**Identification of genomic regions associated with productivity, specific qualitative traits and low P adaptation using BCNAM populations**

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**Challenges addressed**

This research activity was conducted to access agronomic performance of five BCNAM biparental populations (Lata//SC566, Lata//IS15401, Lata//DouaG, Grinkan//IS15401 and Grinkan//SC566), which are supposed to carry different alleles for Al-tolerance gene *SbMATE.* Through this work, the effect of the different *SbMATE* alleles on grain yield production under low and high phosphorous conditions, was evaluated.

**Objectives:**

* Access *SbMATE* gene effect on grain yield performance under Low and high phosphorous conditions
* Identify association or QTLS for the different adaptation traits.

**Materials and method**

Four populations BC1F4 progenies (490 progenies) were phenotyped in 2015 and 2016 under contrasted conditions (low P and high P fields) at Samanko/Mali. This progenies were selected from BCNAM populations, over 1080 progenies, developed between 2009 and 2012. The progenies were also genotyped by sequencing (GBS). Association analysis (GWAS) using phenotypic and genotypic data was then ran to identified QTLs/genomic regions associated to grain yield, plant height and other adaptation and quality traits.

**Results and interpretation**

Five BC-NAM biparental populations carrying *SBMATE* gene for aluminum tolerance have been chose base on Leiser et al 2014 study to evaluate their effect under low and high soil phosphorous condition. The first evaluation was done in 2015, this report is the results of second year assessment in ICRISAT-Samanko station. We find in general the good repeatability for almost three parameters (table1). The results of data analysis revealed also a large genetic variation for the grain yield within the populations and between the different populations in +P and –P (figure 2) as consequence we had low grain yield in –P and the poor development of the plant. A Significant delayed of the heading stage in –P compared to the +P about 2 to 10 days (figure 1).

Four QTLs that are explained the heading stage in +P and -P were detected in chromosome 1, 3, 6 and 7. Three QTLs also were identified for plant height, but some QTLs have being identified in the same population at the same a position in +P and –P for heading and plant height. Two QTLs were identified for grain yield only in +P (table1). In general almost these detected QTLs are probably identified by some preview study in deep analysis will be applied to declare if any new QTLs is detected.

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*A: Heading B: Grain yield*

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*C: Plant height*

**Fig. 2 (A, B & C):** Performance of progenies for heading, grain yield and plant height in high P and low P.

**Table1: QTLs identified for different traits and repeatability.**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Trait/Env | POP1 | Locus | chr | pos | lod | Repeatability |
| EP\_HP | LIS15401 | S3\_51359438 | 3 | 78.03133 | 14.42667 | 0.95 |
| EP\_HP | LIS15401 | S6\_72442 | 6 | 0.262461 | 9.946915 | 0.95 |
| EP\_HP | LSC566 | S6\_811191 | 6 | 2.938942 | 7.938887 | 0.93 |
| EP\_HP | GRSC566 | S6\_3228290 | 6 | 18.57483 | 16.08057 | 0.96 |
| EP\_LP | LSC566 | S1\_62582038 | 1 | 141.0988 | 5.854888 | 0.71 |
| EP\_LP | LIS15401 | S3\_51671464 | 3 | 78.73148 | 14.08113 | 0.84 |
| EP\_LP | LIS15401 | S6\_465732 | 6 | 1.687369 | 7.523057 | 0.84 |
| EP\_LP | GRSC566 | S6\_45455228 | 6 | 55.39742 | 4.201899 | 0.73 |
| EP\_LP | GRSC566 | S7\_54732559 | 7 | 74.3615 | 21.26247 | 0.73 |
| HPL\_HP | LDOUAG | c3.loc156 | 3 | 156.2439 | 4.847944 | 0.67 |
| HPL\_HP | GRSC566 | c6.loc38 | 6 | 39.42816 | 8.202252 | 0.93 |
| HPL\_LP | LDOUAG | S3\_72803026 | 3 | 158.6141 | 5.323078 | 0.61 |
| HPL\_LP | GRSC566 | S6\_45455228 | 6 | 55.39742 | 4.05698 | 0.84 |
| HPL\_LP | GRSC566 | S7\_54732559 | 7 | 74.3615 | 22.23538 | 0.84 |
| *PGrm2\_HP* | *GRSC566* | *S6\_45455199* | *6* | *55.3973* | *4.09966* | 0.74 |
| *PGrm2\_HP* | *GRSC566* | *S7\_54732559* | *7* | *74.3615* | *22.3253* | 0.74 |

*Ep = heading, HPL = plant height, HP = high Phosphorus or high P and LP = low phosphorus or low P.*

**Next step**

This study is carry in the framework of PhD thesis. Import set of data were collected however, analysis is still on-going to be more specific about results presented. Association analysis will be also performed on quality traits such as glumes opening, grain vitrosity, panicle form, etc.