MAJOR LOCI CONTROLLING RESISTANCE TO THE ANGULAR LEAF SPOT OF COMMON BEAN

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Angular leaf spot (ALS) caused by the fungus *Pseudocercospora griseola* is currently one of the most widespread and destructive disease of common bean (*Phaseolus vulgaris* L.) in Latin America and Africa (Pastor-Corrales *et al.* 1998). Yield losses up to 80% have been reported in Brazil (Jesus-Junior *et al.* 2001). Genetic resistance is the most cost-effective, easy to use and ecological strategy to manage the disease. However, progress in breeding for resistance to ALS has been difficult. The high virulence diversity of *P. griseola* and the recurring discovery of new races of this pathogen are challenging for the development of cultivars with effective resistance to ALS (Sartorato & Alzate-Marin 2004; Abadio *et al.* 2012).

During the Common Bean Disease Workshop on Angular Leaf Spot and Root Rot, held in Skukuza, South Africa, in July 2015, a work group was established to review the progress in genetic analysis and breeding for ALS resistance. At that time, only three ALS resistance genes had been mapped and named following the guidelines for gene nomenclature proposed by the Bean Improvement Cooperative (BIC) Genetic Committee: *Phg-1* (AND 277) on chromosome Pv01 (Carvalho *et al.* 1998; Gonçalves-Vidigal *et al.* 2011), *Phg-2* (Mexico 54) on Pv08 (Sartorato *et al.* 2000), and *Phg-3* (Ouro Negro) on Pv04 (Corrêa *et al.* 2001; Gonçalves-Vidigal *et al.* 2013). However, in addition to these genes, unnamed major resistance loci have also been reported in different resistance sources used by common bean breeding programs in Uganda, Colombia and Brazil. Among these resistance sources are BAT 332, CAL 143 and G5686 (Table 1).

Caixeta *et al.* (2005) named tentatively additional ALS resistance genes in AND 277, Mexico 54, MAR 2 and Cornell 49-242. However, none of these studies included physical linkage information and their results or genetic hypotheses still need to be validated. Consequently, the gene names proposed by these authors were not accepted by the BIC Genetic Committee. Based on allelism test results by Namayanja *et al.* (2006), the ALS resistance gene in BAT 332 shall be considered as allelic to *Phg-2*, present in Mexico 54. A physical position analysis using the reference genome sequence of *P. vulgaris* (Schmutz *et al.* 2014) indicated that the ALS resistance genes in MAR 2, Cornell 49-242, G10474 and G10909 may also be alleles of *Phg-2*. The physical map developed using sequence information obtained from molecular markers linked to *Phg-2* and to the major loci controlling ALS resistance in these ALS resistance sources showed the presence of one single gene cluster on Pv08 (Figure 1). However, additional studies on the genomic characterization of *Phg-2* are necessary to better clarify the allelic relationship of *Phg-2* and the ALS resistant genes present in MAR 2, Cornell 49-242, G10474 and G10909, and guide the nomenclature of these genes.

It was also proposed that the major QTL ALS4.1^{GS,UD} on Pv04, present in G5686, and the ALS10.1^{DG,UC} on Pv10, identified in both G5686 and CAL143, shall be officially named as *Phg-4* and *Phg-5*, respectively (Table 1). This proposal considered that these major loci had consistent and significant effects across different environments and populations (Mahuku *et al.* 2009; Oblessuc *et al.* 2012, 2013; Keller *et al.* 2015). These QTLs have been physically mapped

on positions different from those of the ALS resistance genes *Phg-1*, *Phg-2* and *Phg-3* (Figure 1). This effort to better characterize and formally name the major ALS resistance loci identified so far will be useful to support common bean breeding programs for ALS resistance regarding to selection and use of resistance sources. In addition, it will also guide the characterization of new ALS resistance loci.

Considering all information presented above, in the last BIC Genetic Committee meeting held during the 2015 BIC Meeting, in Niagara Falls, Canada, in November 2015, the work group on genetic analysis and breeding for ALS resistance has proposed new gene symbols for unnamed major ALS resistance genes and QTLs previously reported, as summarized in Table 1. Based on the evidences presented, results from classical genetic studies, fine-mapping information and physical position analysis using the reference genome sequence of *P. vulgaris*, the BIC Genetic Committee has formally accepted the proposed new gene symbols.

Genetic and molecular evidences indicate that common bean loci controlling resistance to diseases caused by high variable pathogens are organized in clusters in which individual genes confer resistance to one specific isolate or race of the pathogen (Ferreira *et al.* 2013). For this reason, direct or indirect mapping using information from molecular markers linked to known ALS resistance genes and QTLs is recommended to support the characterization of new ALS resistance loci.

Table 1. Named and mapped loci that control resistance to the angular leaf spot of common bean.

Gene symbol		Resistance Source	Gene Pool[b]	LG[c]	Pathogen race	Reference
New[a]	Original					
Phg-1	*Phg-1*	AND 277	A	Pv01	63-23	Carvalho *et al.* (1998) Gonçalves-Vidigal *et al.* (2011)
Phg-2	*Phg-2*	Mexico 54	MA	Pv08	63-19 63-39	Sartorato *et al.* (2000) Namayanja *et al.* (2006) Mahuku *et al.* (2011)
Phg-2[2]	*Phg-?*	BAT 332	MA	Pv08	63-39	Namayanja *et al.* (2006)
Phg-3	*Phg-ON*	Ouro Negro	MA	Pv04	63-39	Corrêa *et al.* (2001) Gonçalves-Vidigal *et al.* (2013)
Phg-4	ALS4.1^{GS,UD}	G5686	A	Pv04	31-0 Field[d]	Mahuku *et al.* (2009) Keller *et al.* (2015)
Phg-5	ALS10.1^{DG,UC}	CAL 143	A	Pv10	0-39 Field	Oblessuc *et al.* (2012, 2013)
	ALS10.1^{DG,UC}	G5686	A	Pv10	31-0 Field	Keller *et al.* (2015)

[a] Highlighted are the ALS resistance genes previously mapped, named and accepted by the BIC Genetic Committee. Those that are not highlighted are the new gene symbols proposed based on results from classical genetic studies, fine-mapping information, and physical position analysis using the reference genome sequence of *P. vulgaris* (Schmutz *et al.* 2014), which have recently been accepted by the BIC Genetic Committee. [b] Andean (A) or Mesoamerican (MA) gene pool. [c] Linkage group (LG) or chromosome based on genetic mapping and genomic analysis information. [d] Resistant reaction under natural infection in the field.

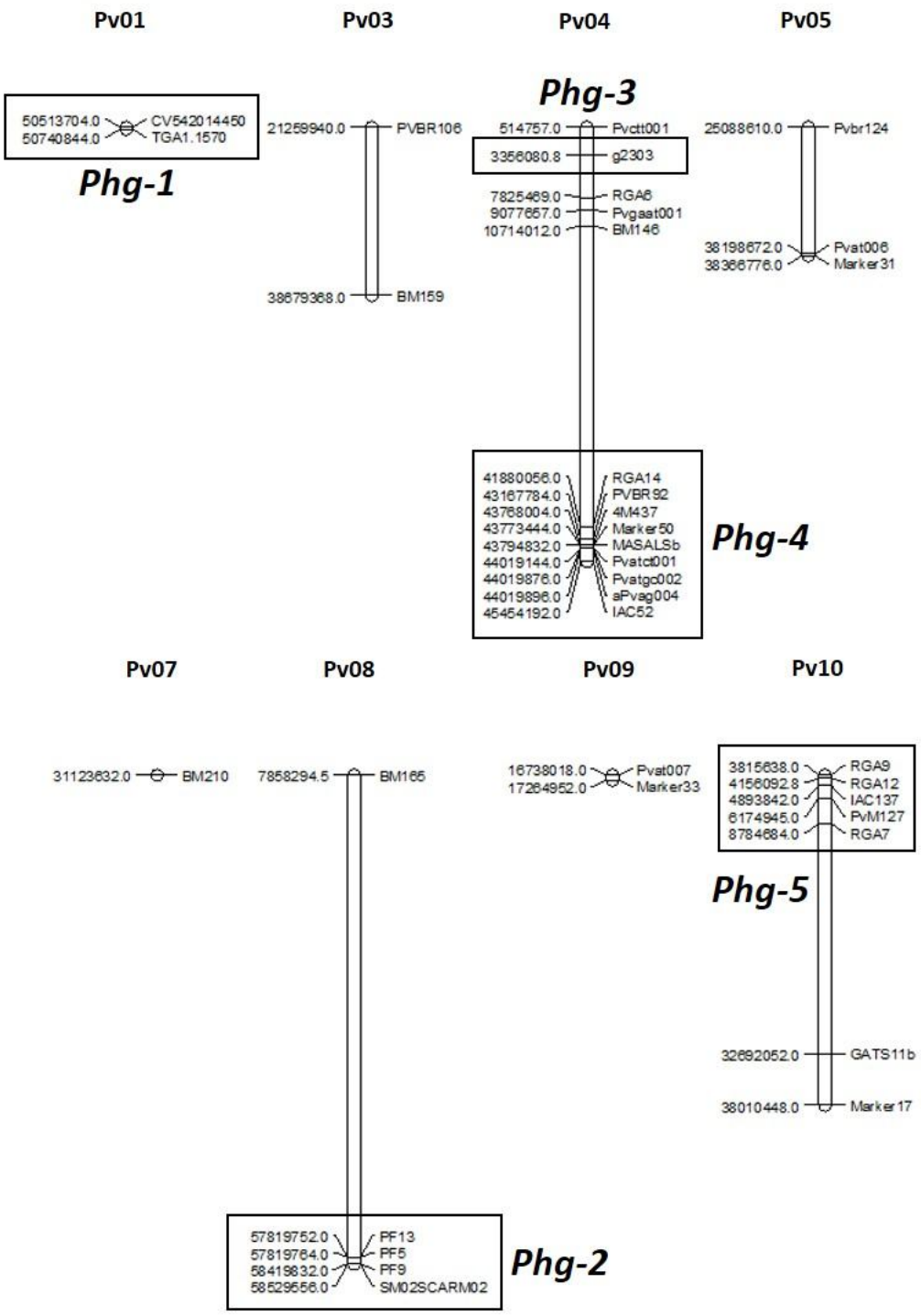

Figure 1. Linkage groups showing the physical position of the molecular markers linked to the major loci controlling resistance to the angular leaf spot of common bean. This physical map was developed based on sequence information obtained from the markers.

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