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GENETIC AND MOLECULAR BASIS OF FRUIT QUALITY TRAITS: FROM GENOMIC DISCOVERY TO PRECISION BREEDING- A REVIEW

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ABSTRACT
Fruit quality determines consumer acceptance, nutritional value, market price and suitability for storage and processing. However, quality is hard to improve because it is a multifunctional trait instead of a single measurable property. Fruit form, size, colour, sweetness, sourness, aroma, texture, nutritional composition and postharvest behaviour arise from developmental and metabolic pathways that are interconnected and can vary with genetic, maturity, environmental and management factors. Recent advances in reference genomes, population resequencing, high density phenotyping and pangenomics have revealed genetic variation not easily accessible to conventional breeding. Quantitative trait locus mapping and genome-wide association studies have identified quality-related regions, while transcriptomics, metabolomics and functional studies have linked candidate genes to biologic processes. These discoveries are transforming breeding practice: proven markers are working in early selection, and genomic prediction can foresee complex traits, and genome editing to manipulate specific genes or promoter elements. However, association studies are only the first step. Good improvement demands reliable phenotypes, validation across various genetic backgrounds and environments, and trade-offs among quality, yield, resilience and shelf life. This review focuses on the genetic architecture and molecular regulation of major fruit quality traits, evaluates the tools that connect genomic discovery to breeding decisions, and outlines a practical framework for developing fruit cultivars with quality that remains desirable from harvest to consumption.

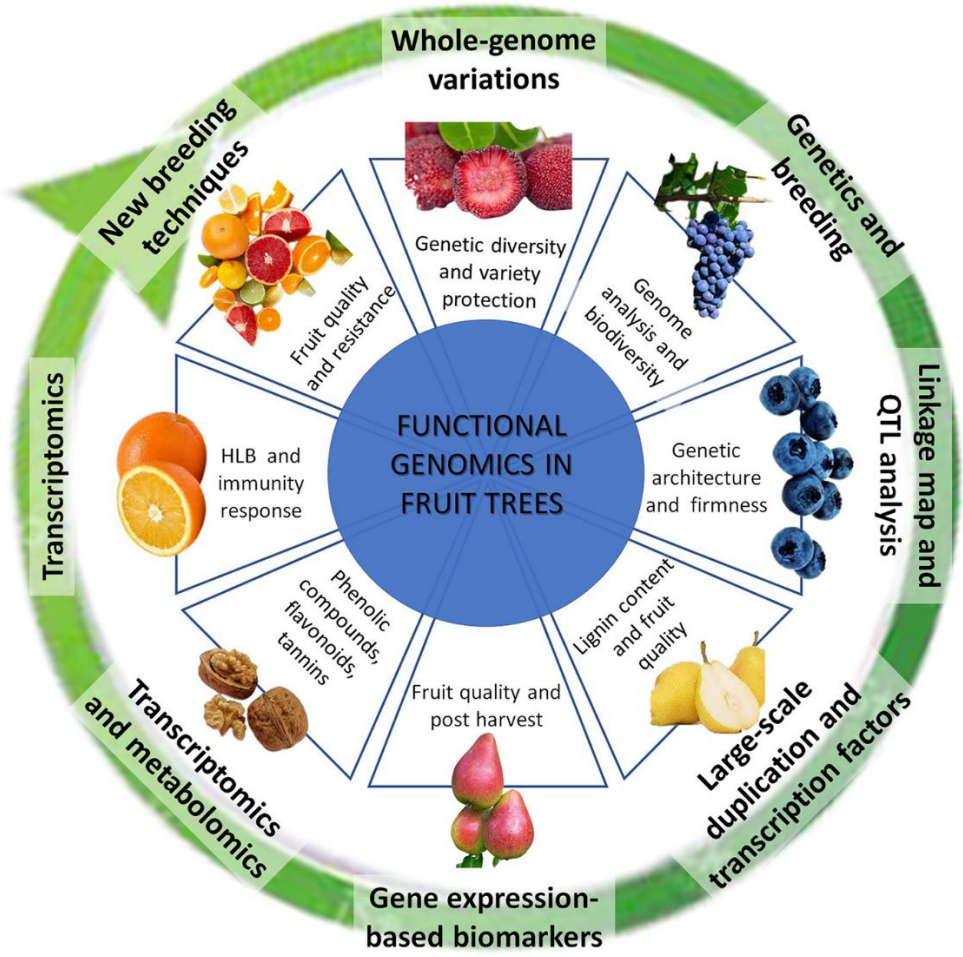
KEYWORDS: Fruit quality; fruit genetics; molecular breeding; pangenomics; flavour; genomic selection; genome editing

1. INTRODUCTION
A fruit may meet commercial standards of size and appearance, but fail in the perception of the consumer because they had low flavour, texture which is not desirable or its eating quality declines before it reaches the market. Conversely, seeds of an exceptionally flavoured genotype may not be suitable for the farm if it produces poorly, fragile, or does not store well (Baccichet *et al*., 2025). Thus, fruit quality is effectively the combined performance of a biological product and the supply chain associated with it. In addition to traits expressed in the orchard or field, incorporate the changes during ripening, responses to harvest and storage, and the sensory experience of consumption that the breeder must take into account. This is particularly true in perennial fruit crops, with long juvenile periods, large plants, and expensive field trials prolonging the assessment of new selections (Zhang *et al*., 2025).
Genomic research has transformed the study of this problem. Prior breeding programmes were mostly dependent on phenotypic traits, pedigree, and repeated field test results. Modern programmes can examine DNA sequence variation, quantification of thousands of metabolites, transcriptome dynamics throughout development steps, and predicting the performance of seedlings before they bear fruit (Nazir *et al*., 2025). These fold from a quality difference to its genetic basis to eventually a breeding decision. The route is rarely direct. If a marker linked to sweetness is good in one population, it may not be at all useful in another. Additionally, a gene that increases colour might change other metabolites or respond to heat differently. The main challenge is to identify real

biological connections, and not ones that are only specific to a particular population, environment or measurement methodology (Minamikawa *et al*., 2024).

Fruit crops also fall under very different biology nonetheless. A grape berry, citrus hesperidium, mango drupe and strawberry receptacle will not simply develop or ripen alike. One crop may be highly heterozygous or polyploid, others are clonally propagated, highly self-incompatible or have to ripen for many years before they can be reliably tested (Ahmad *et al*., 2026). No single quality breeding model could accommodate all species. Common mechanisms between fruits sugar transport, vacuolar acid accumulation, pigment biosynthesis, cell wall remodelling and hormone-mediated ripening provides a baseline for comparison. This review uses that framework while recognising where crop-specific genetics, market preferences and breeding constraints require different solutions (Pinto *et al*., 2026).

Figure 1. Applications of Functional Genomics in Fruit Tree Improvement and Quality Enhancement



Source- Licciardello *et al*., 2021

2. Defining and Measuring Fruit Quality

2.1 Quality is a collection of related traits

Fruit quality has external, internal, nutritional and postharvest dimensions. External characteristics like size, shape, uniformity, skin colour and lack of visible defects reflect the external quality. Internal quality traits include sweetness, fruit acidity, aroma, juiciness, flesh firmness, flesh colour and absence of fibres or seeds (Grabska *et al*., 2023). Constituents like carotenoids, vitamin C, anthocyanins, minerals and other bioactive compounds are considered in nutritional quality. Postharvest quality indicates whether these attributes remain after prior handling, transport, storage, and display. The significance of each component is dependent on the crop and intended use. Breeding targets must, therefore, be set around a defined product and consumer rather than an irreversibly objective of better quality (Zhao *et al*., 2024).

Many routine measurements are useful but imperfect substitutes to what consumers experience. Total soluble solids, usually called degrees Brix, provide evidence of the level of material dissolved but they fail indicate amounts of individual sugars and the level of perceived sweetness. Titratable acidity tests the amount of acid neutralised during the analysis and not pH which is the measure of hydrogen-ion activity: they measure the response to different but interrelated questions (Ikegaya, 2024). Instrumental firmness may be predictive of resistance to compression but less apt at reflecting crispness, mealiness or the temporal sequence of the sensations involved in chewing. Likewise, detecting a volatile compound does not guarantee it contributes appreciably to aroma. Its concentration, odour threshold and interactions with other compounds are key. Genetic studies are more

insightful when they add familiar measurements to chemical profiles and well-designed sensory assessment (Perkins-Veazie *et al*., 2021).

2.2 Phenotyping across development and environments

The quality shown for a genotype relies heavily on when and where its fruit is sampled. Sugar accumulation and acid decline may continue through maturation while colour development, softening and volatile production can pursue at different rates. Two genotypes harvested on the same calendar date might therefore be at different physiological stages (Roh *et al*., 2025). Mature trials provide crop-appropriate indicators and note the harvest conditions such as crop load, the position of the fruit, etc., and storage conditions. Sampling through ripening provides performance metrics of a genotype that is always at its best or one that displays a target expression only for some time. For traits such as storage firmness, measurements at harvest and after a defined storage period answer separate breeding questions (Kwon *et al*., 2025).

Environmental effects must be built into quality assessment rather than being treated as unexplained errors. It is availability of assimilates, pigment formation, acid metabolism and aroma that are influenced by the temperature, light, water supply and crop load. In some cases, fruit soundness, mineral absorption, and water relations are affected by rootstocks (Micheloud *et al*., 2025). Multi-year and multi-location trials to identify if a favourable genotype is stable or condition-dependent. Statistical models can separate genetic effects from environment and genotype-by-environment interaction, provided that trials are replicated and measurements are consistent. Reliable phenotyping is often more valuable than simply generating additional DNA markers: even a dense genomic dataset cannot rescue a poorly defined trait (Babiker *et al*., 2025).

3. The Genetic Architecture of Fruit Quality

Fruit quality traits have varying levels of genetic complexity. For some traits like the presence of certain pigments or major changes in acidity, one locus might have very strong influences. Others, such as flavour preference, crispness, and storage performance, are influenced by many loci having relatively subtle or context-dependent effects (Poonam *et al*., 2023). A major locus can still work as part of a complex genetic background, such that its effect can become more or less pronounced. For instance, an allele that promotes red pigmentation under good light may create a weaker form of the same phenotype under the same conditions known to inhibit pigment formation. Describing a trait as controlled by a gene can therefore conceal the contribution of developmental stage, interacting loci and environment (Bouillon *et al*., 2025).

This creates more Genetic correlations. The concentration of some soluble compounds may be lowered by selection for larger fruit, through dilution or changes to source-sink dynamics. Likely, the traits of self-guided transport and firmness may be positively correlated, but could become unpalatable especially if slight down-regulation of softening is significantly delayed or uneven (De Visser *et al*., 2026). These associations are not necessarily important biological relationships: they are dependent upon the pathways and alleles through which a characteristic is modified. We can sometimes relax a trade-off by aiming at the regulatory step impacting quality and impact to the rapid response of the growth and yield. It is more than the correlation between two traits in an existing population, to identify the underlying biology of those traits if they are actually amenable to sorting (Ric-Varas *et al*., 2024).

The reproductive biology of fruit crops is reflected in Inheritance. Heterozygosity might hide recessive alleles and polyploidy creates problems for interpreting dosage and markers. Once a superior variety is isolated in clonally propagated species, its offspring can vary widely. Long juvenile periods limit the number of selection cycles that can be finished in a programme (Nagasaka *et al*., 2024). While these attributes make for early prediction, they also require rigorous testing. A marker that performs well among related seedlings may be unreliable across diverse germplasm if the causal allele is absent, the marker is no longer linked to it, or the same phenotype arises through another pathway (Zadokar *et al*., 2025).

4. Genomic Discovery of Quality Variation

4.1 Reference genomes, diversity panels and pangenomes

High-quality reference genomes map the coordinates needed for gene identification, allele comparison and integration of molecular datasets. Advances in long-read sequencing and chromosome assembly have resolved many previously enigmatic regions, such as long ranges of repeated sequence, complex subtle structural rearrangements and duplicated genes (Wijesundara *et al*., 2024). Resequencing of wild relatives, landraces and cultivars can then show how selection has impacted diversity during domestication and improvement. These comparisons are particularly informative when a commercially important trait has reduced variation in cultivated germplasm or when a desirable flavour component remains more abundant in less improved material. Discovery alone does not establish breeding value, however: a useful wild allele may be linked to undesirable characters that require several generations of selection to remove (Liu *et al*., 2024).

A single reference genome cannot represent every gene and allele in a diverse crop. Pangenomes solve this by contrasting many assemblies, thereby capturing presence-absence variation, copy-number differences and structural variants in conjunction with single-nucleotide changes. These types of variation can change expression or other metabolic outputs but might be poorly represented by marker arrays (Sabety *et al*., 2024). Grapevine and Citrus genomic studies demonstrate how new genomic resources allow researchers to assay loci tied to berry traits and fruit acidity and then focus functional studies here. When products created from earlier studies can enhance a breeder's ability to predict across breeding material, this is where the practical benefit occurs: a more complete

genome is valuable because you get to hear of alleles that breeders could potentially test, track and combine (Chen *et al*., 2025).

4.2 Mapping, association studies and causal validation

QTL mapping is the inheritance of markers and phenotypes within a family. It is very suitable for detecting regions in which the contrasting parents carry different quality alleles, but the family determines the resolution and range of alleles that can be detected with it. Genome-wide association studies examine diverse germplasm and can detect historical links between variants and traits at finer resolution (Bala *et al*., 2025). It has to be interpreted carefully in fruit crops, where pedigree relationships, population structure and cultivars can generate apparent associations which are not biologically causal. Both approaches find regions of the genome or statistical signals. But it does not guarantee that the closest annotated gene causes the phenotype (Fan *et al*., 2025).

Causal inference is more reliable when multiple independent forms of evidence converge. A candidate allele could match a mapped signal, have expression levels in the proper tissue that are within expectations, predict a metabolite difference and also yield the projected outcome when manipulated (Jimenez-Munoz *et al*., 2026). Segregation in more families and performance across environments further test this. Fine mapping can resolve closely linked candidates, while biochemical assays can demonstrate what a protein actually does. This chain of verification is especially crucial for regulatory genes, which might affect several pathways. A convincing discovery should justify the phenotype and provide a reliable way to identify it instead of simply adding another named candidate to a genomic interval (Cao *et al*., 2024).

5. Molecular Control of Fruit Size and Shape

Fruit size is established through processes that begin before fruit expansion becomes visible. Ovary structure, number of developing cells, rates of cell division, cell enlargement and availability of carbohydrates all play a role. Seed development and hormonal signals can promote growth but importance varies between species and fruit types (Baral *et al*., 2025). If growth is unequal along different axes, it can lead to an elongated, flattened or irregular fruit, determining shape. Consequently, genes related to developmental patterning, meristem organization, cell-cycle regulation and hormone responses have emerged as targets in these studies. A larger final fruit does not reveal which developmental step changed; anatomical and temporal observations are needed to identify the mechanism (Tian *et al*., 2024).

Breeding for size must consider composition and production at the same time. A large fruit may impact sugar concentration, skin-to-flesh ratio, firmness, or number of fruit bear per plant, but mainly enhance the appearance and pack-out. Cell number, cell expansion, assimilate partitioning or the fruit set are traits that can be modified by an allele (Du *et al*., 2025). Meanwhile, the shape can determine, directly, the manner of being packed, its susceptibility to damage, and its suitability for mechanized sorting. Molecular markers for major shape loci are useful when a market requires a clear category, but precise breeding aims to preserve a balanced phenotype. Selection indices that include yield, eating quality and uniformity are more useful than maximising fruit weight in isolation (DeViller *et al*., 2025).

6. Sweetness and Organic Acid Balance

6.1 Sugar supply, transport and storage

Sweetness begins as carbon fixed in photosynthetic tissues and provides the sugars to grow when the fruit is developing. The proportion of sucrose in the final fruit is also influenced by Sucrose transport, sucrose unloading into fruit tissues, conversion to glucose and fructose, metabolic conversion and vacuolar storage. They have different importance of these steps between crops and stages. A gene that affects a fruit's sugar import could alter both fruit growth and concentration, while an allele involved in the sugar metabolism inside the fruit may exhibit a different spectrum of effects. The action of sugar transport regulators associated with transporters, invertases, sucrose synthases, and regulators are thus contextualized in a whole plant source-sink system. Measuring one enzyme or transcript at one stage cannot, by itself, explain the sweetness of a ripe fruit (Ren *et al*., 2023).

Recent functional work in tomato provides a useful example of pathway-specific improvement. Editing the related regulators *SlCDPK27* and *SlCDPK26* increased fruit glucose and fructose in the reported experimental material without the expected penalty in fruit weight or yield, showing that an observed size-sweetness trade-off can sometimes be modified through a more precise target (Marchal, 2024; Chae *et al*., 2026). The result is promising because the study connected a molecular mechanism to a measurable fruit phenotype. Its breeding implications still require attention to background, production conditions and the full flavour profile. Sugar concentration is one component of consumer preference, and success in a tested tomato background should not be assumed to transfer unchanged to other cultivars or fruit crops (An *et al*., 2026).

6.2 Acidity and perceived flavour

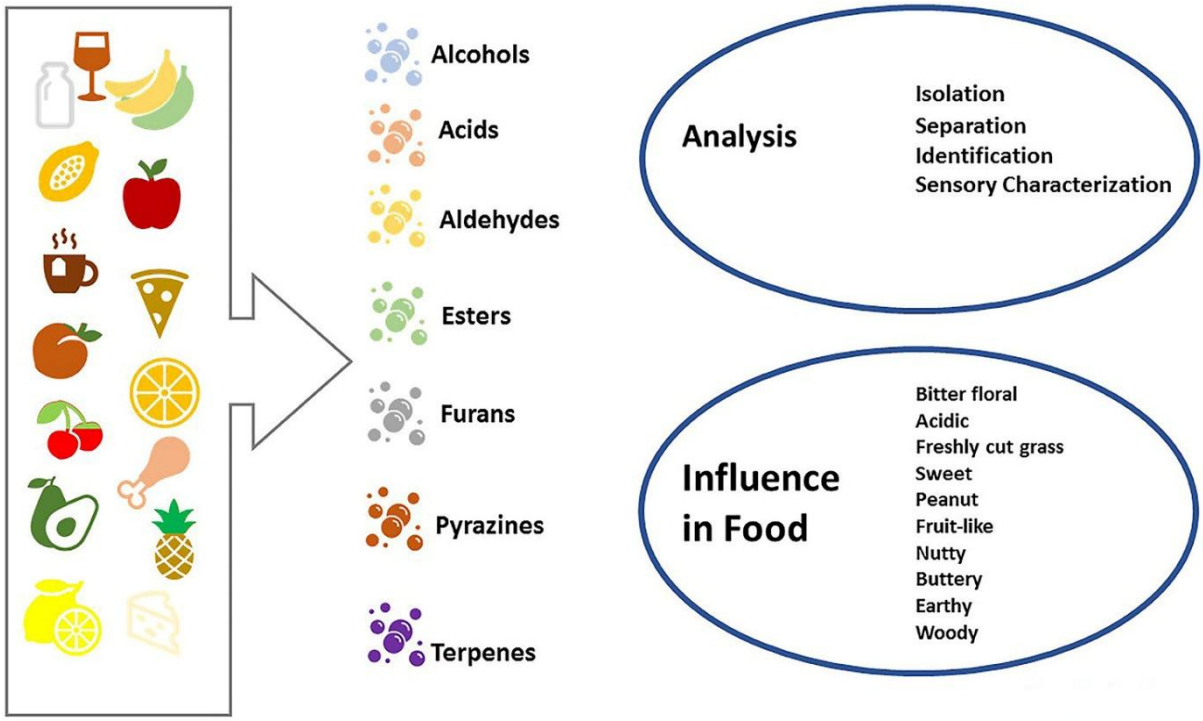
Organic acids impart tartness, freshness, and flavour balance. Citrate and malate make up the most important organic acids in many fruit species but they only differ in amounts and are developed during the fruit developmental patterns. Fruit acidity reflects accumulation of synthesis, degradation, and transport through membranes of cell compartments (Miao *et al*., 2024). Vacuolar conditions are also important because they affect how much acid can be accumulated, and so membrane transport and proton regulation are key components to be investigated genetically. The relationship between acids and sweetness is sensory as well as chemical: the same soluble-solids value can taste very different at two acidity levels. Breeders therefore need both the concentrations of individual sugars and acids and, where feasible, direct sensory evidence about their balance (Miao *et al*., 2024).

A very large change in acidity is often due to a master regulator but subtler changes occur via many pathways. Genomics comparison and experimental tests in citrus demonstrated the central role of PH4 in citric acid accumulation, highlighting the route from a pangenome discovery through to a mechanistic testing (Butelli *et al*., 20219). Such findings do not mean that all citrus acidity can be genetic. Fruit maturity, background genes and storage conditions are unrivalled, and preferences vary between fresh-market, juice and processed uses. Selection should aim for the level of acidity to achieve the desired flavour and shelf life. Removing acid indiscriminately may increase apparent sweetness while leaving fruit bland or changing its performance after harvest (Song *et al*., 2026).

7. Aroma and the Genetics of Flavour Complexity

Aroma arises from volatile compounds made via a variety of pathways, including through fatty acids, amino acids, carotenoids, and other precursors. Alcohols, aldehydes, esters, terpenes and related compounds provide different flavour notes, though their contributions are not proportional to concentration ratios (Tang *et al*., 2025). A compound can have a significant effect even at a lower concentration if it has a lower odour threshold. Some may be present in larger amounts than others, but hardly influence the general aroma. This is more than the sum of its parts: altering one volatile should unmask or mask the sensory effect of another. This accounts for why selections based on a very broad total volatile measure are unlikely to produce reliable flavour improvement (Bezerra *et al*., 2024).

Figure 2. Major Volatile Aroma Compounds and Their Role in Food Flavour



Aroma derives the underlying biology from genes that are involved in precursor availability, enzyme specificity, transcriptional control and the timing of ripening. These include some of these pathways since domestication and selection for yield, appearance or transportability may have moved some of them, preserving desired diversity in older cultivars or wild relatives (Duan *et al*., 2025). Breeders can assess that variation using targeted chemical analysis and sensory panels and then assign alleles associated with favourable profiles. The most useful aroma marker is that one which corresponded to a compound with established sensory impact and the favourable allele works in the desired background. Volatiles can also change quickly after harvest, so experiments should describe when the fruit was harvested and how long it was stored before analysis (Khera *et al*., 2023).

Flavour is an integration of aroma with sweetness, acidity and mouthfeel. Fruit with an attractive set of volatiles could still get a low score if sugar accumulation happens before high maturity or the excess firmness, which stresses the fruit, restricts aroma release while eating (Corrado *et al*., 2025). This integration has a practical consequence for breeding: a selection index should not consider flavour as a combination of laboratory readings in isolation of consumer response. Trained panels can distinguish sensory attributes, while consumer studies reveal whether those attributes drive acceptance in a target market. Combining these data with genomics will uncover key molecular targets that affect the eating quality, not just those that change a laboratory profile without changing the product (Porter *et al*., 2023).

8. Colour and Nutritional Composition

The synthesis, degradation and distribution of compounds across the flesh and peel of a fruit pale the colour of the fruit. The loss of chlorophyll often reveals pigments already present, while carotenoids and anthocyanins may accumulate through development or ripening (Fernandez-Cancelo *et al*., 2025). Genes encoding the biosynthetic

enzymes dictate which compounds may be made, transcription factors govern their expression; transport or storage processes then shape the overall appearance and visible intensity. Even though the same external colour can derive from a range of pigment compositions, there is no substitute for a chemical analysis when nutrition is the breeding goal. In addition, various factors such as exposure to light, temperature and developmental stage lead to expression of different pigments, making a controlled comparison necessary when searching for genetic differences (Anchana *et al*., 2026).

Anthocyanins are responsible for the red, purple, and blue hues in many parts of fruit, whereas carotenoids add yellow, orange and red colours and contain some nutritionally important compounds. Vitamin C and polyphenols add further nutritional dimensions that may be only weakly reflected in appearance. An increase in one measured component has to be put in the context of edible portion, serving size, stability during storage and processing, and the diet as a whole (Narra *et al*., 2204). The practical usefulness of a cultivar concentrated in a few or an infrequently-eaten tissues will often be less than the laboratory result would suggest. New nutritional improvement claims are most convincing when the compound is measured in the harvested, eaten tissue when it is normally mature to eat and under predicts the system stability of the trait across production (Habibi *et al*., 2025).

Pigment pathways can be exploited for marker-assisted breeding since some colour differences have distinctive phenotypes and influential regulatory loci. However, colour traits should reflect the crop that is grown and its biology (Kong *et al*., 2025). Heavily pigmented skin is aesthetically pleasing but does not alter the flesh chemistry, and even when it has nutritional merit, a newly introduced colour could face consumer bias. Coloration can be a marker of quality and product identity. Precision breeding should state whether its aim is appearance, a specific biochemical constituent or both. That distinction determines which tissues to sample, which genes to prioritise and how success should be measured (Kong *et al*., 2025).

9. Texture, Softening and Shelf Life

Texture relates to the size and organization of the cells, cell adhesion, and wall composition, turgor and the nature of the skin and flesh. Cell-wall polymers are altered during ripening, which can lead to cell adhesion breaks and softening (Malacarne *et al*., 2024). This then has an impact on the eating experience; the fruit takes on a melting, mealy, crisp or just fragile texture based on the structure and timing of these changes. Genes for wall modification can affect firmness, but instrumental testing rarely evaluates complete phenotype. Acoustic parameters, tissue fracture tests and sensory assessment distinguish fruit that has firmness is same but different when bitten or chewed (Pękala *et al*., 2025).

Texture is one of the main determinants of shelf life but a lot more than firmness plays a role. The extent of water loss, cuticle characteristics, cold chilling responses, susceptibility to bruising and delayed ripening also determine the market readiness of fruit. The most common form of postharvest softening curtailment: fruit should survive through distribution but reach a good eating stage over a typical period (Elmanawy *et al*., 2025). Focusing on simply slow-cooling fruit alone is risky in the sense that these fruits may never reach their intended sensory characteristics. In this regard, studies into the genetic basis of apple fruit texture have shown that both known loci associated with firmness and the challenge of pinning down complicated characteristics of crispness to a single marker are relevant in the case of this polysaccharide (Gidado *et al*., 2024).

Texture breeding once more illustrates that a lot goes to step under protocol in the genetic experiments. In its ripening programme, a genotype may have started out being genetically firmer as compared to another genotype when their texture is equivalent to the same eating maturity. Genotype ranking can change or, can eye defects that were not seen at harvest by storage temperature and duration (Gilpin *et al*., 2025). A program of evaluation must include clearly defined stages and conditions of commercial grade handling. Measurements such as firmness at harvest, injury resistance during transport and eating texture following maturity would go well when refreshing a fresh market cultivar. These outcomes are related, but each may be associated with a distinct blend of biological processes and breeding priorities (Khalifeh *et al*., 2025).

10. Ripening as a Regulatory Network

Changes in colour, flavour, texture and other quality traits prediction is aided by ripening coordinates. Its control by hormones, transcription factors, chromatin state and feedback between metabolism and development at the same time (Aprilyanto *et al*., 2025). Climacteric fruits, for instance, show a statistically-significant increase in ethylene production and respiration during ripening, but non-climacteric fruits follow various other regulatory patterns. While this can be a useful distinction, they are not two entirely different gene classes. Ethylene can influence some processes outside of a strictly climacteric response, and other hormones are found in both groups. For breeding, the key question is how a proposed allele changes the timing and coordination of desirable traits, rather than whether it changes a general ripening label (Ouyang *et al*., 2025).

Regulators with wide-ranging effects can lead to substantial benefits but also may increase risks of undesirable side-effects. Delaying ripening, might increase shipping life, but fade aroma or create uneven colour. Conversely, a broad effect results from modifying a single downstream enzyme, which however might not be considered effective if several pathways are simultaneously limiting quality (Ortega-Salazar *et al*., 2024). This allows for a hierarchy of potential targets: broad regulators fit when the target is a feature of the entire ripening process, pathway-specific targets fit a defined chemical or structural trait. Time-course studies can indicate whether an intervention affects the rate of ripening, its onset or breaks up processes that were previously simultaneous. Breeders can use these cues to select alleles that specifically enhance the ultimate eating experience (Srivastava *et al*., 2026).

11. Connecting Genes, Transcripts and Metabolites

Genome sequence will only reveal a hypothesis of what a plant could possibly do, whereas transcript, protein, and metabolite measurements tell us what its fruit is doing at a particular stage. Transcriptomics reveals genes that change in expression during development or between contrasting genotypes (Mengist *et al*., 2026). Metabolomics records the biochemical end-products of any differences, including sugars, acids, pigments and aroma precursors. Extrapolating the two can propose regulatory relations that would not be revealed by either datas*et al*one. However, correlation between a transcript and a metabolite does not prove direct control: both may respond to maturity or to a third regulator. Genetic segregation, perturbation and biochemical evidence are needed to test a proposed mechanism (Shi *et al*., 2025).

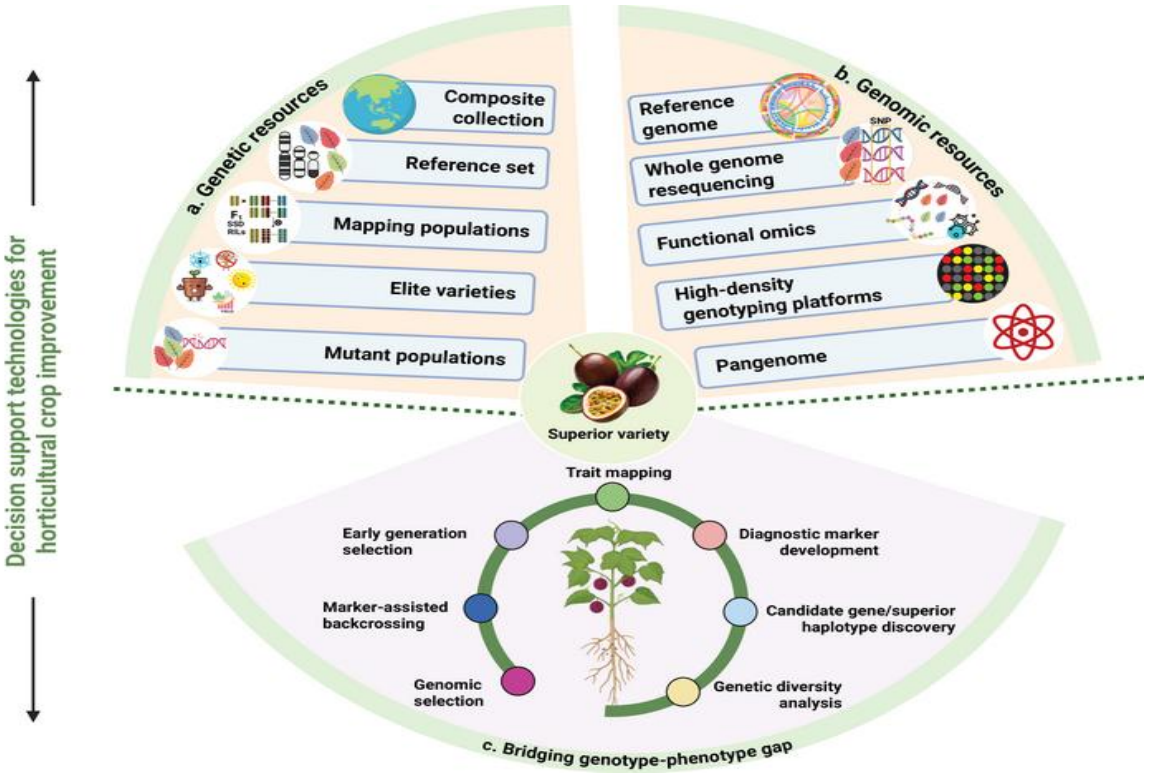
Sampling design is especially important in integrated studies. Peel and flesh may have different functions and expression patterns; even regions within one fruit can differ in light exposure or maturation. A mixed sample can mask a tissue-specific effect. Measurements taken at only one date may miss an early acting gene that causes a later metabolic effect (Xiao *et al*., 2026). Well-designed studies consider tissue, developmental stage, biological replication and analytical methods before attempting to detect molecular correlates. The most useful outcome of such an exercise is a testable model: a causal allele affecting expression or protein activity, thereby altering a pathway and produces a quality difference that can be measured in fruit and perceived when relevant (Nasiopoulou *et al*., 2025).

12. Marker-Assisted Selection and Genomic Prediction

Marker-assisted selection is most effective when a locus has a substantial, repeatable effect and the marker closely tracks the favourable allele. It allows breeders to discard unsuitable seedlings before committing years of field space to them. This can be particularly helpful for attributes that manifest only in mature trees, require costly assays, or are difficult to assess in all environments (Pincot *et al*., 2026). One should evaluate a diagnostic marker in the germplasm actually utilized by the breeding programme. Harnessing evidence from other traits and validation sets will be needed where the relationship between marker and trait may not hold in unintended populations where multiple crosses or even other outbred populations interbreed (Jang *et al*., 2024).

Many of the quality characteristics are simply too complicated for a small number of markers to predict. Genomic selection solves this issue by using markers spread throughout the genome which predict pedigree-based breeding values which are estimated from a training population of phenotype individuals (Sleper *et al*., 2025). Its success depends on the size, diversity and relevance of that population; the quality of phenotypes; relatedness of the training population to candidate selection; and the environmental stability of genetic effects. Prediction models trained on one cultivar group or production region should be tested before it is used elsewhere. The training population must be constantly updated with newly tested plants to make predictions still good as the breeding germplasm changes (Jung *et al*., 2025).

Figure 3. Integration of Genetic and Genomic Resources for Precision Breeding and Horticultural Crop Improvement



Source- Fulara *et al*., 2026

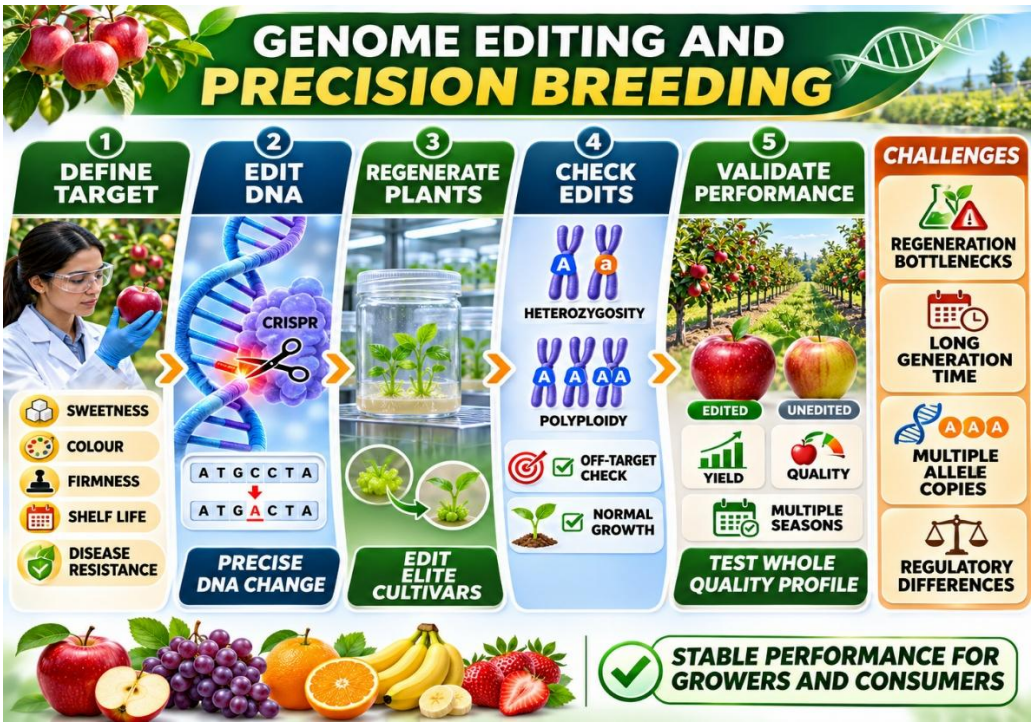
A practical programme will often combine methods. Strong, validated loci can be selected with diagnostic markers, while genomic prediction ranks candidates for complex traits such as texture or overall quality. Field evaluation remains necessary to confirm performance, detect unexpected defects and assess consumer response (Pacheco *et al*., 2026). Economic decisions also matter: the value of early prediction depends on genotyping cost, field-space savings, juvenile period and the proportion of seedlings that would otherwise be advanced. The purpose of molecular selection is to improve the timing and accuracy of decisions. It should be assessed by the quality of cultivars ultimately released and the resources required to develop them (Hislop *et al*., 2026).

13. Genome Editing and Precision Breeding

Genome editing alters a defined sequence without having to use breeding to get the desired recombination or the need to carry out the product through crossing. It is especially promising when a causal gene has been validated, its likely side effects are known, and conventional breeding would bring in undesirable linked variation. Editing may disrupt a gene, change a regulatory region or reproduce a useful allele in an elite background (Sohail *et al*., 2025). Different interventions can have very different biological outcomes: a complete loss of function may be too strong, while a modest expression change will give the intended improvement. Precision means location and type of genetic change, not a guarantee that every output can be anticipated (Pal *et al*., 2025).

Fruit crops are considered difficult to apply to editing. Regeneration and transformation, in particular, can be undesirable due to poor efficiency or dependence on specific genotypes, whilst long generation times add additional time delays to screens, as required to purge out introduced editing machinery through crossing. Heterozygosity and polyploidy require careful attention to which allele copies were altered (Enciso-Rodriguez *et al*., 2026). A regenerated plant has to be examined for the desired editing, other changing sequence, normal growth, and stable fruit quality. Clonal propagation can retain a successful genotype, but it does not replace a multi-year assessment of quality and productivity. Delivery methods and regulatory requirements differ between crops and jurisdictions, so editing strategy will need to be determined within the context of the specific realities of a given breeding programme (Creeth *et al*., 2026).

Figure 4. Genome Editing and Precision Breeding for Fruit Quality Improvement



The strongest applications of this approach come from a logical chain of evidence: a quality limitation is defined; a credible target is recognized as the product of natural variation and functional experiments; a change designed to produce through editing; and the resulting fruit is tested against an appropriate unedited comparator (Berman *et al*., 2025). Evaluation should encompass the entire quality profile, yield, and performance across relevant conditions. This discipline prevents a striking improvement in one trait from concealing an unacceptable defect elsewhere. Editing expands the breeder's options, particularly for modifying an elite cultivar, but its success is measured by the same standard as any breeding method: a stable product that performs well for growers, supply chains and consumers (Ortega-Salazar *et al*., 2024).

14. Breeding Across Species, Environments and Markets

Comparative genomics can identify conserved genes and pathways across fruit crops, but the same pathway may not provide an equally effective breeding target in every species. Fruit anatomy, ploidy, ripening behaviour and consumer preferences influence the breeding value of an allele (Pacheco-Ruiz *et al*., 2025). For example, a sugar-

related gene identified in apple may suggest a candidate for improving sweetness in pear or peach, but its expression pattern, protein interactions and effects on yield require species-specific validation. Similarly, pigment regulators controlling anthocyanin accumulation in grape berries may function differently in apple peel or plum flesh. Cross-species genomic knowledge is most valuable when it generates hypotheses for experimental validation rather than assuming direct transferability of breeding outcomes (Beaumont *et al*., 2025).

Climate and production conditions increasingly define the concept of quality. Temperature changes can affect colour formation or acid balance; a change in the era of water availability can influence size and concentration of soluble solid, and the rate of physical damage of the crop can be increased by extreme weather conditions (Soufi *et al*., 2026). Conversely, a cultivar with world-renowned quality in one environment may offer an entirely different product elsewhere. Breeding programmes need to distinguish genetic stability from useful responsiveness. Depending on the assumptions of a market strategy, it may be worthwhile testing among representative environments to ensure these decisions are articulated and hopefully avoid the disappointment of a powerful genomic breakthrough failing commercially (Pascual *et al*., 2024).

Consumer preference adds another layer of specificity. A sweet fruit with low acidity may appeal to one market and seem flat in another. Texture expectations can differ between fresh consumption, shipping and processing. Implementations of quality objectives by partnering with growers, postharvest specialists and consumers and converting it into measurable selection criteria (Mashrapova *et al*. 2026). Sensory panels are valuable because laboratory traits do not always predict acceptance, but they require consistent samples and careful design. Associating sensory outcomes and chemical and genomic data can identify which attributes deserve priority. Such work enables precision breeding to target desired traits people want rather than any molecular trait that is easiest to measure (Harker *et al*., 2024).

15. A Practical Path from Discovery to Cultivar Development

A robust quality-breeding pipeline begins by defining the product: who will consume it, at what stage, after what storage period and with which minimum standards for appearance and production. Breeders then establish a phenotype protocol that captures both commercially important measurements and sensory attributes (Kennison *et al*., 2026). Diverse germplasm and breeding families are evaluated to locate useful variation, while genomic analyses identify associated regions and candidate genes. Functional experiments distinguish plausible causes from nearby markers. At this point, the programme can decide whether a validated marker, genomic prediction, conventional crossing or editing offers the most efficient way to move a favourable allele into suitable material (Agre *et al*., 2026).

Each transition requires a decision based on evidence. Maturity scoring and environmental effects must be revisited if a weak association withstands repeated tests before approval as a selection criterion. A favourably edited line that shows improved sugar concentration should also be evaluated for acid balance, aroma, fruit size, and seed performance (Osorio *et al*., 2026). All in all, a seedling with a high genomic prediction should be included in field trials evaluating production and postharvest traits. A threshold that is too high for a material to qualify can result in one solution overlooked in favour of a single intriguingly bright trait. The end goal of the breeding programme is to develop a consistent quality, and we must orchestrate the pipeline to find gains and costs as early as possible (Chacon *et al*., 2025).

Collaboration is important as no single dataset can capture the entire problem. Genetics can resolve inheritance, molecular biology to test mechanisms, analytical labs to profile compounds, and sensory specialists to determine if differences that have been measured are meaningful to consumers (Hettiarachchi *et al*., 2026). Studies in controlled laboratory settings can miss the soft spots that growers and postharvest researchers can discover. Common terminology for maturity, sampling and quality traits allows the results of these groups to be compared. Because data systems that link genotype, pedigree, field environment, fruit chemistry and sensory response are just as important as sequence depth. They are valuable as they allow a breeding program to make the same decisions based on different observations (Ma *et al*., 2026).

16. Research Priorities and Remaining Challenges

The main bottleneck for many fruit crops is turning the ability to produce sequence data into the capability to frequently and sensibly measure it. Unlike high-throughput imaging and non-destructive sensing can increase the number of fruits studied, these technologies have to be benchmarked against chemical and sensory reference points (Kim *et al*., 2026). More intricate phenotypes are required for other traits, e.g. crispness, off-flavour and quality changes during distribution. Genetic resources used in studies should also be diverse in nature. Narrow collections, though legit in the eyes of a scientist, could mean very little to a breeder working with an entirely different material. Sampling methods that are publicly documented and datasets that are well-journaled would facilitate fast and widespread application of results to be valid (Fass *et al*., 2025).

Greater attention is also needed to the diversity of genetic variation. Structural variants, allele dosage, and regulatory changes may help elucidate quality differences that were sub markedly by standard single-nucleotide marker studies. At the same time, increasingly complex datasets should not encourage claims of causality without experimental support (Munoz *et al*., 2024). An ideal model links variation to gene function, fruit composition, and the relevant sensory or commercial outcome. It is best to compare opposing alleles when conditions are as mediated as possible and report favourable and unfavourable effects this way. This is one of the best ways of identifying interventions that have benefits beyond the conditions in which they were initially identified (Yuan *et al*., 2025).

Finally, breeding objectives must accommodate change without losing their focus on eating quality. Production environments, distribution systems and consumer markets will continue evolving. Programmes to succeed will maintain genetic diversity over many years and periodically retrain their models. Precision breeding is still a practical decision-making tool: selected phenotypes, confirmed markers and useful crosses can make considerable gains even without going for national-scale editing or multi-omics factories. The progress will ultimately be measured in genomics knowledge: fruit that people are comfortable with, growers can grow with confidence, and supply chains can delivery intact (Escamilla and others, 2025).

17. CONCLUSION

Fruit quality emerges from the interaction of development, metabolism, ripening and the environment. Genomics has made these interactions more tractable by revealing alleles and pathways underlying size, sweetness, acidity, aroma, colour, texture and storage behaviour. The greatest advances occur when discovery is connected to rigorous phenotyping, functional validation and a clearly defined breeding objective. Major loci can support early marker selection, genome-wide information can improve prediction of complex traits, and editing can refine specific targets in valuable genetic backgrounds. None of these approaches eliminates the need to evaluate fruit at eating maturity and under realistic production and postharvest conditions. Future cultivar development will depend on combining molecular precision with a complete view of quality: one that includes yield and resilience, but ultimately succeeds through consistent consumer satisfaction.

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