

Executive Summary (299 words): Sorghum is the most drought-tolerant dual-purpose (grain + straw) cereal crop of the semi-arid tropics and subtropics, where development challenges are the greatest and market failure is most acute. As such, it is both a priority for further improvement and a botanical model from which we might glean information about drought tolerance that might be leveraged in improvement of many other cereals by comparative approaches. Sorghum has recently become only the second cereal (after rice), to have its genome fully sequenced, opening new doors to its improvement and enhancing its value for comparative biology.

In a partnership joining African and Asian sorghum improvement researchers with genomic scientists experienced in crop breeding and germplasm enhancement, we will engage the sorghum sequence in a balanced approach to durably increase rates of sorghum improvement. Toward a pathway joining discovery research of increasing scope and sensitivity with application to the needs of resource-poor farmers living in drought-prone environments, early study of a few genes already known to have qualitative effects on drought tolerance will set the stage for identifying a growing pipeline of additional genes/alleles with more subtle effects, engaging several previously GCP-funded resources. Key to both discovery research and product development/delivery will be our focus on breeding populations in which drought tolerance will be combined with other traits that address production constraints in West and Central Africa, Eastern and Southern Africa, and South Asia. By applying sorghum's fully-sequenced genome to study of these field-proven genetic resources, we will elucidate genotype x environment interactions that render drought tolerance a difficult trait to work with. Improved knowledge of sorghum presents a singularly-promising opportunity to leverage comparative genomics approaches to benefit improvement of many other cereals. NARS scientists are full research partners, and will also benefit from training visits to UGA and/or ICRISAT.

Scientific Summary (277 words): Fine-scale characterization of qualitative factors related to sustained photosynthetic output under drought stress, will yield improved understanding of the structure and functions of genomic regions of importance to sorghum improvement, advancing genetic dissection and molecular cloning of genes conferring the phenotypic effects mapped to these regions.

Empirical testing of key combinations of *stay-green* QTLs will reveal the comparative efficacy of various combinations under stress conditions in Ghana, India, and Sudan, also providing for obtaining additional recombinants needed to reduce linkage drag. The sorghum sequence will provide us with the means to design comparative DNA markers that are suitable for utilization both in sorghum and in many additional cereals.

Transcriptome profiling of a diverse sampling of field-proven germplasm will support development of hypotheses about roles of specific genes and pathways in drought response. We will begin to test these and other hypotheses based on analysis of the sorghum sequence, using breeding populations in which drought tolerance will be combined with other traits addressing production constraints in West and Central Africa, Eastern and Southern Africa, and South Asia.