



Sorghum in the 21st Century

Global Sorghum Conference

Resiliency and Sustainability in the Face of Climate Change

June 5-9 2023 The Corum Event Center, Montpellier, France

Lead Sponsor

KANSAS STATE
UNIVERSITY

College of Agriculture

Supporting the

 INTERNATIONAL YEAR OF
MILLETS
2023

BOOK OF ABSTRACTS

PROGRAM - ABSTRACTS

List of posters - List of participants

List of exhibitors - Exhibition plan



Mapping race differentiation along the cultivated sorghum genome

Jovanie Mendy^{1,2} (jovanie.mendy@cirad.fr), Abdoulaye Beye^{1,2}, Julien Frouin^{1,2}, Fabien De Bellis^{1,2}, Concetta Burgarella³, David Pot^{1,2}, Guilhem Sempere^{4,5}, Claire Billot^{1,2}, Christian Leclerc^{1,2}, Jean-François Rami^{1,2}, Monique Deu^{1,2}, Aude Gilabert^{1,2}, Jean Christophe Glaszmann^{1,2}

¹ AGAP Institut, Cirad, Montpellier, France ; ² AGAP Institut, Univ Montpellier, Cirad, INRAE, Institut Agro, Montpellier, France ; ³ Evolutionary Biology Centre, Uppsala University, Uppsala, Sweden ; ⁴ Intertryp, Cirad, Montpellier, France ; ⁵ Intertryp, Univ Montpellier, Cirad, IRD, Montpellier, France

Sorghum genetic diversity features morphological races such as Bicolor, Caudatum, Durra, Kafir and Guinea, as well as geographical origins throughout Africa and Asia. Among the different genetic groups, the Guinea margaritifera subrace receives a particular status suggesting a secondary domestication event. Whole genome sequencing data provide new ground to better understand sorghum genetic diversity. We have access to the wealth of sequencing data produced by the Sorghum Genomics Toolbox (SGT) project. We have complemented the SGT sample with 37 accessions that have extended the coverage of the margaritifera subrace. After a new SNP call, we recovered a dataset of 972, mostly cultivated, accessions characterised with 31 million SNP loci. We performed principal component analyses (PCAs) after applying different thresholds for minimum allele frequency and for missing data. Overall, we obtained high-level components that differentiate Guinea margaritifera materials, confirming the special status of this subrace. On this basis, we are characterising the distribution of this differentiation along the genome and the extent of genetic exchange between the margaritifera subrace and the other cultivated forms. The data is ready to be accessed on our South Green platform using the Gigwa data management tool and various analytical options that will make it an excellent resource for data mining by researchers and students interested in germplasm management and improvement.