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GENETIC AND BREEDING FOUNDATIONS FOR DEVELOPING ABIOTIC STRESS TOLERANT CUCURBIT CULTIVARS

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Abstract: Developing cucurbit cultivars that maintain marketable yield under water limitation, high temperature and salinity requires genetic improvement linked to realistic stress evaluation. This narrative review examines the genetic and breeding foundations of abiotic stress tolerance, with emphasis on melon, watermelon and pumpkin or squash. Selected primary studies are considered alongside a proposed framework for germplasm evaluation, parent selection and cultivar development. The reviewed evidence includes genomic diversity resources, functional investigation of drought-associated genes, physiological comparisons among melon genotypes, mutation-based selection in Cucurbita, and field assessment under combined stresses. These studies demonstrate useful opportunities for identifying donor material, but they do not establish a universal physiological marker or a single genetic solution across species and environments. The proposed framework integrates replicated stress phenotyping, validation of marker effects, crossing within compatible genetic backgrounds, selection for fruit quality, and multi-environment evaluation. Particular attention is given to distinguishing stress escape from physiological tolerance, early-stage survival from reproductive performance, and rootstock-mediated protection from inherited tolerance in the scion. Molecular tools should support, rather than replace, selection for reliable yield under the target production conditions. The review provides a research-oriented basis for cucurbit improvement; it reports no new field experiment or newly developed cultivar.

Keywords: cucurbits; abiotic stress; genetic resources; plant breeding; drought tolerance; heat tolerance; salinity; marker-assisted selection; genotype by environment interaction.

INTRODUCTION

Abiotic stress tolerance is a breeding objective whose meaning depends on the crop, production system and stage of development. A genotype that survives a severe seedling treatment may still produce few marketable fruits when stress occurs at flowering. Conversely, an early cultivar may avoid late-season water shortage without possessing greater tissue-level tolerance. For breeding purposes, tolerance therefore needs an operational definition: acceptable productivity and fruit quality under a specified stress regime, compared with relevant checks and with performance under favourable conditions.

This review focuses on melon (*Cucumis melo* L.), watermelon (*Citrullus lanatus*) and cultivated Cucurbita species, corresponding to the principal crop groups commonly included in the Uzbek term “poliz ekinlari.” They share some physiological responses but constitute distinct breeding

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systems. Species identity, reproductive compatibility and market class must remain explicit when findings are compared. A promising allele in melon cannot simply be treated as a transferable breeding marker for watermelon, and a vigorous pumpkin rootstock does not demonstrate heritable stress tolerance in the melon scion.

The central challenge is to connect the discovery of variation with a useful cultivar. Genomic information can help identify contrasting parents and track favourable alleles. Physiological measurements can clarify why plants differ. Neither approach alone establishes stable agronomic value. The purpose of this article is to examine selected evidence for genetic improvement and propose a breeding pathway that links these tools to yield, fruit quality and repeatable performance in target environments.

MATERIALS AND METHODS

The article is a narrative review based on a targeted online search of research publications and publisher records available on 12 October 2026. Search terms combined melon, watermelon, Cucurbita, drought, heat, salinity, genetic variation, candidate gene, physiological screening and breeding. Primary studies were prioritised when they directly examined genetic resources, stress-associated variation, functional gene evidence or agronomic responses. The selected material spans genomic, controlled-environment and field research. It is not a systematic review, and no exhaustive coverage, formal evidence grading or meta-analysis is claimed.

Evidence was assessed according to the biological material, developmental stage, stress environment and type of outcome measured. Genetic associations were distinguished from functional tests, and physiological responses were distinguished from demonstrated yield advantages. Findings in grafted plants or heterologous experimental systems were retained only with their original context. The breeding workflow developed below is an analytical proposal, not a description of trials performed by the authors. No accession from Uzbekistan is designated as tolerant without experimental evidence.

GENETIC RESOURCES AND THE EVIDENCE BASE

The diversity available within a crop determines the scope for selection. Zhao and colleagues generated a melon variation map from 1,175 accessions and identified genomic associations with agronomic traits [1]. This resource supports germplasm characterisation and the study of fruit-related variation. It should not, however, be described as direct proof that those accessions are tolerant to drought or salinity. A genomic collection becomes a stress-breeding resource when its members are evaluated under relevant stress treatments and their identity is traceable.

Landraces, breeding lines and compatible wild relatives may provide complementary forms of variation. Their usefulness should be judged through both donor traits and the cost of recovering an acceptable crop phenotype. A donor may carry advantageous stress responses alongside undesirable maturity, fruit size or quality. The proposed use of diverse material therefore includes pre-breeding: confirming the target response, making suitable crosses and selecting progeny that retain the useful trait while recovering the required agronomic background.

Direct genetic evidence is illustrated by the investigation of *CmPPR4* in melon. Xia and colleagues used a recombinant inbred population and complementary functional approaches to implicate this gene in drought resilience [2]. This moves beyond a simple correlation between a

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marker and a stress score. Nevertheless, its breeding value in a new population still requires validation of the relevant allele and phenotype. A drought-associated allele should not be assumed to confer heat tolerance, salt tolerance or acceptable fruit yield in every genetic background.

In watermelon, an association-mapping study evaluated 48 genotypes under controlled drought and examined relationships between iPBS markers and measured traits [3]. This illustrates the use of diversity-based screening to nominate material and markers for further breeding work. The associations should be tested in independent populations before routine selection. In particular, evidence from a limited marker panel should not be presented as a complete description of the genetic architecture of drought tolerance.

Evidence from pumpkin also requires attention to the experimental system. Li and colleagues characterised alcohol dehydrogenase genes in *Cucurbita moschata* and reported improved drought performance in *Arabidopsis* plants overexpressing *CmoADH9* [4]. This provides a basis for further investigation of gene function. The result is not equivalent to a validated, high-yielding drought-tolerant pumpkin cultivar. Follow-up work in the target crop is needed before the gene can be used as a practical selection criterion.

Mutation-derived variation offers another route. Alonso and colleagues screened an EMS-derived *Cucurbita pepo* collection and identified salt-tolerant lines, with subsequent evaluation beyond initial germination screening [5]. This demonstrates that induced variation can broaden the material available for improvement. A breeding programme using such lines would still need to examine inheritance, unwanted linked or background mutations, reproductive performance and fruit quality. The existence of a selected mutant does not remove the need for a conventional cultivar evaluation process.

PHYSIOLOGICAL TRAITS AS BREEDING EVIDENCE

Physiological traits help distinguish plant responses, but their value depends on the selection question. Chevilly and colleagues compared contrasting melon cultivars under drought and salinity and found that useful physiological and metabolic distinctions differed between the two stresses [6]. The implication is that a common “stress tolerance score” should not be built by assuming that the same indicator has the same interpretation under every treatment. Trait relevance must be established within each crop, stress regime and developmental stage.

Sarabi and colleagues documented variation in physiological, biochemical and ionic responses among melon landraces exposed to salinity [7]. Their work supports evaluating multiple response domains rather than relying on visible injury alone. For breeding, the important question is whether an indicator predicts continued growth or yield when genotypes are compared under equivalent exposure. A large response to stress may reflect effective adjustment, substantial injury or both. Its direction is not sufficient to identify a superior parent.

Ansari and colleagues examined drought responses in the melon genotype SC-15, including changes in photosynthetic activity, antioxidant enzymes and protein profiles [8]. Such mechanistic studies help formulate hypotheses about adaptation, but a response observed in one genotype cannot establish a selection threshold for an entire germplasm collection. The proposed breeding use is to identify a manageable set of candidate measurements and then test their predictive value in a broader, replicated population.

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Combined stress introduces a further complication. Flores-León and colleagues assessed cucurbit accessions under field drought and combined heat–drought conditions, linking physiological observations with agronomic outcomes [9]. Their results support evaluating combined exposure directly. In this review, the breeding inference is that selection under drought alone may miss genotypes whose reproductive performance changes when high temperature accompanies water limitation. Field validation should therefore resemble the combination and timing of stresses that the target cultivar is expected to encounter.

Rootstock research provides useful complementary evidence. Ulas and colleagues showed that selected Cucurbita rootstocks improved physiological and nutritional responses of melon scions under hydroponic salinity [10]. This is relevant to rootstock selection and production-system design. It must be kept separate from the claim that the scion itself has acquired heritable salt tolerance. A breeding programme should specify whether its final product is an own-rooted cultivar, a rootstock, or a tested graft combination, because these products require different selection criteria.

FROM PHENOTYPING TO GENETIC INFERENCE

Reliable genetic analysis begins with reliable exposure. For a proposed drought trial, reporting only the number of days without irrigation is inadequate: plant size, soil volume and evaporative demand can cause unequal stress among entries. Soil water status, irrigation amounts and weather should be recorded alongside plant measurements. For heat evaluation, the timing and duration of elevated temperature should be described, particularly around flowering. For salinity, irrigation-water conductivity, root-zone salinity and salt composition should be distinguished. These records make genotype comparisons interpretable.

The experimental unit must also match the treatment. If heat is imposed on a chamber, plants inside that chamber are subsamples of one treatment environment, not independent chamber replicates. A proposed design should use independent environmental replication or repeated experimental runs and describe their limitations. Likewise, field plots sharing one irrigation unit should not automatically be analysed as independently treated replicates. Good genetic material cannot compensate for a design that confounds genotype, treatment and position.

Quantitative trait locus mapping and genome-wide association analysis answer related but different questions. A segregating family tracks variation between particular parents, whereas a diversity panel explores variation across a broader set of accessions. In both cases, a marker can be associated with a trait without being causal. The proposed validation sequence is to reproduce the association, test the marker in additional backgrounds and determine whether its effect persists under relevant field conditions. Population structure, relatedness and multiple testing should be considered when interpreting association results.

Expression evidence requires similar restraint. A gene whose transcript increases after stress may contribute to protection, participate in damage responses or reflect a secondary change. Functional experiments strengthen inference, but the crop, tissue and developmental stage used in those experiments remain relevant. Consequently, transcript abundance alone should not be used to classify a breeding line as tolerant. The practical objective is a reproducible relationship between inherited variation and useful crop performance.

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PROPOSED BREEDING FRAMEWORK

The first stage should define a target product profile. This includes species and market class, growing season, irrigation system, expected stress combinations, acceptable maturity, marketable yield and fruit-quality requirements. Separate targets may be necessary for drought-prone and salt-affected production systems. Without this definition, selection can reward traits that look favourable in the laboratory but have little value in the intended market or environment.

The second stage should assemble and document a diverse germplasm panel. Passport information, seed source and regeneration history need to be retained. Initial multiplication should minimise avoidable differences in seed quality, because uneven emergence can otherwise be mistaken for genetic stress tolerance. A preliminary screen can remove poorly adapted entries, but severe one-step elimination should be avoided when the stress treatment has not been calibrated. Sensitive and tolerant checks, where independently validated, help reveal whether the treatment is discriminating rather than universally lethal.

The third stage should combine controlled screening with reproductive-stage evaluation. Early measurements may include establishment, relative growth, water status and visible injury. Later measurements should include flowering, fruit set, marketable fruit number, fruit mass and crop-specific quality traits. The same genotype should be assessed under a suitable control and stress treatment. Absolute performance under stress should be considered together with relative decline: a low-yielding genotype can show a small percentage loss simply because its unstressed yield was already low.

The fourth stage should select parents for complementary value. A donor with a repeatable stress response can be crossed with a compatible elite parent possessing the required fruit type and local adaptation. Progeny evaluation should retain both stress and non-stress environments so that tolerance is not selected at the expense of basic productivity. Backcrossing is a possible route when the purpose is to transfer a relatively defined donor contribution; broader population improvement may be more suitable when useful variation is distributed across several traits. The choice should follow the observed inheritance rather than a fixed technological preference.

The fifth stage can incorporate molecular selection where it adds demonstrable value. Marker-assisted selection is most useful when the marker–trait relationship is sufficiently reliable in the breeding material. For complex performance involving many small effects, a genomic prediction approach may be investigated, but only with an appropriate training population and independent validation. These are proposed options, not established performance claims for the present authors' material. Prediction should be tested on new families or environments, because random splitting of closely related observations may overstate its practical accuracy.

The sixth stage should evaluate advanced lines across representative environments and seasons. A mixed-model analysis can be planned to separate genotype, environment and genotype-by-environment effects, with treatment structure represented correctly. The aim is not necessarily to identify one universally best line. Some lines may be broadly useful, while others may suit a specific stress pattern. Stability should therefore be interpreted together with mean performance and the intended deployment area. Fruit sweetness, texture, appearance, storage behaviour and seed-production feasibility remain part of advancement decisions.

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SELECTION INDICES AND QUALITY CONTROL

A selection index is proposed as a transparent decision aid rather than a substitute for biological judgement. It could combine marketable yield under stress, yield under control conditions, reproductive success and a small number of validated secondary traits. Adverse outcomes, such as unacceptable fruit quality or poor establishment, can be treated as exclusion criteria. Index weights should reflect breeding priorities and measurement reliability; they should not be presented as universal constants. Highly correlated traits should be checked to avoid repeatedly rewarding the same underlying response.

Multivariate analysis can help describe trait relationships and identify unusual material, but a principal-component score is not automatically a tolerance score. A component may summarise plant size or maturity rather than stress adaptation. Any ranking derived from such analysis should be tested against an independent agronomic endpoint. Confidence intervals, replication and the consistency of rankings across experiments are more informative than an unqualified list of “best” genotypes from one screening run.

The breeding record should preserve both successes and failures. Accessions rejected because of weak fruit quality, unstable tolerance or poor crossing performance provide information about trade-offs. Candidate markers that fail in new backgrounds should also be recorded. This prevents repeated investment in associations that are population-specific and helps distinguish a genuine donor from a genotype that performed well only under an unusual combination of experimental conditions.

DISCUSSION

The selected literature supports several complementary entry points into cucurbit improvement: genomic characterisation, functional gene investigation, physiological screening and generation of new variation. Their evidential strength differs. Large diversity resources reveal opportunities; gene studies clarify mechanisms; stress trials identify candidate donors; and multi-environment yield evaluation establishes practical value. Treating these stages as interchangeable would exaggerate the readiness of a promising discovery for cultivar development.

For a programme relevant to Uzbekistan, the proposed priority is to connect local germplasm evaluation with clearly measured production constraints. Local origin alone should not be used as proof of adaptation to every form of stress. Imported material likewise needs local testing before its performance can be inferred. An efficient starting point is a documented panel, a limited set of repeatable physiological measurements and yield trials under representative conditions. Molecular analysis should be added where it resolves a specific breeding question or improves selection efficiency.

This review is limited by its targeted source selection and by differences among the reviewed experiments. It does not quantify a pooled genetic effect or establish a validated ranking of donor accessions. Evidence is also uneven across crop species, developmental stages and stress combinations. The proposed framework should therefore be regarded as a testable research plan. Its success would need to be measured through selection response, field performance and the quality of resulting cultivars.

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CONCLUSION

The genetic improvement of abiotic stress tolerance in cucurbits depends on combining useful inherited variation with precise phenotyping and realistic agronomic selection. Candidate genes, molecular markers and physiological indicators are valuable when their effects are reproduced in the target breeding material and linked to acceptable yield. They cannot by themselves establish broad stress tolerance or cultivar readiness.

A defensible development pathway begins with a clear product profile, progresses through germplasm characterisation and compatible crossing, and concludes with multi-environment testing that retains fruit quality as a central criterion. Drought, heat and salinity should be evaluated separately where their mechanisms differ and jointly where combined exposure defines the production problem. This approach provides a practical basis for developing improved melon, watermelon and Cucurbita cultivars without overstating the evidence available from early-stage screening.

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