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From Loci to Landscapes: The Molecular Determinants of Plant Adaptation and Migration Under Climatic Stress

Climate Change * Conservation * Evolution

Introduction: The Sessile Imperative

The survival of plant species in an era of rapid climatic flux depends on two fundamental strategies: migration to favorable habitats or adaptation in situ. Unlike mobile animals that can behaviorally escape thermal stress, plants are rooted in place; when precipitation regimes, temperatures, or seasonal cues shift, a population must tolerate change through phenotypic plasticity, evolve genetic adaptations, or disperse seeds across the landscape.[1] Anchored by the 2025 synthesis by Hancock et al. in the Annual Review of Ecology, Evolution, and Systematics, recent advances in evolutionary genomics have illuminated the molecular and demographic machinery governing these responses.[1]

Anthropogenic climate change has compressed evolutionary timescales from millennia to decades, catalyzing an integration of population genetics, molecular biology, and landscape ecology.[1] As Hancock et al. (2025) demonstrate, adaptive trajectories are constrained by the interplay between standing genetic variation and de novo mutation, the mutational target size of selected traits, and the demographic costs of range expansion -- specifically expansion load and allele surfing.[1][2] Across model annuals such as Arabidopsis thaliana and Capsella rubella, long-lived boreal conifers, and domesticated maize, convergent evolution recurs at key regulatory hubs, yet no single molecular pathway dominates the adaptive landscape.

Theoretical Frameworks of Genetic Adaptation in Plants

Evolutionary adaptation proceeds through shifts in allele frequency across generations, governed by the origin of beneficial variants and the genetic architecture of selected traits.

Standing Genetic Variation vs. De Novo Mutation

Rapid evolutionary responses to contemporary climate change rely predominantly on standing genetic variation (SGV) rather than slow, stochastic de novo mutations.[1] Because standing variants already circulate within a population, selection acts without mutational lag time, and pre-existing alleles have often been pre-tested by past environments.[5] Adaptation from SGV typically generates "soft" selective sweeps, in which multiple haplotypes carrying beneficial variants rise in frequency simultaneously.[6] For example, during maize domestication, the Tb1 (Teosinte branched 1) apical-dominance allele was selected from standing variation present in wild teosinte.[4] Nevertheless, de novo mutations remain important across longer timescales and at colonization fronts.[5]

Mutational Target Size and Polygenic Architecture

A key determinant of evolutionary speed is mutational target size -- the number of loci, cis-regulatory elements, and pathways capable of altering a phenotype.[1] Polygenic traits (biomass, flowering time, drought tolerance) possess large mutational target sizes across hundreds of loci exhibiting epistasis, enabling rapid, incremental adaptation via subtle allele-frequency shifts across the genome.[8][9] Conversely, oligogenic traits (such as target-site herbicide resistance) have small mutational target sizes and evolve via hard sweeps of large-effect substitutions.[11] Because most climate-resilience traits are polygenic, single-gene genetic engineering rarely replicates full adaptation without considering the broader genomic matrix.[10][12]

| Adaptation Mode | | Genetic Basis | | Detection Method | | Evolutionary Speed | | Empirical Example |

| Oligogenic | | Few loci of large effect | | High FST outliers, QTL mapping | | Rapid (if SGV or hotspot exists) | | FRIGIDA vernalization loss |

| Polygenic | | Hundreds of small-effect loci | | Polygenic scores, subtle allele shifts | | Continuous, incremental | | Drought tolerance, biomass |

| Convergent | | Distinct lineages recruit same genes | | Comparative environmental genomics | | Variable across clades | | Boreal cold hardiness in conifers |

Genomic Consequences of Range Expansion

As isotherms shift poleward and upslope, plant populations tracking their thermal niches undergo range expansion -- a demographic process that profoundly restructures genomic diversity.[1]

* Expansion Load: Colonization fronts are founded by small numbers of pioneer individuals, reducing effective population size and amplifying genetic drift relative to purifying natural selection. Consequently, moderately deleterious mutations escape purging and accumulate at the leading edge, depressing mean population fitness.[2] In Campanula americana (American bellflower), populations farthest from glacial refugia exhibit severe inbreeding depression and strong heterosis upon inter-population crossing, confirming the accumulation of recessive expansion load.[3]

* Allele Surfing: Neutral, beneficial, or deleterious variants present at the wave front can "surf" demographic growth to fixation across newly colonized landscapes, generating spatial allele gradients that mimic local adaptation and require explicit demographic modeling to disentangle from selection.[2][7][13]

* Reproductive Assurance (Baker's Law): Mate and pollinator scarcity at range margins strongly selects for autonomous self-fertilization.[1][3] While selfing guarantees short-term colonization success, it reduces effective recombination and genetic diversity, potentially constraining long-term adaptive capacity.[14]

Key Molecular Pathways and Convergent Evolution

Phenology and Dormancy: FRIGIDA, FLC, and DOG1

Synchronizing vegetative growth and reproduction with seasonal thermal windows is critical for plant fitness.[1] In Arabidopsis thaliana, the FRIGIDA (FRI) locus activates FLOWERING LOCUS C (FLC) to enforce a winter vernalization requirement. While northern European populations maintain functional FRI alleles for winter-annual life cycles and southern populations harbor loss-of-function deletions for rapid cycling, functional and non-functional haplotypes often co-occur to bet-hedge against interannual climate variability.[15] In its relative Capsella rubella, independent 5' UTR cis-regulatory deletions in FLC independently attenuate expression and accelerate flowering.[16] At the germination stage, DELAY OF GERMINATION 1 (DOG1) functions as a maternal thermal-history sensor that modulates gibberellin (GA) catabolism and endosperm-cap weakening; DOG1 haplotypes diverge across climatic clines and exhibit pleiotropic trade-offs with adult drought tolerance.[17][18][19]

Developmental Heterochrony and Deep-Time Convergence

Morphological adaptation frequently targets master transcription factors. During colonization of the Azores by Cardamine hirsuta, a selective sweep at the SPL9 transcription factor QTL altered developmental heterochrony and shoot architecture to match insular seasonal moisture regimes.[20] Across macroevolutionary timescales, comparative genomics of White Spruce (Picea glauca) and Lodgepole Pine (Pinus contorta) -- diverged by over 100 million years -- revealed convergent recruitment of ~47 conserved cold-hardiness and abiotic stress genes.[21] Similarly, domesticated maize (Zea mays), which suffered a ~95% effective population bottleneck accompanied by linked deleterious load, achieved highland cold tolerance through both convergent pathway mutations and adaptive introgression from wild highland teosinte.[22][23]

| Gene / Locus | | Taxon | | Primary Function | | Adaptive Significance & Molecular Mechanism |

| FRIGIDA (FRI) | | Arabidopsis thaliana | | Flowering repressor | | Latitudinal phenology clines via loss-of-function vernalization release.[15] |

| FLC | | Arabidopsis / Capsella | | MADS-box repressor | | Parallel early-flowering evolution via 5' UTR cis-regulatory deletions.[16] |

| DOG1 | | Arabidopsis thaliana | | Seed dormancy sensor | | Maternal thermal sensing and GA regulation; pleiotropic drought link.[17][19] |

| SPL9 | | Cardamine hirsuta | | Developmental timing | | Selective sweep on heterochronic shoot QTL in Azorean morphotype.[20] |

| Tb1 | | Zea mays (Maize) | | Apical dominance | | Soft sweep from teosinte standing genetic variation.[4] |

| Cold Suite (~47 loci) | | Picea / Pinus | | Freezing tolerance | | Deep-time convergent recruitment of conserved stress modules.[21] |

Conclusion: Navigating the Anthropocene Adaptive Landscape

As synthesized by Hancock et al. (2025), plant adaptation to climatic stress and range shifts is an emergent property of genomic architecture interacting with demographic history.[1] Discrete phenological switches with small mutational target sizes (such as FRI/FLC) evolve repeatedly via targeted regulatory mutations, whereas quantitative stress tolerance relies on polygenic allele-frequency shifts fueled by standing genetic variation.[8][10] Simultaneously, poleward migration imposes severe demographic trade-offs, where allele surfing, expansion load, and transitions to selfing can erode adaptive potential at the colonization front.[2][3] Conserving wild genetic reservoirs and integrating demographic modeling with field-validated functional genomics will be decisive in determining which plant lineages persist across the Anthropocene.[1][24]

Updates... (Nov 22, 2026): Enriched all 24 peer-reviewed plant evolutionary genomics references with verified exact publication dates from CrossRef and OpenAlex metadata.

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