance, antixenosis may reduce colonization, antibiosis may retard insect development, and tolerance may allow for percentage of yield loss in infested plants. Selection indices can also apply appropriate economic weight to these components and to correct for the unfavorable correlations they have with yield, maturity, or quality. Genomic prediction may also facilitate the identification of crosses with a high probability of generating progeny carrying complementary resistance alleles, while maintaining an adequate level of genetic diversity. Balancing short-term genetic gain against long-term inbreeding may also be desirable in optimal-contribution selection to avoid that the resistance base becomes concentrated in very few, highly related parents (Allier *et al.*, 2020).

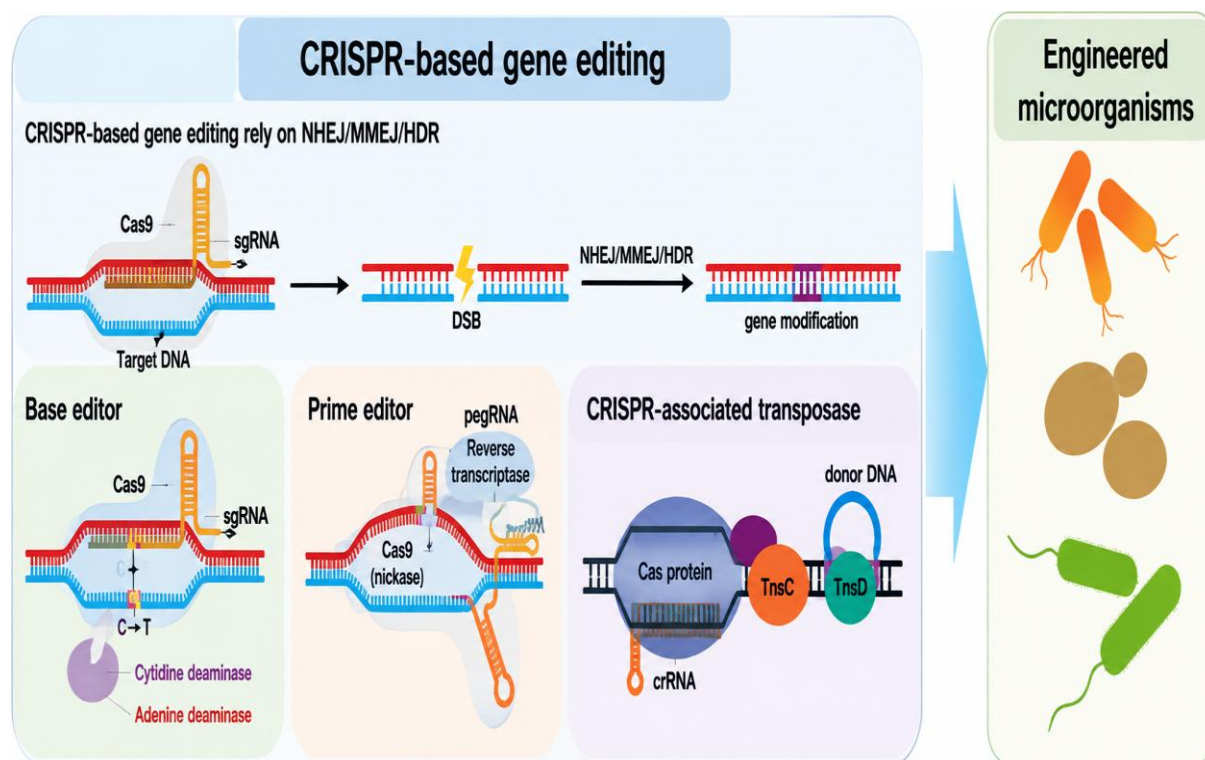
Resistance must also be assessed among pest populations and within production systems. Biotypes of a single insect species may differ in virulence, host preference, ability to detoxify or tolerate defensive compounds. Thus a cultivar selected for resistance against one laboratory population may not perform when released into a wider geographical area. Representative pest collections, panels of well-characterized biotypes or controlled mixtures of populations should be used to evaluate training populations whenever biosafety regulations allow (Jaganathan *et al.*, 2026). Both average resistance and environmental stability can then be estimated using reaction-norm and multi-environment genomic models. Temperature, humidity, soil moisture, planting date and crop nutrition can be included as covariates to account for variation in resistance expression. This method is becoming more relevant with climate change, as warming can influence insect growth, movement, overwintering and the timing of crop-pest interactions. A next-generation cultivar needs to be effective not only against current pest populations, but also under projected future infestation profiles and environmental conditions (Toda *et al.*, 2024).

6. Gene Editing as a Precision Resistance Tool

6.1 CRISPR Systems and Advanced Editing Technologies

Gene editing enables breeders to introduce targeted changes at specific sites in the genome, generating valuable variation without having to repeatedly cross an elite cultivar with a genetically distant donor. CRISPR-associated systems are particularly powerful because guide RNAs can be used to aim the editing machinery at selected DNA sequences (Dhugga, 2022). The simplest applications generate small insertions or deletions that interrupt gene function, while newer methods allow more controlled nucleotide substitutions, short sequence replacements, and simultaneous modification of multiple targets (Molla *et al.*, 2021). Base editing can modify specific nucleotides without causing a traditional double-strand break, and prime editing offers more options for precise substitutions and small insertions or deletions. Multiplex editing can target multiple members of a gene family or different defence pathways in a single transformation event. These technologies expand breeding beyond the transfer of existing alleles by allowing researchers to recapitulate naturally advantageous alleles, remove deleterious sequences, control gene expression and combine defence-related changes that are hard to achieve through recombination alone (Zhou *et al.*, 2019).

Figure 2: CRISPR-Based Gene Editing Strategies and Their Applications in Microbial Engineering



Source- Wei and Li, 2023

6.2 Editing Susceptibility and Defence Pathways

One of the main approaches is editing plant susceptibility genes that insects use for feeding, nutrient acquisition, colonization or to suppress immunity. However, complete gene disruption can cause a severe growth penalty when the same gene has important physiological functions. Thus, tissue-specific, inducible or promoter editing may offer a more refined strategy, by only reducing susceptibility to pests where and when they attack (Sun *et al.*, 2024). Gene editing can also improve defence recognition, signalling and metabolic pathways that make phenolics, terpenoids, glucosinolates, alkaloids, proteinase inhibitors and defensive volatiles. Other targets are structural traits like cuticle thickness, silica deposition, cell-wall composition and glandular trichomes. All modifications need to be evaluated at the whole-plant level, as enhanced defence may come at the cost of reduced growth, reproduction, nutritional value or marketable quality (Malhotra *et al.*, 2023).

Gene editing can increase the speed at which known resistance alleles are deployed. After a causal nucleotide change has been mapped, associated, or identified through functional genomics, the beneficial allele can be recreated in an elite cultivar directly as an edited version rather than being introgressed via a long backcross program. Editing of regulatory DNA has the potential to upregulate as well as downregulate expression of endogenous defence genes without altering the encoded protein (Van Vu *et al.*, 2025). This strategy might result in moderate and developmentally regulated resistance that may be less metabolically costly than constant overexpression. Multiplex editing can be used to pyramid pest recognition, anti-feeding and tolerance mechanisms, or to modify redundant genes that are difficult to combine through crossing. Targeted insertion could eventually allow for precision placement of larger resistance cassettes though efficient delivery and plant regeneration still represent key bottlenecks. For sustainable resistance, edited plants should not be viewed as single technological products, which are expected to continue being effective forever, but instead as ingredients in wider genetic and ecological solutions (Li *et al.*, 2024).

7. RNA-Guided and Novel Molecular Strategies

The line separating traditional host resistance and molecular pest control is becoming increasingly blurred. Host-induced gene silencing Host-induced gene silencing allows crop plants to express RNA molecules that target important insect genes associated with growth, digestion, nerve, detoxification, reproduction, and defense against plant metabolites. Gene editing can enhance this concept by targeting RNA-expressing constructs to specific sites in the genome, modulating their expression, or multiplexing targets to mitigate resistance (Saakre *et al.*, 2024). Natural resistance may additionally derive from small-RNA pathways, including plant microRNAs. Yet the efficiency of RNA-mediated resistance presumably relies on feeding activity, on stability of RNA, on cellular uptake and systemic transport, and varies among insect species or groups. Consequently, they must be verified empirically. Potential effects on non-target species can also be evaluated through sequence analysis, exposure analyses, and relevant ecological assessments to confirm that RNA-based pest resistance is effective and environmentally sound (Germing *et al.*, 2025).

Emerging strategies involve transient gene regulation, epigenome editing and modulation of plant-associated microorganisms. CRISPR activation and interference systems can activate or switch off defence genes without permanently changing their coding sequences, while epigenome editors can alter DNA methylation or chromatin

states, but the stability and inheritance of these changes are still questioned (Seem *et al.*, 2024). Symbiotic microorganisms can induce plant immunity, generate insect-repelling compounds and influence volatile emissions, and host genetics can play a role in microbiome assembly. As a result, adding another layer of resistance can come from breeding or editing crops for beneficial plant-microbiome interactions. However, microbial colonization and epigenetic responses are strongly affected by soil, climate and crop management. These techniques need to be validated in field trials, and effective breeding programs should focus on resistance traits that are measurable, stable, and consistently maintained under commercial production conditions (Compant *et al.*, 2025).

8. Artificial Intelligence in Resistance Phenotyping

8.1 Automated Detection of Insects and Crop Damage

Phenotyping is often the most costly and error-prone part of insect-resistance breeding. Manual damage ratings are valuable, but they can be subjective, discontinuous, and insensitive to the onset of infestation. Artificial intelligence based on images taken with cameras, smartphones, microscopes, unmanned aerial vehicles and field robots can identify insects, feeding lesions, leaf mines, defoliation, discoloration and canopy collapse. Deep-learning models enable differentiation of symptoms, approximation of damaged leaf area, counting of insects and monitoring of damage over time (Mittal *et al.*, 2024). Hyperspectral and thermal imagers can detect physiological stress prior to symptom expression, and acoustic sensors can identify concealed feeding by borers inside stems, fruits, or stored products. Automated phenotyping expands the diversity of genotypes and time points of observation. Repeated measurements can differentiate delayed infestation from slow damage accumulation and rapid crop recovery, which are indistinguishable with a single terminal damage score (Murphy *et al.*, 2024).

8.2 Data Quality, Model Validation and Explainability

Reliable phenotyping with AI requires diverse and carefully labelled training data. Images obtained from a single lighting condition or a single crop genotype may not generalize to different backgrounds, plant architectures, cameras or symptom intensities. Models may confuse insect injury with nutrient deficiency, drought, disease or mechanical damage unless these conditions are properly represented during training. Data augmentation, standardized colour references and multisensor measurements can enhance the reliability, but independent validation is still required. Human experts should investigate predictions they are unsure about and cases that are biologically unusual, introducing an active-learning component where the model learns from successive breeding cycles (Yao *et al.*, 2024). Explainable models can explain which parts of an image or which spectral bands were most influential in a classification, which can help breeders to spot technical artefacts and potentially discover previously unrecognized resistance traits. Thus, AI should increase the repeatability and biological resolution of measurements, while entomologists will continue to be responsible for confirming the identity of pests, their feeding behaviour and the biological meaning of phenotypes predicted (Miao *et al.*, 2024).

9. AI for Gene Discovery and Genomic Prediction

9.1 Multi-Omics-Based Gene Discovery

Modern breeding programs produce genomic variants, transcript profiles, metabolite quantifications, protein interactions, environmental records, and phenotypic observations at scales not browsable for human interpretation. Machine learning algorithms may combine these data sets to identify genes, pathways, and regulatory networks implicated in insect resistance. Feature-selection techniques can rank genomic regions simultaneously supported by association mapping, differential expression, co-expression networks, chromatin accessibility and metabolite profiles (Yan and Wang, 2023). Protein structure prediction and molecular modelling may be used to screen receptor-effector, the defensive enzyme, and candidate proteins to test protein interactions prior to lengthy experimental trials. Natural-language processing can be used to extract and organize information from scientific literature, gene databases and breeding reports, although experimentally validated information should always be kept separated from computational-based inference. Artificial intelligence is most useful when it whittles down the thousands of candidates to a small, biologically coherent set, rather than producing an inscrutable ranking with no functional rationale (Murmu *et al.*, 2024).

9.2 Machine Learning for Genomic Prediction

Machine learning-based genomic selection is not limited to purely additive marker effects. Methods such as random forest, gradient boosting, support vector machines, and multilayer perceptron can incorporate epistasis, nonlinear interaction, and high-order interaction. Deep-learning-based frameworks can integrate marker sequences with gene annotations, expression profiles, and environmental covariates. However, increasing the model complexity does not necessarily yield better prediction accuracy (Zingaretti *et al.*, 2020). Data sets for crop breeding tend to be smaller and more structured than those for large-scale commercial AI applications, with a high risk of overfitting. Genomic based simple models can outperform deep networks when the size of the population is small or the resistance is largely additive. Hence comparisons of models should be based on independent populations, on prediction into the future across breeding cycles and on testing in truly new environments. The aim is not to have the most complex or trendy algorithm, but to provide accurate, robust and interpretable predictions that maximize genetic gain while minimizing field evaluation costs (Montesinos-Lopez *et al.*, 2024).

10. AI-Assisted Design of Gene-Editing Experiments

Artificial intelligence can enhance various aspects of gene-editing design. Predictive models can rank guide RNAs based on predicted editing efficiency, genomic sequence context, and potential off-target activity at similar sites. They can also rank the targets for editing by considering the gene function, network position, tissues-specific expression, natural variation, and predicted impact on agronomic traits (Dixit *et al.*, 2024). Protein-language and structural models may also be useful for designing editing enzymes with different targeting rules, higher specificity, or better recognition of challenging genomic areas. Experimentally trained models of editing outcomes can be used to make predictions about which guides are likely to produce specific mutation patterns in a given crop. With increasing experimental data, artificial intelligence could enable the design of promoter edits that modulate gene expression rather than abolish it. This is particularly useful for defensive pathways where over-activation or constitutive activation impacts plant growth and yield (Nayfach *et al.*, 2026).

Computational predictions should not be confused with biological validation. An otherwise top-ranked guide RNA might be rendered inactive due to chromatin accessibility, DNA methylation, genotype-specific sequence variation or delivery limitations. A putative resistance gene may also have an effect on development, fertility, nutritional profile or on other stress responses (Villiger *et al.*, 2024). Therefore, AI-based editing must be subjected to staged validation, including sequence verification, molecular characterization, laboratory insect bioassays, evaluation of pest performance and multi-environment testing. Whole-genome or targeted sequencing can be used to investigate potential off-target sites, while transcriptomic and metabolomic studies might help identify unanticipated pathway disruption. Edited plants should be tested against appropriate segregating controls, and independent events to ensure that the effect attributable to the intended edit is not a product of tissue-culture variation. Artificial intelligence enhances experimental prioritization, but well-established genetics, physiology, and phenotyping are still needed to prove causality and breeding value (Wu *et al.*, 2022).

11. An Integrated Breeding Pipeline

11.1 Target Definition and Resistance Discovery

An entire integrated programme is planned around the product profile. Crop breeders need to define the crop, production area, target insect, anticipated pest pressure, level of resistance sought, and any agronomic or quality traits that are non-negotiable. Germplasm panels, breeding populations and wild relatives are then phenotyped using standardized insect assays and high-throughput sensing. Genomic, transcriptomic, metabolomic and environmental data may be integrated to discover sources of resistance and to predict breeding value (Donovan *et al.*, 2022). Genomic selection can be used to rank parents and progeny for quantitative resistance, as well as identify candidate genes/regions through genome-wide association, linkage mapping, and functional analyses. Artificial intelligence enables image analysis, data fusion, cross prediction and candidate prioritization. This discovery stage should deliver both superior breeding lines with favourable polygenic backgrounds and a short list of molecular targets that can potentially be refined through precise gene editing (Escamilla *et al.*, 2025).

11.2 Editing, Selection and Continuous Model Improvement

Gene editing is most beneficial when natural recombination is limited, the elite germplasm does not contain a beneficial resistance allele, or an exact modification is more advantageous than traditional introgression. Edits should be made in agronomically strong cultivars with pre-existing quantitative resistance and then validated prior to genomic-selection population deployment of the lines (Greenwood *et al.*, 2023). This means breeders can combine the edited trait with yield, quality and adaptation. Speed breeding, doubled-haploid production, and rapid generation advancement facilitate reduction in the time from editing to field evaluation. Outcomes from molecular assays and field-trials should result in iterative updates to prediction models. Even failed edits still inform which targets do not work, or are environmentally sensitive, or harbor cryptic fitness costs (Ghosh *et al.*, 2024).

The combined system functions as a closed prediction-validation loop. Phenotyping resistance is enhanced by AI, which in turn enhances genomic prediction and the selection of the best backgrounds. Multi-omics then identifies candidate resistance mechanisms while AI prioritizes promising editing targets. Causality is validated or favourable variants introduced through gene editing, and new data for model retraining is generated by the resulting plants (Yang *et al.*, 2020). Human breeders set the goals, the constraints, and the tolerable uncertainty. Genomic selection models polygenic value, gene editing makes targeted changes, and AI synthesizes complicated data to inform better decisions. Predicting durable insect resistance therefore requires a marriage between prediction and experiment and the testing of molecular innovations in realistic breeding populations and production environments (Bradbury *et al.*, 2025).

12. Breeding for Multitrait Performance and Ecological Compatibility

Insect tolerance cannot be improved separately from yield, crop quality, maturity, abiotic-stress tolerance, or disease resistance. Defense pathways are resource-intensive and may affect flavour, texture, processing properties, or nutritional content. Dense trichomes deter insect pests but also hinder harvest and beneficial organism activity. Elevated levels of some specialized metabolites can enhance antibiosis while also causing the products to taste bad or become toxic (Marone *et al.*, 2022). Strong immune activation can suppress plant growth especially in conditions of low pest pressure. Multi-trait genomic selection allows to strike a balance between these consequences by considering the relative economic and biological importance of each trait. Machine learning can recombine potential selection indices and select genotypes closer to an optimum trade-off between resistance, productivity and quality. Editing of regulatory regions rather than coding sequences may additionally contribute to fine-tuning defensive strength, and the inducible or tissue-specific expression of

defense may localize protection to the organs and developmental phases of the plant where it is most beneficial (Qi *et al.*, 2024).

Compatibility with integrated pest management should be an explicit goal of breeding. Resistant varieties have the potential to reduce reliance on insecticides and slow the growth of pest populations, but their usefulness is enhanced if they are also compatible with biological control, crop rotation, cultural control, and pest monitoring. Parasitoids and predators can be attracted by plant volatiles with the modification of volatile blends influencing also pollinators or secondary pests. Therefore, surface proteins and defensive metabolites should be characterized in tritrophic system including crop, herbivores and natural enemy (Qian *et al.*, 2024). AI-enabled field monitoring enables the measurement of pest and beneficial-insect communities across the growing season, and genomic models can predict plant traits linked to desirable ecological outcomes. Breeders can eventually breed for ecological resistance, which is not just the direct suppression of pests but the ability of the plant to work with natural enemies and landscape-level management. These cultivars would impart more robust protection than plants relying solely on a single toxic mode (Adams *et al.*, 2024).

13. Managing Insect Evolution and Resistance Breakdown

13.1 Evolutionary Monitoring of Pest Populations

Any effective plant defence creates selection pressure on insect populations. Pests may overcome resistance by changing their feeding habits, enhanced detoxification, changes in molecular target sites, suppression of plant signalling, altered gut physiology or association with protective microorganisms. Short generation intervals and large population sizes can speed up this type of evolutionary response. Genomic surveillance of pest populations can reveal allele frequency changes related to virulence, while artificial intelligence can combine genomic, geographic and monitoring data to serve as an early warning system (Fujii *et al.*, 2024). Resistance-management models can help estimate the impact of various cultivar deployment strategies on adaptation. Cultivar mixtures, temporal rotation, spatial mosaics, refuges and pyramids of mechanistically different resistance factors may reduce the likelihood that a single pest genotype will overcome all defensive barriers. The optimal deployment strategy depends on the pest's mobility, reproductive biology, virulence inheritance, regional cropping systems and landscape structure (Ellegaard *et al.*, 2018).

13.2 Resistance Pyramiding and Strategic Deployment

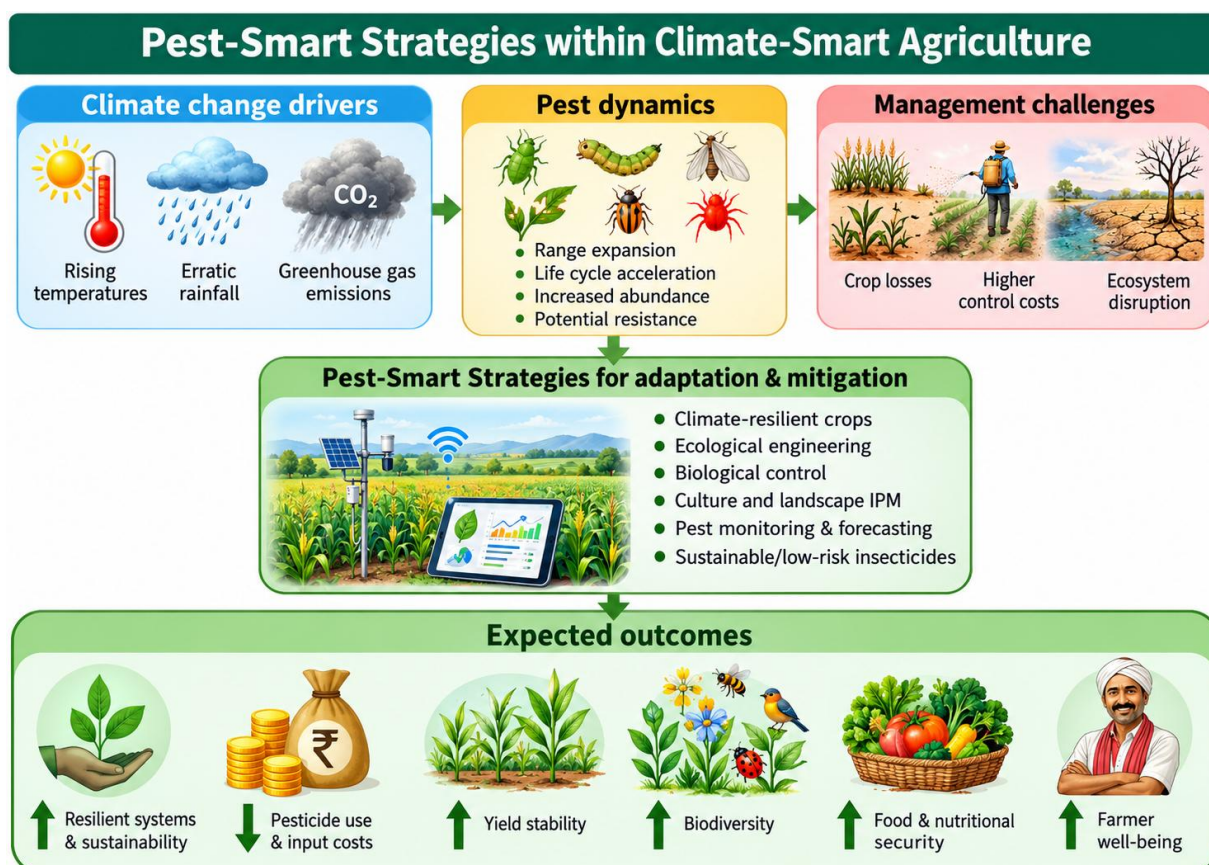
Breeders also need to consider not just whether a cultivar can withstand a current pest population, but how long that resistance might last. Experimental evolution, serial passage, and recurrent-selection experiments can subject insects to candidate cultivars for several generations and may predict potential adaptation routes. Assays for insect fitness on susceptible, resistant, and mixed host backgrounds can assess if virulence has biological costs (Guru-Pirasanna-Pandi *et al.*, 2025). Edits that potentially decouple conserved insect-plant interactions may also provide greater durability, though alternative feeding or detoxification routes can be selected with similar intensity. Quantitative resistance often exerts less strong, more diffused selection than a single major gene, but it can be challenging to phenotype and pyramid. A rational design might combine moderate quantitative resistance with one or more strong defensive genes that only modestly slow pest population growth, rather than depending completely on any one genetic barrier. Monitoring after cultivar release remains critical because durability is a thing that is demonstrated over time, not a feature that can be bestowed on a cultivar at development (Pilet-Nayel *et al.*, 2017).

14. Climate-Smart Insect-Resistance Breeding

Climate change is influencing the distribution, abundance and timing of the generations of many insect pests. Increased temperatures can increase the rate of development and the number of generations, while altered rainfall and elevated CO₂ can affect host quality, insect survival and feeding behaviour. As a result, resistance that is effective now may become less reliable in a future climate (Vencl *et al.*, 2024). Thus, genomic prediction should incorporate environmental and physiological variables associated with heat, drought and nutrient stress. Controlled environment studies and regional field networks can test crop-pest interactions under climate change scenarios, and AI can combine weather forecasts, pest monitoring data and crop development models to predict where certain resistance traits will remain effective (Jat *et al.*, 2024).

Resistance under climate-resilience should be considered as the breeding target rather than resistance assessed under only one environment deemed as being favourable. Heat and drought can influence defensive metabolites, stress signalling and the ability of the plant to compensate for herbivory. Genomic selection in a multi-environment context could also elucidate alleles that sustain defence and recovery under combined stresses (Tadese *et al.*, 2025). Gene editing might also be used to modify regulatory nodes that connect abiotic and insect-stress responses, such genes must be thoroughly validated as they tend to have pleiotropic effects on many other physiological processes. AI-enabled crop models can be used to model allelic combinations and deployment environments to rank materials for testing in the field. Such predictions are expected to aid and not substitute for rigorous evaluation under representative climates, pest pressures and crop management systems (Pandey *et al.*, 2017).

Figure 3: Pest-Smart Strategies for Climate-Resilient Agriculture



Source- Fand *et al.*, 2026

15. Data Quality, Infrastructure and Capacity

Integrated breeding programmes are more dependent on coordinated high-quality data than they are on the incorporation of new technologies. Phenotypic records need to be standardized with consistent trait definitions, rating scales, pest-density information, environmental metadata, and trustworthy genotype identification. Similarly, images, sensors and genomic datasets need to be consistently calibrated, quality controlled, reference assembled, variant formatted and annotated, and insect populations need to be characterized by origin, collection date and biological traits (Selby *et al.*, 2019). Interoperable data can enable data reuse across breeding cycles and institutions, assuming farmer rights, genetic resource agreements and sensitive information are safeguarded. For smaller programmes, costs can be reduced by using shared genotyping services, cloud-based analyses, open-source software, and regional phenotyping networks, instead of building all the infrastructure independently (Papoutsoglou *et al.*, 2020).

Capacity-building would incorporate plant breeding, quantitative genetics, entomology, molecular biology, bioinformatics, engineering, economics and social science. Yet breeders should have a sufficient computational background to evaluate the model assumptions, and data scientists must be familiar with biological variation and experimental designs. Entomologists are needed for representative insect colonies and relevant resistance traits and molecular scientists need to link editing results to whole-plant performance. May highlight Economics can determine if resistant cultivars reduce production risk for a positive cost (Nogue *et al.*, 2024). Farmers should also provide information on pest complexes, management practices and varietal preferences, especially where conditions for smallholders are not the same as those at the research stations. Advanced technologies and multidisciplinary research hence are essential for a balanced and efficient application of these approaches sophisticated models can make up poorly designed experiments or breeding goals which do not consider the needs of farmers (De Sousa *et al.*, 2024).

16. Biosafety, Regulation and Public Acceptance

Insect-resistant edited crops should be evaluated based on the nature of the end product, its mode of action, and the production environment. Potential issues include unintended changes to the genome, modified composition, effects on non-target species, gene flow, weediness and effects on pest management. Regulatory evaluation needs to separate small edits that re-create natural alleles from those that create novel pesticidal traits, as their exposure routes and risk profiles are distinct. Variation between national systems of regulation may lead to uncertainty for research, seed movement and trade (Groover *et al.*, 2024). Early regulatory engagement, with transparent reporting of methods of editing, target sequences and separation of editing components along with phenotypic performance, can facilitate reproducibility, and trust in edited cultivars (Ricroc *et al.*, 2026).

Public acceptance is a function of more than just technical safety; it also depends on clear communication, equitable access and transparent governance. Farmers and consumers need to know what problem is being

solved, what kind of genetic modification has been made, what are the expected benefits and what are the limitations. Unsupported claims like "pesticide-free" should be avoided, as resistant cultivars may still require management of secondary pests or resistance-breaking populations. Intellectual property systems should enable public breeding programmes and locally important crops to access innovation (Atimango *et al.*, 2024). Participatory priority setting, accessible licensing and investment in public transformation facilities can reduce technological inequality. Trust is built when the process of decision-making is transparent, the benefits are tangible and resistance-stewardship is maintained even after commercialization (Bearth *et al.*, 2024).

17. Current Limitations and Research Priorities

Several biological and technical limitations remain. Genomic prediction is expected to lose accuracy when applied to distantly related populations and under different environments, and accurate insect phenotyping at large-scales is still challenging. Gene editing is limited by low transformation efficiency, genotype-dependent regeneration, delivery constraints, and, in the case of polyploids, the requirement to edit multiple homologous copies. Functional redundancy can also conceal editing effects. Machine-learning models can inherit biases from their training data, perform poorly when deployed in novel environments, and lack interpretability; multi-omics investigations are often correlative rather than causative. To overcome these challenges, standardised bioassays, enhanced experimental populations, transformation-independent delivery systems, explainable AI, and robust functional validation across multiple genetic backgrounds and environments are necessary (Alseekh *et al.*, 2021).

Future research should aim to incorporate techniques that enhance field reliability and are more relevant to breeding value. Multi-pest and multi-environment genomic prediction requires large, diverse training populations, and phenotyping needs to incorporate measures of insect behaviour, pest fitness, plant damage and yield compensation, instead of single visual scores. Pangenomes and haplotype-resolved assemblies can identify structural variants and resistance alleles not present in reference genomes. Single-cell, spatial omics and metabolomics can inform tissue-specific defence responses and their relationships with crop quality (Verma *et al.*, 2026). AI models should be tested using prospective breeding decisions, and gene-editing research should focus on promoter engineering, allele replacement, multiplex editing and efficient regeneration. Long-term insect-evolution experiments and landscape monitoring are also necessary to assess resistance durability (Raza *et al.*, 2026).

18. Future Prospects: From Selection to Predictive Crop Design

Breeding systems are expected to increasingly operate in a seamless biological-prediction space. Digital twins could integrate genotype, crop growth, insect development, and weather to predict resistance prior to field validation, and generative algorithms could hypothesize crosses that trade resistance, yield, quality, and genetic diversity (Messina *et al.*, 2025). High-throughput phenotyping pipelines might quickly evaluate chosen pairs under pest and climatic stresses, and portable sensors combined with farmer observations could enhance pest surveillance. Collectively, these tools may shift breeding from screening through very large populations towards designing small, information-rich populations that are more likely to produce successful cultivars (Bradbury *et al.*, 2025).

Predictive crop design must remain rooted in evolutionary and ecological theory, since insect adaptation is an ongoing process and resistance to insects is often costly in terms of plant physiology. Hence, the strongest forms of that resistance may come from a mixture of constitutive barriers, inducible defences, quantitative antibiosis, tolerance and compatibility with natural enemies rather than a single very strong resistance factor (Bohloolzadeh *et al.*, 2024). Methods such as genomic selection have the potential to build good polygenic backgrounds, gene editing can fix particular weaknesses, and AI-based guidance can make decisions within complex data landscapes. These integrated approaches may enable adaptive resistance portfolios that best balance protection against pests, productivity, affordability to farmers and maintenance of genetic diversity within and among crops and production environments (Kshatriya and Gershenzon, 2024).

19. A Strategic Roadmap for Breeding Programmes

A practical transformation can be initiated with current breeding material by harmonizing insect phenotyping, digitizing historical datasets and developing representative training populations. Genomic selection can subsequently be performed for resistance and agronomic characteristics by using models appropriate for the data at hand (Scheffel *et al.*, 2025). High-throughput imaging prioritizing major phenotyping bottlenecks and prioritization of candidate genes based on evidence from mapping, expression, allelic variation and functional studies. Gene editing should focus on well characterized genes where there are clear benefits compared to conventional introgression, and then be reintegrated into crossing, selection, and multilocation testing. This tiered approach could provide immediate breeding gains and simultaneously facilitate the accumulation of the data, skills and infrastructure required for deeper integration of technology (Gothe *et al.*, 2024).

Programme success should be evaluated through genetic gain, prediction reliability, lower phenotyping costs, environmental stability and measurable pest-management benefits after release. Resistance is not useful if it does not protect yield in the field, nor precise edits if they reduce quality or rely on expensive delivery systems (Bhosale *et al.*, 2025). Breeding programs Also: Nurture diverse parents/resistance types, enhance host-pest monitoring, and produce stewardship plans pre-deployment. Although decision-support tools can be designed to incorporate genomic predictions, phenotypes, editing status, uncertainty, regulatory information, the final advancement decision should be clearly justifiable by breeder judgment and evidence. Employed judiciously,

innovative technologies have the potential to enhance the foundational breeding processes of recombination, selection, testing and continuous improvement (Cobb *et al.*, 2019).

20. CONCLUSION

Genomic selection, gene editing and artificial intelligence can provide a transformative approach for creating next-generation insect-resistant crops. Genomic selection allows breeders to select for multiple resistance alleles simultaneously, while continuing to enhance yield, quality and adaptation. Gene editing allows for targeted changes in susceptibility genes, defence pathways and beneficial alleles, while artificial intelligence enhances phenotyping, genomic prediction, multi-omics analysis and target identification. Combined, these technologies can reduce breeding times and generate more effective, broad-spectrum and stable resistance. But long-term protection requires genetically diverse germplasm, careful phenotyping, appropriate field testing and consideration of insect evolution, climate change, beneficial organisms, biosafety and farmer needs. The use of diverse defence mechanisms in a strong polygenic background and integrated pest management programmes can reduce insecticide use, maintain productivity and produce robust, sustainable crop varieties for future agricultural climates.

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