Genomic Basis of Climatic Adaptation of Ethiopian Sorghum [S. bicolor (Moench)] Landraces

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Abstract
Population structure analysis showed that the Ethiopian sorghum germplasm consisted of 12 subpopulations with high levels of admixture (47%). Redundancy analysis indicated that a larger proportion of SNP variation was not explained by either agro-ecology or geographical location. Most of the subpopulations grouped to the dura botanical race. The dura type was distributed throughout most of the Ethiopian agroecological zones. Genome-environment association (GEA) study identified 18 significant SNP markers for adaptive traits. These significant environmental SNP markers were co-located with previously identified drought and cold adaptation QTLs. Several priority candidate genes were identified around the significant GEA markers which have homologous genes in Oryza sativa Japonica genome with the function of abiotic stress tolerance. The associated GEA and candidate genes could significantly contribute in understanding the genetic control of adaptive traits in sorghum. Based on this result, the Ethiopian sorghum germplasm collection could be a source of traits for abiotic stresses adaptation for future breeding programs.

INTRODUCTION
The world environment is changing due to rising temperatures globally and erratic precipitation especially in developing countries. This environmental change not only affects the limits of species distribution but also the centres of distributions[1]. Hence, sorghum landraces originating from stress environments are major sources of adaptive traits for crop improvement[2]. A recent study reported that relatively more variance was explained by environment than by geographical locations in Senegalese sorghum[3]. Other studies in sorghum[4] have shown genome-environment associations (GEA) for high genetic differentiation among populations, identifying adaptive loci and predicting phenotypic variation. Understanding of the genetic diversity related to environment and geographical location using genome-environment association studies are important for breeders. Therefore, the objective of this study was to understand the extent and pattern of genetic diversity across different environments and genome-environment association (GEA) in Ethiopian sorghum germplasm.

MATERIALS AND METHODS
Genetic Materials
A total of 940 diverse sorghum germplasm landraces were used for this study. The genetic materials were obtained from the Ethiopian Biodiversity Research Institute (ETRI),2 Agricultural Research Center. The materials were selected systematically (Fig 1D) to include all agro-ecologies (Fig 1A), altitudes (Fig 1B), and sorghum producing regions of the country (Fig 1C).

Genotyping
Leaf samples of four individual plants were collected from 15 days-old seedlings. The leaf samples were dried using a freeze dryer (Alpha 1-2 LDplus). Total genomic DNA extraction and sequencing were conducted at Diversity Analytics Technology (DAT T PI), Canberra, Australia (http://www.diversityarrays.com)

RESULTS
The landraces were clustered into 12 subpopulations (Fig 2 & Fig 3) with high minor allele frequency (65.5%) and admixture (47%). The spatial interpolation of ancestry coefficients analysis showed the maximal local contribution of geographical location in Ethiopian landraces to ancestry, with individuals in specific subpopulations found to be located in geographic regions (Fig 4).

SNP variance partitioning across agro-ecology and geographical location
SNP variance explained only 7% by agro-ecology, 3% by geographical location and 3% colinearity (Fig 6). A large proportion of variance was not explained by either agro-ecology or geographical location, suggesting that other factors such as human activities, or human settlement and seed sharing among farmers could be significant.

CONCLUSIONS
Ethiopian sorghum germplasm is diverse with high level of admixture which dominated by the dura botanical race, with no representation of the kafir botanical race. Agro-ecology plays more role in Ethiopian sorghum variation than geographical location. This study confirmed that diverse Ethiopian sorghum germplasm has unique adaptive alleles which could be a source of useful genes for environmental stress adaptation.

References

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