

## Introduction

Improving nutrient use efficiency is an important objective in modern breeding programs. Our group attempts to elucidate the components that contribute to greater efficiencies of potassium (K) acquisition and utilization in wheat (*Triticum aestivum*), and its nexus with sodium (Na) dynamics.

## Objectives

1. Evaluate genomic regions potentially associated with Na accumulation at limiting K supply and their relevance for potassium utilization efficiency (KUE).
2. Deepen the physiological characterization of contrasting lines.
3. Validate candidate regions by studying segregating biparental populations.

## Methodology

- Genome Wide Association Study (GWAS) using 212 spring wheat lines from diverse origin, genotyped with the Infinium Wheat SNP 90K iSelect assay.
- Ranking of lines according to their capacity to partition Na<sup>+</sup>.
- Two biparental F<sub>2</sub> populations, developed by crossing phenotypically contrasting lines, and genotyped by SSR markers.
- Evaluation at seedling stage of plants grown under hydroponic condition with adequate (K<sup>+</sup>) and limiting (K<sup>-</sup>) K supply.
- Measured traits: dry matter (DW), relative growth rate (RGR), Na<sup>+</sup> content (cNa), Na<sup>+</sup> partitioning between shoots and roots (Na S/R), K<sup>+</sup> Utilization Efficiency (KUE), acquisition and translocation rates (SAR and STR).

## Results

1) Significant SNPs were found in two contiguous regions placed on the long arm of chromosome 1B for Na S/R differences in the GWAS.

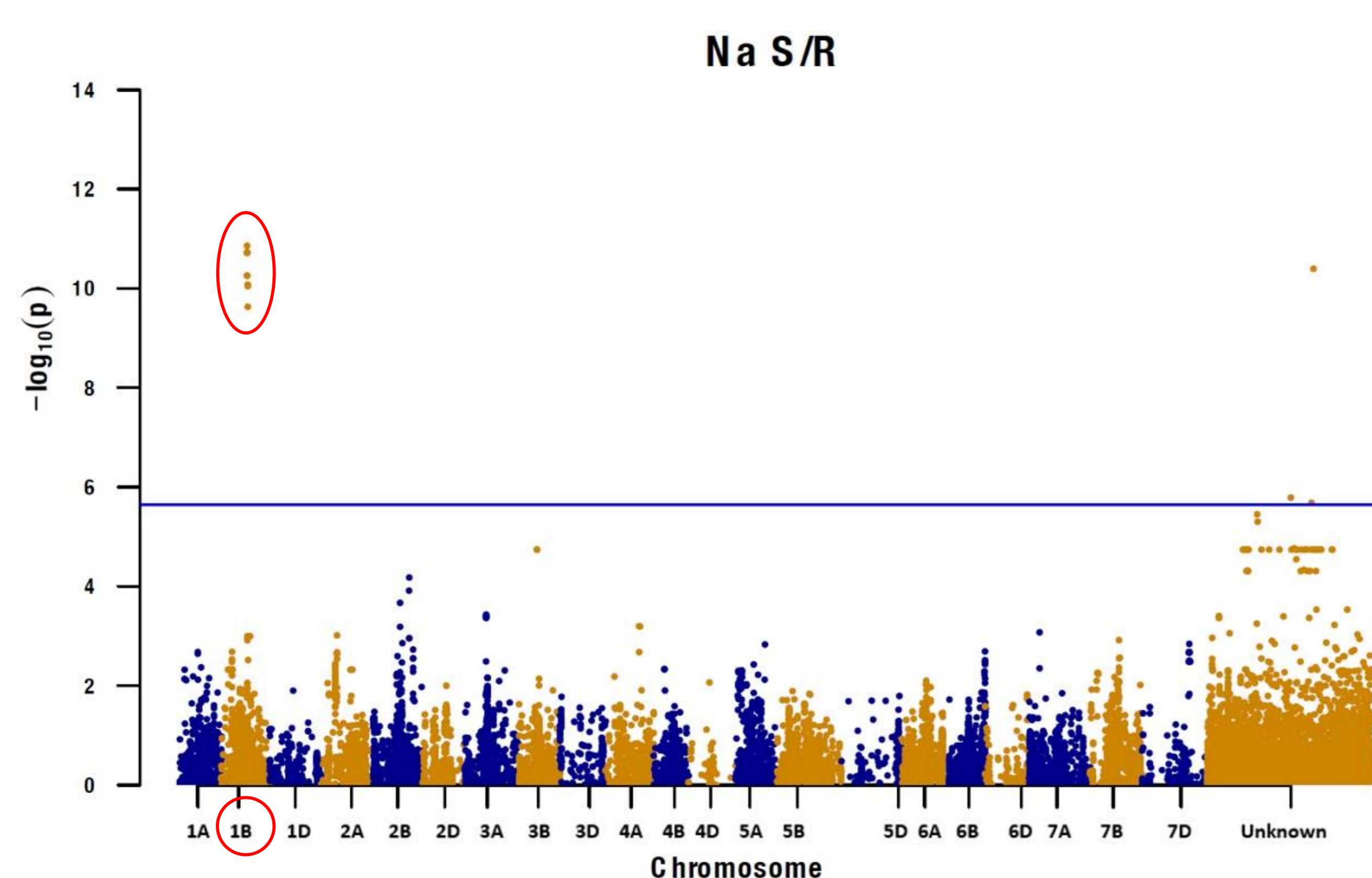


Figure 1: Manhattan plot of SNPs for Na<sup>+</sup> partitioning (Na S/R) for each chromosome. The blue line indicates the threshold value for significant associations.

2) Differences between contrasting ranked lines in Na<sup>+</sup> homeostasis tended to increased under limiting K<sup>+</sup> supply, and they involved differences in Na<sup>+</sup> uptake, Na<sup>+</sup> translocation and KUE.

Trait	Mean	Min	Max	CV	Amplitude	K effect	Line effect	K*Line effect
cNa R	246.87	21.45	656.93	80.24	30.6	<0.0001	<0.0001	<0.0001
cNa S	123.61	4.19	522.8	149.8	124.8	<0.0001	<0.0001	<0.0001
Na S/R	0.77	0.17	3.05	105.08	17.9	<0.0001	<0.0001	0.0014
Na SAR	59.71	3.74	205.73	113.98	55	<0.0001	<0.0001	<0.0001
Na STR	32.52	0.97	148.76	152.57	153.4	<0.0001	<0.0001	<0.0001
Na STR/SAR	0.35	0.14	0.76	54.6	5.4	<0.0001	<0.0001	<0.0001
DW T	0.25	0.14	0.38	25.18	2.7	<0.0001	<0.0001	0.045
RGR t	0.14	0.1	0.18	12.36	1.8	<0.0001	<0.0001	NS
RGR S	0.16	0.12	0.2	12.14	1.7	<0.0001	<0.0001	NS
KUEe T	1.10E-03	2.40E-04	2.40E-03	73.98	10	<0.0001	<0.0001	<0.0001
KUEe S	1.50E-03	3.50E-04	3.60E-03	72.76	10.3	<0.0001	<0.0001	<0.0001

Table 1: Variability of traits under study for 6 selected lines from the GWAS, assayed at an adequate and a limiting K<sup>+</sup> supply.

K	Line	Na accumulation			Na dynamics			Growing pattern			K <sup>+</sup> utilization efficiency	
		cNa R	cNa S	QNa S/R	Na SAR	Na STR	Na STR/SAT	DW T	RGRT	RGRS	KUEe T	KUEe S
K-	IDO851	503,3 a	482,0 a	2,25 a	185,0 a	130,3 a	0,70 a	0,21 cde	0,129 ed	0,155 de	2,0E-03 a	2,9E-03 a
K-	MN07338	462,7 a	456,1 ab	2,24 a	173,7 a	120,3 ab	0,69 a	0,23 cd	0,140 bcd	0,159 cde	2,1E-03 a	3,0E-03 a
K-	MT-0813	534,5 a	341,5 b	1,51 a	152,5 a	90,6 b	0,56 a	0,26 bc	0,138 cd	0,156 de	1,7E-03 b	2,3E-03 b
K-	12010-29	461,3 a	58,4 c	0,25 c	61,6 b	12,4 c	0,20 c	0,16 e	0,114 e	0,137 f	1,6E-03 b	2,2E-03 b
K-	CWAM2-9178	308,2 b	53,9 cd	0,37 bc	47,3 c	12,8 c	0,27 bc	0,18 e	0,132 d	0,137 f	1,9E-03 a	2,2E-03 b
K-	9229	316,8 b	44,1 d	0,30 bc	43,4 c	10,1 c	0,23 bc	0,20 de	0,116 e	0,144 ef	1,6E-03 b	2,2E-03 b
K+	IDO851	79,6 c	11,0 e	0,45 b	11,8 d	3,6 d	0,31 b	0,30 ab	0,153 abc	0,184 a		
K+	MN07338	55,0 c	8,2 f	0,49 b	8,5 e	2,6 e	0,33 b	0,34 a	0,169 a	0,192 a		
K+	MT-0813	59,2 c	7,9 f	0,42 bc	8,6 e	2,3 e	0,29 bc	0,33 a	0,154 ab	0,175 abc		
K+	12010-29	58,3 c	6,8 fg	0,25 c	7,4 e	1,5 f	0,21 c	0,23 cd	0,139 cd	0,163 bcd		
K+	CWAM2-9178	59,7 c	6,5 g	0,29 bc	8,0 e	1,8 f	0,23 c	0,23 cd	0,152 cd	0,158 cde		
K+	9229	63,9 c	7,2 fg	0,30 bc	8,7 e	2,0 ef	0,23 c	0,31 ab	0,148 bc	0,179 ab		

Table 2: Responses of selected lines under limiting (K<sup>-</sup>) and adequate (K<sup>+</sup>) potassium supply. The three highest value for each treatment are highlighted. IDO-851 and MN-07338 are signaled as lines with major values for the traits under study.

3) cNa in the third leaf blade (proxy of Na S/R) showed a mendelian segregation for a single locus (3:1), being the high Na<sup>+</sup> accumulation the dominant trait.

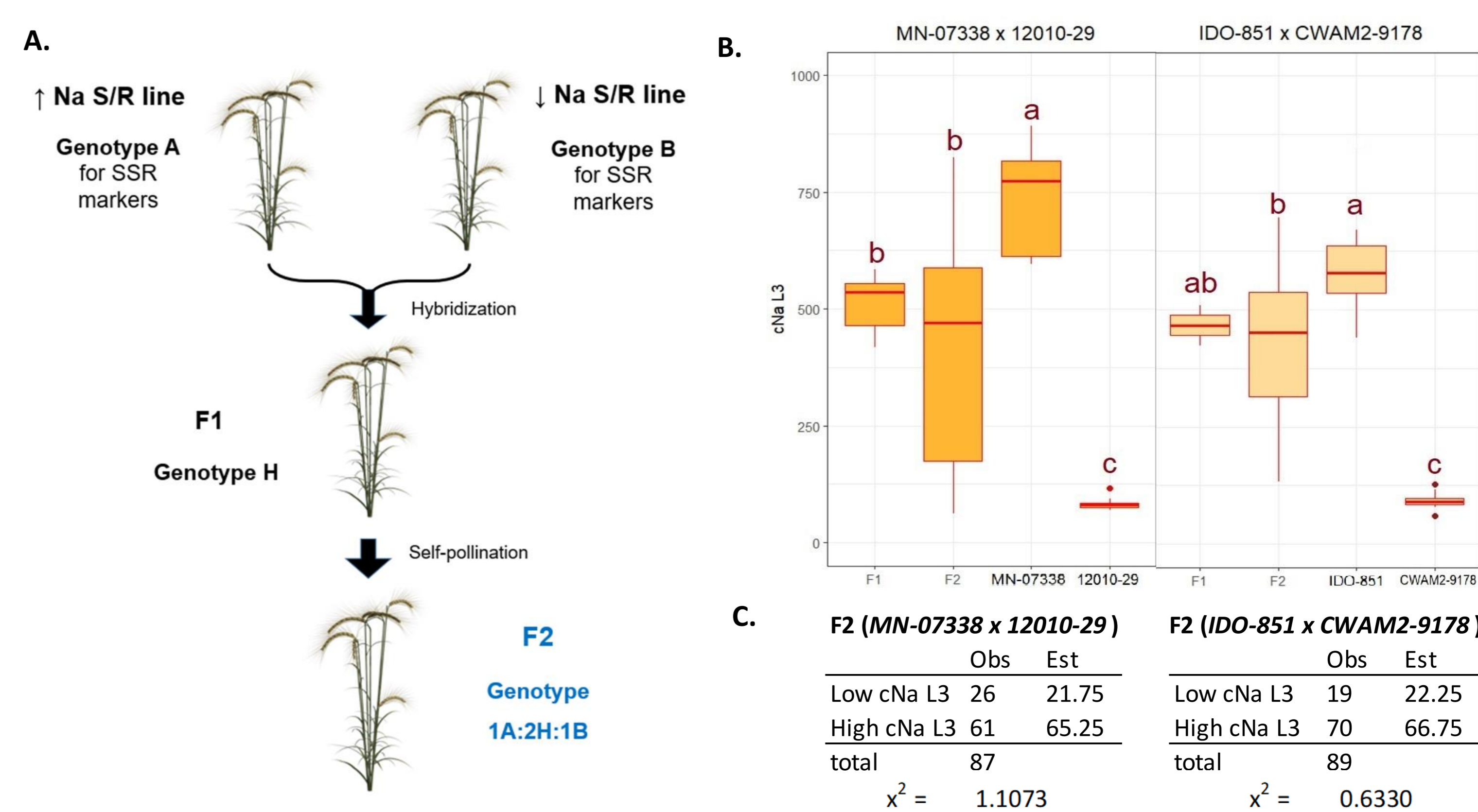


Figure 2: A. Development diagram of F<sub>2</sub> populations from contrasting lines. B. Boxplot of Na<sup>+</sup> content in the third leaf blade (cNaL3) -proxy of Na S/R- for two biparental populations under a limiting K<sup>+</sup> supply. C. X<sup>2</sup> analysis for a Mendelian 3:1 distribution of a trait (p < 3.8416).

4) Flanking SSR markers explained at least 22% of cNa and showed a significant cosegregation with this trait in both F<sub>2</sub> families.

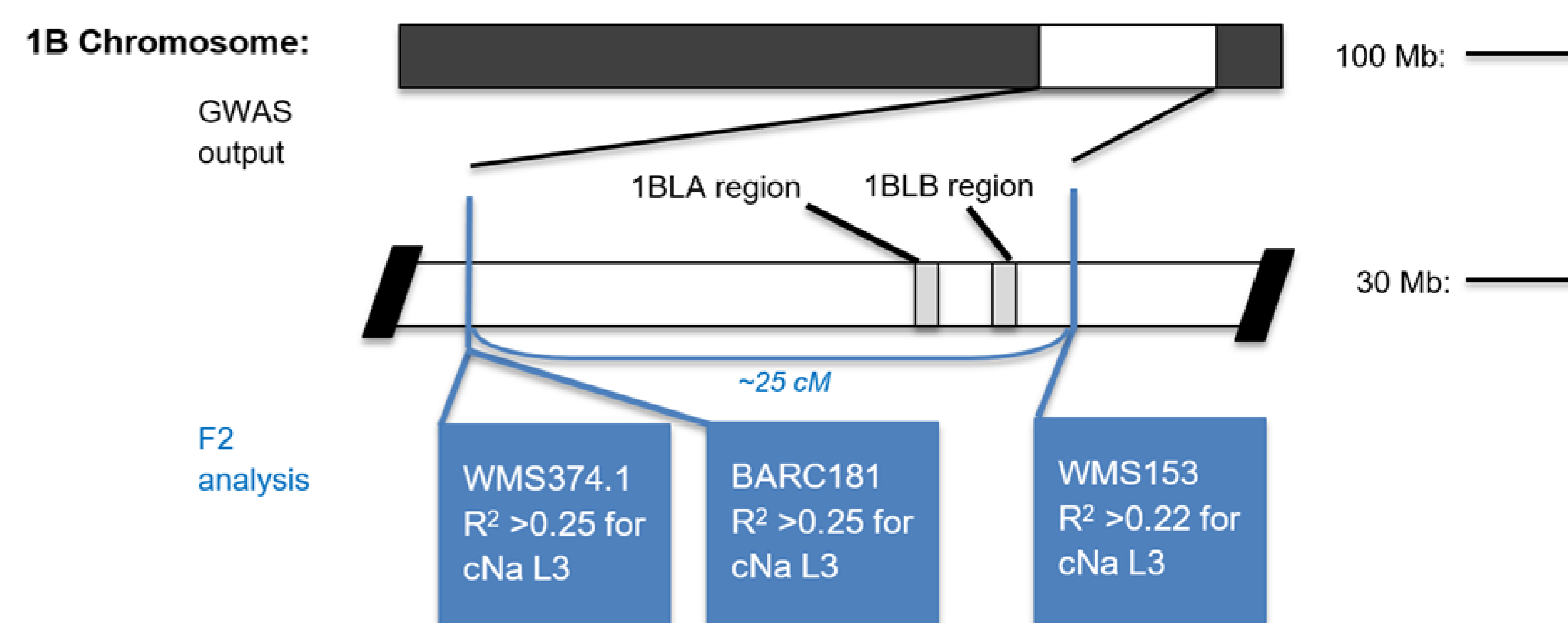


Figure 3: Physical map showing 1BLA and 1BLB regions associated to Na<sup>+</sup> partitioning in the GWAS and flanking SSR markers used for the F<sub>2</sub> analysis. Genetic distances between markers were estimated in centimorgans (cM).

## Conclusions

- Wide variability was observed among genotypes for Na<sup>+</sup> accumulation in the aerial plant fractions, which were considerably increased under limiting K<sup>+</sup> supply.
- Phenotypic differences in Na<sup>+</sup> accumulation were accompanied by differences in Na<sup>+</sup> uptake, Na<sup>+</sup> translocation and KUE.
- The 1BL chromosome regions may account for >22% of the total variation in Na<sup>+</sup> accumulation and showed a single-locus dominant Mendelian distribution for the trait.
- All evaluated SSR showed a significant cosegregation with Na<sup>+</sup> accumulation for both F<sub>2</sub> families.
- These data confirm regions on 1BL as strong candidates for the major differences found in Na<sup>+</sup> accumulation at limiting K<sup>+</sup> supply and suggests the suitability of Na<sup>+</sup> accumulation-based approaches to improve KUE.