

Wheat lines, suffering structural rearrangements between wheat-1BS and rye-1RS chromosomes, display differential patterns of magnesium accumulation

Poster N°

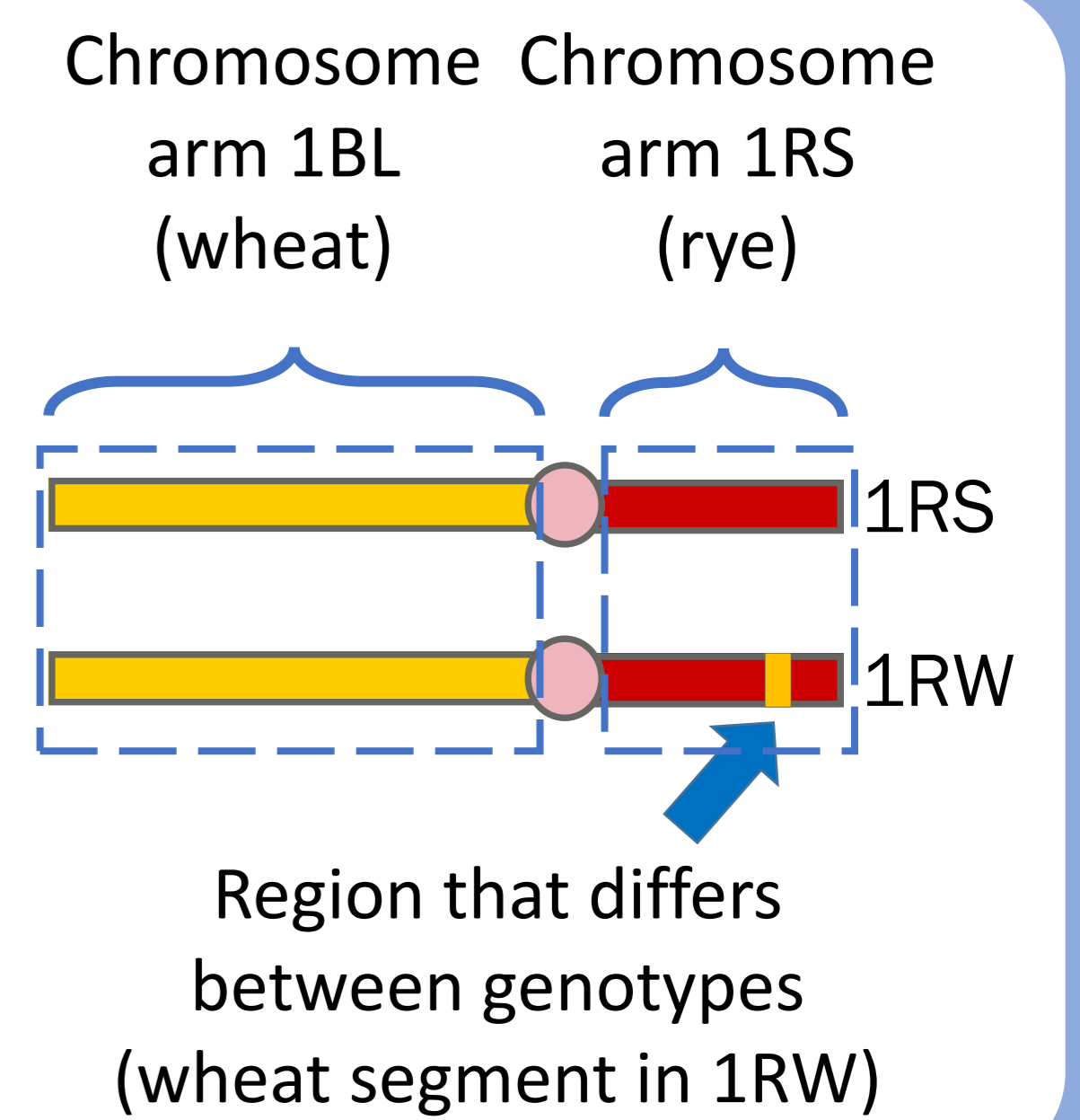
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Introduction: Two near isogenic lines, designated as 1RS and 1RW, resulting from the recombination of the rye (*Secale cereale*) chromosome 1RS with chromosome 1BS of bread wheat (*Triticum aestivum*), differ in a relatively small region of that short chromosome arm. We have recently reported that chromosome rearrangements in this region imply modifications in the dosage of some genes (including OPRIII codifying an enzyme involved in jasmonic acid (JA) biosynthesis pathway). This dosage difference confer differential drought resistance in a way primarily associated to the capacity of roots for soil exploration. An emerging question is whether or not those rearrangements also differentially influence plant mineral nutrition. In the present study we analyzed the ionome of 1RS and 1RW, which unveiled the existence of relevant differences in the distribution of magnesium (Mg) between the shoot and the root of these lines. Following this observation, we explored the physiological and molecular determinants of differential magnesium accumulation observed.



Results:

1- Do 1RS and 1RW plants differ in their ionomes?

Element	Root element concentration	Shoot element concentration	Shoot/root element partition
K	0.8920	0.2384	0.7143
Sr	0.1477	0.1489	0.0032
Mo	0.4383	0.4649	0.0800
Al	0.7874	0.1683	0.9119
P	0.1907	0.4131	0.0091
Cu	0.9204	0.7934	0.0254
Mn	0.4060	0.0010	0.1192
Zn	0.9266	0.9534	0.0905
Ca	0.8709	0.5646	0.0154
Mg	0.0001	<0.0001	<0.0001
Fe	0.0454	0.7794	0.4553
Na	0.7953	0.1777	0.3390

Table 1: ionome analysis of 1RS and 1RW plants. In orange significant p-values are indicated for two experiments treated as blocks.

Consistent differences were detected for Magnesium (Mg)

2- Do the above differences occur over a wide range of Mg supply?

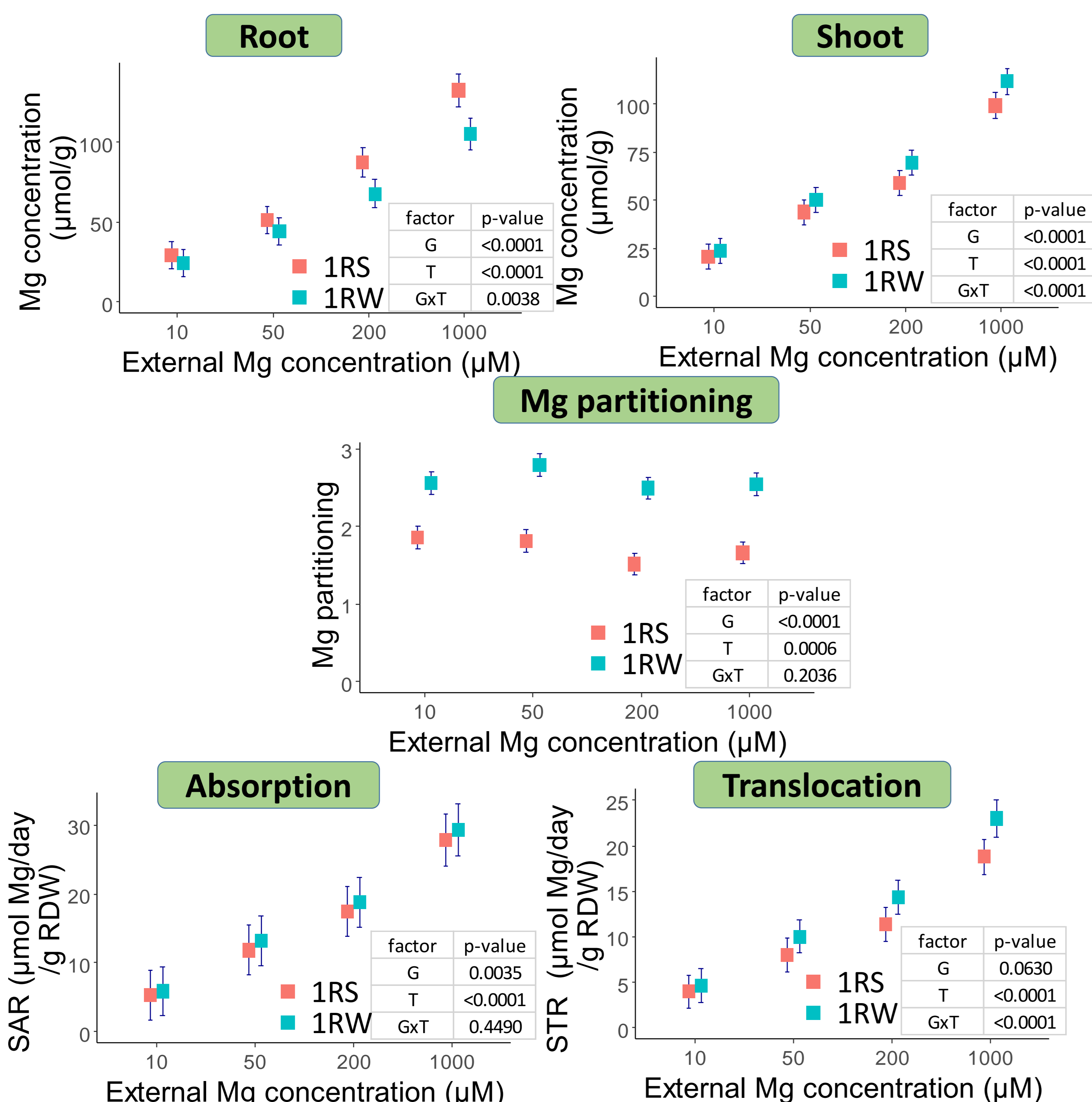


Figure 1: Effect of wide range of external Mg supply on Mg concentration in roots and shoots, partitioning, specific absorption rate and specific translocation rate for hydroponically grown plants. Factorial ANOVA is shown indicating p-values obtained for the genotype (G), the level of Mg supply (T) and their interaction (GxT).

3- Are the translocation differences attributable to a large contribution of the bypass flow?

factor	p-value	External Mg concentration (µM)	
G	0.0104	10	1000
T	0.4123		
GxT	0.0159		
Gen		1RS	1RW
		0.6% ± 0.2	0.2% ± 0.0
		0.4% ± 0.1	0.6% ± 0.2

The apoplastic contribution may be marginal

Table 2: Relative contribution of apoplastic flow to the total amount of water transpired. Data correspond to the mean value of two experiments ± SE considered as blocks. Factorial ANOVA is shown indicating p-values obtained for genotype (G), level of Mg supply (T) and their interaction (GxT).

4- Does 1RS and 1RW transcriptome differ for the expression of genes coding cation transporters?

Family	DEG d6	DEG d16
CPA1		1
CPA2		5
GLR	1	2
HAK	1	3
HMA	2	
IREG		1
MSL		1
NRAMP	1	
OSCA		2
Shaker	1	1
VIT	3	
ZIF		2
ZIP	5	
Total	14	18

Table 3: A catalogue of wheat genes coding for putative cation transporters was built up using the 1.1 wheat genome version. Then, we performed a comparative study of the root tip transcriptome of 1RS and 1RW plants. The number of differential expressed genes (DEG) at 6 and 16 days after germination is shown. It remains to be explored the possible relevance of these genes in the pattern here described.

5- Are gene dosage differences involved? Is OPRIII Involved?

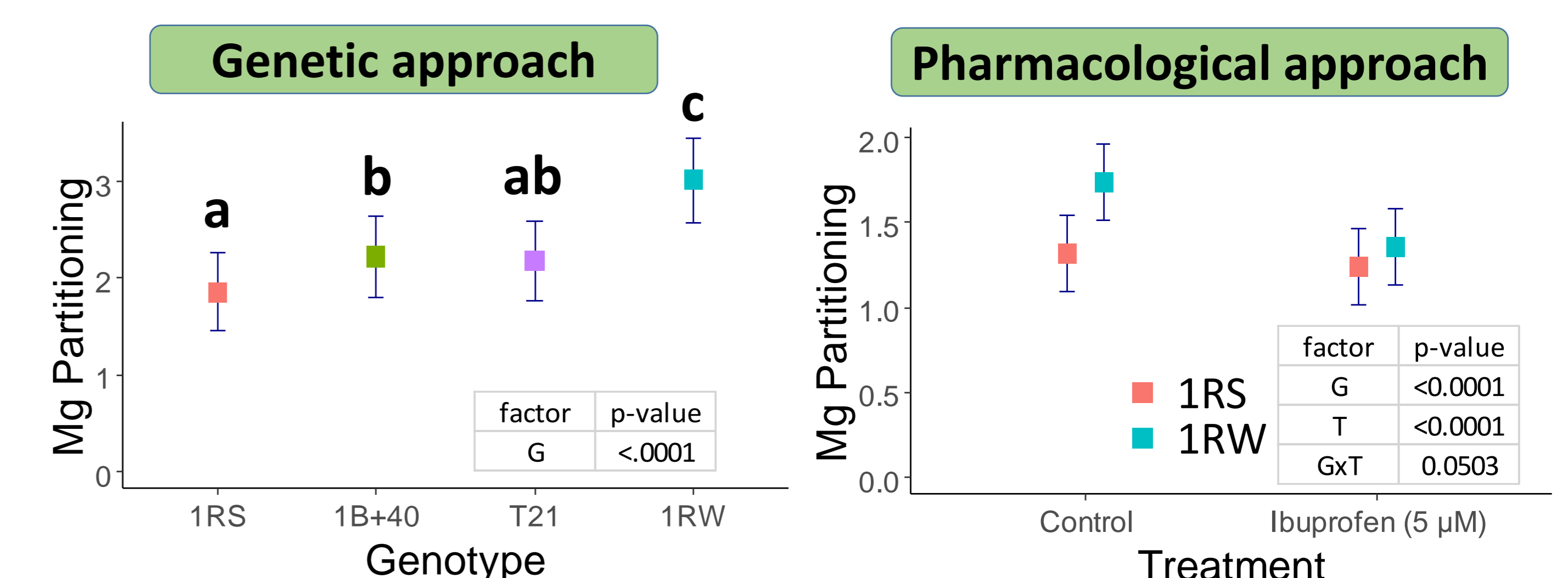


Figure 2: Genetic information suggest that Mg partitioning is affected by gene dosage as lines T21 and 1B+40, with intermediate number of copies of the region, display intermediate partitioning values relative to 1RS and 1RW. Experiments with the JA-biosynthesis inhibitor, Ibuprofen (5 µM), indicate that the pattern of Mg partitioning can be pharmacologically reverted. Data correspond to the mean value of two experiments ± SE considered as blocks.

Conclusion: Our results disclose a chromosome region involved in setting Mg translocation in wheat. Differences in Mg partitioning are maintained over a wide range of external Mg supplies, likely involving the symplastic route. Genetic evidence indicates an effect of differences in gene dosage, potentially attributable to the action of the JA biosynthesis pathway. Noticeably, additional data indicate that these early differences are not translated to differences in Mg grain concentration (data not shown), thus precluding their potential use for biofortification.