

from the development of a biomass phenotyping tool kit to the development of dedicated breeding schemes

¹ UMR AGAP, Cirad, F-34398 Montpellier, France

³ Laboratoire de Biotechnologie de l'environnement, INRA, F-11100 Narbonne, France.

⁵ *Euralis Semence, F-31705 Blagnac*

⁷Centre de Mise en Forme des Matériaux, Ecole des Mines de Paris/Mines ParisTech
F- 06904 Sophia Antipolis, France

⁸ *Centre Régional de Recherche Agronomique de Sotuba, Institut d'Economie Rurale, Mali*

⁹ *Unité de Génétique et d'Amélioration des Plantes Fourragères, INRA, BP6, F-86600 Lusignan, France*

¹⁰ Institut Jean-Pierre Bourgin, INRA, F-78026 Versailles Cedex, France

Sorghum is among the world's most important cereals in terms of human and animal nutrition. It is also currently identified as a promising crop to support the emerging bio-economy value chains that include energy production, biomaterials and molecules for food-feed and non-food-feed applications. In this context, the development of varieties adapted to the different end-uses is critical to provide the industries with relevant feedstock. Breeding sorghum for existing and emerging markets requires several steps, from the definition of "Industrial Ideotypes" down to the identification of "Molecular Ideotypes" in order to speed up the breeding process and optimize the genetic gains per unit of time. Firstly, expectations of the industrials in terms of composition and properties of the sorghum biomass for the different applications ("Industrial ideotypes") have to be defined. Secondly, "Industrial ideotypes" have to be translated in "Biological ideotypes" which refers to the properties of the raw sorghum material in terms of composition and structure. Third, high-throughput phenotyping tools compatibles with genetic analyses and breeding constraints have to be developed. Fourth, strategies to disentangle the genetic determinism of the "Biological Ideotypes" have to be set up. And fifth, relevant breeding schemes able to provide new hybrids and relevant parents have to be initiated. We will illustrate this process through two examples related to the production of sorghum biocomposites and the optimization of sorghum biogas production. For both targets, we will show how, through the use of the sorghum genetic diversity, traits affecting the final product properties were identified. We will then illustrate the efforts that are currently developed to tackle the challenges linked to high-throughput phenotyping. We will finally show how these

phenotyping tools are used on diverse association panels and multiparental designs to identify the genomic regions affecting the traits of interest and develop new hybrids and elite parents.

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