



Identification of new genomic sources for aluminum tolerance in hexaploid wheat breeding lines using phenotypic and genotypic screening

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Abstract:

The present study was investigated in a set of 45 hexaploid wheat breeding lines collected from South Africa, Kenya, Egypt, Cameroon, Ethiopia and Australia for acid soil with aluminum tolerance through phenotypic and genotypic screening. Among these, Betta (acid soil-sensitive), Atlas 66 (acid soil-tolerant) and Chinese spring (partially tolerant) were included as standard controls cultivars for phenotypic and genotypic analysis, while four international standard check varieties (Carazinho, Egret, ES8, ET8) were used when studying the allelic variations of resistance gene (MATE1B). These accessions were phenotyped in a greenhouse experiment and genotyped through genotyping-by-sequencing (GBS). Standard checks showed a citrate efflux concentration of 8.6 μmol (Atlas66), 7.66 μmol (Chinese spring) and 6.1 μmol (Betta) and among the evaluated genotypes, 18 best lines were selected for their high tolerance through phenotypic screening. Furthermore, the GBS protocol used for characterizing genetically accessions have produced 80 124 single nucleotide polymorphism (SNP) markers. So, we defined SNP haplotypes around the MATE1B gene and identified 4 markers defining three distinct haplotypes around, where accessions have carried the alleles CATA for haplotype A, CGCG for haplotype B, and TGCG for haplotype C. For all traits, the phenotypes corresponding to haplotype A were significantly highest than others. To conclude, we suggest that SNP markers associated with haplotype A will provide a useful tool in marker-assisted breeding programs to improve wheat productivity in acid soil under aluminum toxicity conditions.

Biography:

Honore Tekeu has completed his PhD at the age of 32 years from Laval University (Canada), Stellenbosch University (South Africa) and University of Yaoundé 1 (Cameroon). He is using the tools of Next-Generation



Sequencing technologies (Genotyping by Sequencing and SNP Infinium iSelect array), applying bioinformatics (using Unix command line tools as shell scripting, FastGBS and UNEAK pipelines), statistical methods (using R, SAS, Genstat softwares) for wheat breeding and genetics. He attended many international conferences such as the 4th and 3rd Canadian Wheat Symposium (<http://www.cwfhb-cws.com>, respectively the 19-22 November 2018, Winnipeg, Canada and 22-25 November 2016, Ontario, Canada).

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