A Sorghum Pangenome Reference Improves Global Crop Trait Discovery

Background/Objective

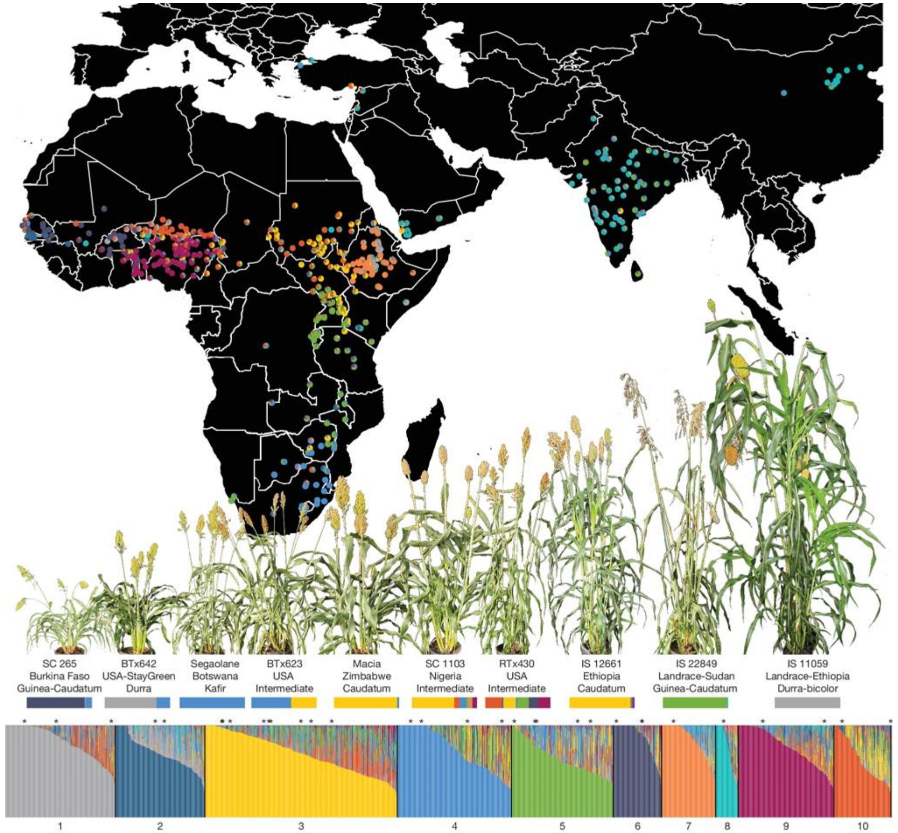
Expanding food security and economic prosperity under rapidly changing environmental stresses will require transformative advances in global crop improvement speed and efficacy. Diversity within grain and bioenergy sorghum offers raw materials for genetic gain and cultivar improvement. However, breeding efforts can be constrained by highly specialized traits and breeding targets. Thus, a global pangenome resource—including a reference genome to anchor analyses, many genomes from locally adapted cultivars and whole-genome re-sequencing of global diverse germplasm—is essential to accomplish this vision.

Approach

We constructed a 33-member pangenome reference and a diversity panel across 1,984 cultivars and landraces. We leveraged these resources to explore the complex interplay among historical contingency, ongoing adaptation and previously uncharacterized structural diversity.

Results

Our analyses conclusively demonstrated multiple nested and deeply diverged structural variants in the domestication gene *SHATTERING1*, which distinguish the previously established multicentric origin of sorghum. Applying landscape genomics revealed how gene flow and secondary contact created the complex genetic mosaic in contemporary breeding networks. As proof of concept for pangenome-accelerated trait discovery, we connected biosynthetic gene cluster structural variation to phenotypic leaf concentration of the cyanogenic glucoside dhurrin.



Geographical and genetic distribution of the sorghum diversity panel.

Significance/Impacts

The resources and methods introduced here for sorghum not only provide valuable community assets to describe global species diversity but also establish a necessary foundation for effective trait discovery using pangenomics. Consequently, it will pave the way for accelerated pangenome-enabled traditional breeding and genome editing of locally adapted alleles across global sorghum germplasm.

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