Exploring root development and architecture in one of the most heat and drought tolerant cereals, pearl millet

SIXTINE PASSOT1, FATOUMATA GNACKO2, JONATHAN ATKINSON3, BRIAN ATKINSON3, MIKAEL LUCAS4, SOAZIG GUYOMARC'H5, FRÉDÉRIC BOUDON6, MARIE COUDERC2, LEÏLA ZEKRAOUI2, CRAIG STURROCK3, NDJIDO KANE7, C. TOM HASH8, PASCAL GANTET5, MALCOLM BENNETT3, DARREN WELLS3, YVES VIGOUROUX4, YANN GUÉDON6, LAURENT LAPLAZE4

1 IRD, CIRAD & Inria, France
2 IRD, France
3 University of Nottingham, United Kingdom
4 IRD, France & LMI LAPSE, Senegal
5 Université de Montpellier, France
6 CIRAD & Inria, France
7 ISRA & LMI LAPSE, Senegal
8 ICRISAT, Niger
Contact: sixtine.passot@ird.fr

Higher global temperatures due to climate change places our agriculture at risk. Pearl millet is a subsistence cereal crop adapted to heat, drought and poor soils, and has potential to produce high grain and fodder yields at high temperatures where other crops fail. Root architecture contributes to this adaptation and thus provides promising traits that could be targeted by selection, but little is known about the genetic regulation of root traits in pearl millet.

To better understand pearl millet root growth pattern in soil and the impact of drought stress, we used the Hounsfield CT Facility (University of Nottingham). This allowed us to non-invasively analyze over time the soil volume explored by the pearl millet root system under different moisture conditions.

Using the RootTrace facility (University of Nottingham), we performed high-throughput phenotyping of a set of 108 genetically diverse pearl millet inbred lines, monitoring their early seminal root growth. These phenotypic data will be combined with genotyping-by-sequencing (GBS) data in order to identify genomic regions controlling this trait via genome-wide association studies (GWAS).