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Breeding for Climate-Resilient Maize Integrating Phenotyping and Genomic Tools

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Maize (Zea mays L.) is a globally important cereal crop, but its productivity is increasingly threatened by climate change. Rising temperatures, erratic rainfall, frequent droughts, and emerging biotic stresses compromise yield stability. Developing climate-resilient maize varieties is therefore essential to ensure food and nutritional security. Conventional breeding approaches, although effective, are limited by long breeding cycles and environmental variability. Integration of high-throughput phenotyping (HTP) and genomic tools provides new opportunities to accelerate the development of climate-resilient maize.

Climate-Related Challenges in Maize

- Drought and heat stress: Reduced photosynthetic efficiency, kernel abortion, and poor grain filling.
- Flooding and waterlogging: Root damage and impaired nutrient uptake.
- Emerging pests and pathogens: Climate-induced shifts in distribution and virulence.
- Nutrient-use inefficiency: Greater demand for resilient genotypes under resource-limited conditions.

Role of Phenotyping in Climate Resilience

Phenotyping is the foundation of breeding for stress resilience. Modern tools allow precise measurement of complex adaptive traits under field and controlled conditions.

- Traits of interest: stay-green, canopy temperature depression, root architecture, anthesis-silking interval, kernel set under stress.
- High-throughput phenotyping platforms:
- ✓ UAV/drone-based imaging for canopy vigor and stress indices.
- ✓ Thermal and hyperspectral sensors for stress detection.
- ✓ Root phenotyping systems (rhizotrons, shovelomics).
- Advantages: enables non-destructive, multi-trait, and dynamic assessment across environments.

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Genomic Tools in Climate-Resilient Maize Breeding

- 1. Marker-Assisted Selection (MAS): Effective for major stress-tolerance genes/QTLs (e.g., *ZeaATM1* for drought tolerance).
- 2. Genomic Selection (GS): Uses genome-wide markers to predict breeding values, accelerating improvement of polygenic stress traits like yield under drought.
- 3. Genome-Wide Association Studies (GWAS): Identifies novel loci linked to stress adaptation.
- 4. Genomic Editing (CRISPR/Cas): Enables targeted modification of stress-responsive genes (e.g., ABA pathway regulators, heat shock proteins).
- 5. Integration with transcriptomics and metabolomics: Helps dissect stress pathways and identify candidate genes for functional validation.

Integration of Phenotyping and Genomics

The synergy of phenotyping and genomics is critical for designing climate-resilient maize.

- Phenomics-guided genomics: Precise trait dissection enables identification of genomic regions associated with stress tolerance.
- Genomic prediction enhanced by HTP: Phenotypic data from sensors strengthen prediction models, increasing selection accuracy.
- Breeding pipelines:
- 1. Define climate-resilient ideotypes (e.g., drought-tolerant, heat-resilient maize).
- 2. Conduct multi-environment phenotyping under stress.
- 3. Apply GWAS and GS for trait-marker associations.
- 4. Deploy MAS or GS to select superior genotypes.
- 5. Validate key genes via genome editing or transgenics.

Case Examples

- Drought Tolerant Maize for Africa (DTMA): Combined field phenotyping with MAS and GS, leading to high-yielding drought-tolerant hybrids adopted in sub-Saharan Africa.
- CIMMYT's Genomic Prediction Models: Integrated UAV-based phenotyping with SNP genotyping to enhance selection accuracy for heat and drought tolerance.
- Root architecture studies in tropical inbreds: Linking shovelomics-derived root traits with genomic regions conferring water-use efficiency.

Future Perspectives

- Machine learning and AI: To integrate large-scale phenotypic and genomic datasets for predictive breeding.
- Pan-genomics and haplotype-based breeding: To exploit untapped diversity for stress resilience.
- Climate-smart multi-stress breeding: Combining tolerance to drought, heat, and emerging pests in single varieties.
- Farmer-participatory breeding: Ensuring climate-resilient varieties are adapted to local conditions and farmer preferences.

Conclusion

Breeding climate-resilient maize requires a holistic integration of advanced phenotyping platforms and genomic tools. By combining precise trait measurement with genome-wide predictions, breeders can accelerate the development of stress-tolerant, high-yielding, and stable maize varieties. Such integrative approaches will be pivotal in safeguarding global maize production under the changing climate.

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