

Unveiling genetic diversity in jute mallow (*Corchorus spp.*): morphological clustering reveals distinctive traits among accessions from Africa and Asia

M. Pamela Afokpe^{1,2,3}, Serge Ologou^{2,3}, S. Romaric Kouihou⁴, Simon Jan de Hoop², Sognigbé N'Danikou^{3,5,6}, Enoch G. Achigan-Dako³, M. Eric Schranz^{1*}

¹ Biosystematics department, Wageningen University & Research, Wageningen, The Netherlands

² Hortigenetics Research (S.E. Asia) Ltd, Chiangmai, Thailand

³ Genetics, Biotechnology and Seed Science Unit (GBioS), Laboratory of Crop Production, Physiology and Plant Breeding (PAGEV), Faculty of Agricultural Sciences (FSA), University of Abomey-Calavi, Abomey-Calavi, Republic of Benin

⁴ BASF Innovation Center Gent, Belgium

⁵ Eastern and Southern Africa, World Vegetable Center, P.O. Box 10, Duluti, Arusha, Tanzania

⁶ Ecole d'Horticulture et d'Aménagement des Espaces Verts (EHAEV), Université Nationale d'Agriculture (UNA), BP 43, Kétou, Republic of Benin

*Corresponding author: eric.schranz@wur.nl

Supplemental File 4: Example of distinctive morphological traits of species found in the 283 jute accessions studied (a) Long pod shape of *C. olitorius* var. *olitorius* (b) Palmate leaves and long pod shape of *C. olitorius* var. *incisifolius* and (c) Round pod shape of *C. capsularis*

