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Shedding light on the evolutionary history of wild and cultivated african sorghum : “the *guinea margaritiferum* case”

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❖ Context

⇒ Crop-wild gene flow, through hybridization and introgression, may lead to important evolutionary consequences for both wild and cultivated plants living in sympatry.

⇒ An adequate sampling with correct identification of both wild and cultivated plants is a pre-requisite to study the evolutionary history of domesticated plants.

⇒ In sorghum, which is cultivated in sympatry with its wild relatives, gene flows between the two compartments may occur, and unambiguous assignments of accessions in these two compartments may become problematic, precluding a correct reconstruction of the evolutionary history of sorghum.

Wild sorghums

Wild sorghum in a guinea field

Guinea margaritiferum field

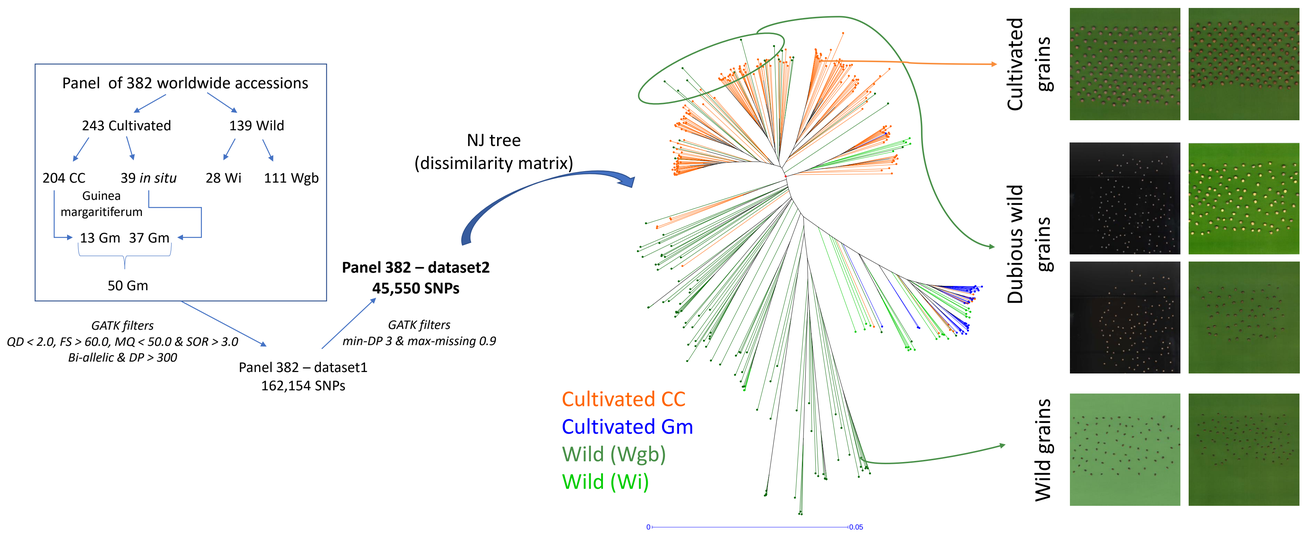
❖ Objectives

⇒ Validation of the status of wild and cultivated African sorghum accessions using morphological and genetic data

⇒ Analysis of wild ↔ crop gene flow

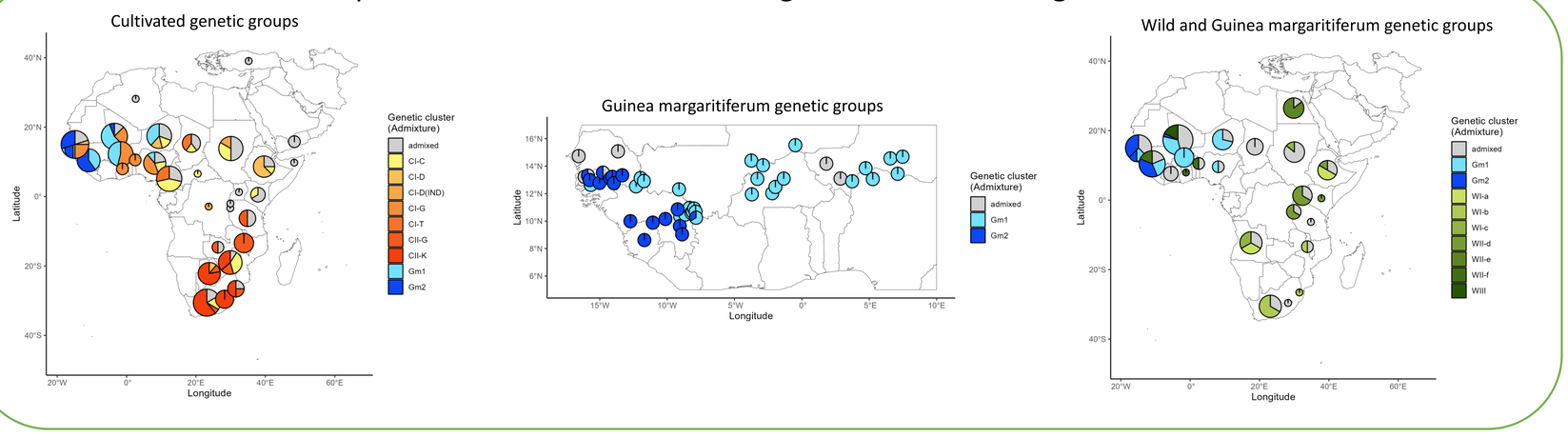
❖ Materials & methods

⇒ Genotyping-by-sequencing of 382 sorghum accessions, 243 cultivated from the CIRAD Core Collection (Cultivated CC) [1,2] and original prospections (*in situ*) [3,4,5], and 139 wild from gene banks (Wgb) and original prospections (Wi) [3,4,5].

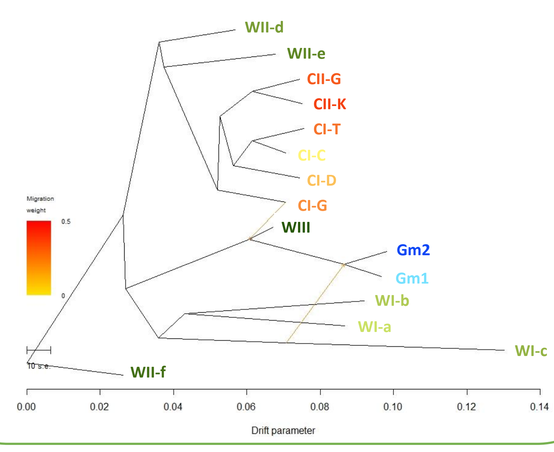


❖ Results

Population structure of African sorghum identified using Admixture



Analysis of gene flow using Treemix



⇒ Geographic structure of wild and cultivated sorghum accessions.

⇒ Two geographic Guinea margaritiferum groups that are genetically close to a group of wild accessions from Mali have been identified.

⇒ These groups bear signals of introgression with wild accessions from out of Western Africa but also with cultivated group of guinea from Western Africa

⇒ A complex history of sorghum, especially in Western Africa where gene flows between local wild and cultivated sorghums might have led to the emergence of a peculiar group.

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[1] Deu et al. 2006 Genome, 49(2):168 ; [2] Bouchet et al. 2012 PLOS One, 7(3):e33470 ; [3] Deu et al. 2008 Theor. Appl. Genet., 116(7):903 ; [4] Barro-Kondombo et al. 2010 Theor. Appl. Genet., 120(8):1511; [5] Sagnard et al. 2011 Theor. Appl. Genet., 123(7):1231