A CLOSER LOOK AT THE RESISTANCE GENE CLUSTER ON COMMON BEAN CHROMOSOME 11

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INTRODUCTION

Several resistance genes of international importance are situated within the resistance gene cluster on common bean chromosome 11. These include three genes (*Ur-3, Ur-11* and *Ur-Dorado-53*) conditioning resistance to rust, the anthracnose resistance gene *Co-2*, and quantitative trait loci (QTL) conditioning resistance to common bacterial blight (CBB) and anthracnose (Freyre *et al.*, 1998; Miklas *et al.*, 2006). Liebenberg *et al.* (2008) reported a possible linkage in coupling between *Ur-3* and the SCAR marker $sAE19_{890}$, (linked in repulsion to *Ur-11* from 'PI 181996') (Johnson et al, 1995; de Queiroz *et al.*, 2004) in 13 lines from Beltsville possessing *Ur-3* and *Ur-11;* and Awale *et al.,* (2008) reported a possible linkage between the SQ4 marker for the *Co-2* anthracnose resistance gene and *Ur-11*. Further indications of possible linkages between SCAR markers for *Co-2*, namely SQ4 (Awale *et al.,* 2008) and SCAreoli (Geffroy *et al.*, 1998) and *Ur-3* or *Ur-11* were provided by Madubanya *et al.* (2009). The aim of the present study was to investigate the possible association of the *Co-2* markers SQ4 and SCAreoli with *Ur-11*, using populations segregating for *Ur-11*, and so doing, to increase our understanding of the organization of resistance gene(s) in this section of chromosome 11.

MATERIALS AND METHODS

The African rust races RSA-Ua1 and TZ-Ua11 (Liebenberg, 2003) were used to determine rust reactions of three populations ('Jenny'/'PI 181996', 'OPS-RS4'/'PI 181996' and 'Kranskop'/'PI 181996' segregating for *Ur-11* using previously described methods (Liebenberg & Pretorius, 2004). Two additional races (RSA-Ua4 and RSA-Ua10) were inoculated on the 'Kranskop'/'PI 181996' population. Genomic DNA from F_2 plants was isolated from leaves as according to (Saghai-Maroof *et al.,* 1984). PCR analysis was performed for SCAR markers SQ4 (*Co-2;* Awale *et al.,* 2008) and SCAreoli (*Co-2*; Geffroy *et al.*, 1998). Results were visualized on 2% agarose gels stained with ethidium bromide. SCAR SQ4, polymorphic in the three populations, was subsequently mapped in these populations using JoinMap 3.0 or MapManager QTX (2002).

RESULTS AND DISCUSSION

Stavely (1990), observed that *Ur-11* is not a simple dominant gene but is made up of a series of tightly linked genes that can segregate as a Mendelian unit. This was confirmed by the present authors. Although the segregation ratio (R:S) for the rust ratings obtained for the Kranskop/PI 181996 population is 3:1 in the F_2, as can be expected with a single dominant gene, portions of the gene are relatively easily lost, so that various nuances of resistance are observed, often characterized by marked, but differing degrees of necrosis with or without sporulating pustules. Not all rust races, however, are able to differentiate these grades of resistance. Certain races have also been observed to differentiate similar nuances of resistance in segregating populations of *Ur-3*, but to a lesser degree. A similar phenomenon has been observed for the anthracnose gene *Co-2*. Using data from

the three segregating populations, SQ4 mapped between 11.9 and 18.4 cM from the *Ur-11* gene. The postulated positions of the markers, the complex nature of the genes concerned, and relative distances observed, have been visualized in Fig. 1, using cM distances determined in this study and by the various SCAR authors. If this representation is correct, the (SCAreoli-*Ur-3*-sAE19) segment was inserted between SQ4 and *Ur-11* by means of a double crossover.

Ur-3 and *Ur-11*, previously linked in repulsion but now available in coupling (Stavely, 1998) are a valuable combination in rust resistance breeding. In order to insert this combination as a unit, two or more markers are necessary to prevent the loss of gene block segments. Existing markers linked to *Co-2* and *Ur-11* appear to be on the *Ur-3* side of *Ur-11* (Fig 1), and their use may prevent loss of *Ur-3*. However, an additional, flanking marker linked to the *Ur-11* gene ('A'in Fig. 1) is necessary to minimize the chances of loss of fragments from *Ur-11*. Future plans also include the validation of all existing markers using a population segregating for *Ur*-3, and the validation of existing markers linked to *Ur-Dorado-53* as well as the CBB and anthracnose QTL. The *Co-2* status of some lines must also be determined. Disadvantages of using this relatively large segment include the possible inclusion of undesirable genes and the probable exclusion of the defeated *Co-2* gene for anthracnose resistance. Other more suitable resistance genes for anthracnose resistance on different linkage groups are, however, available.

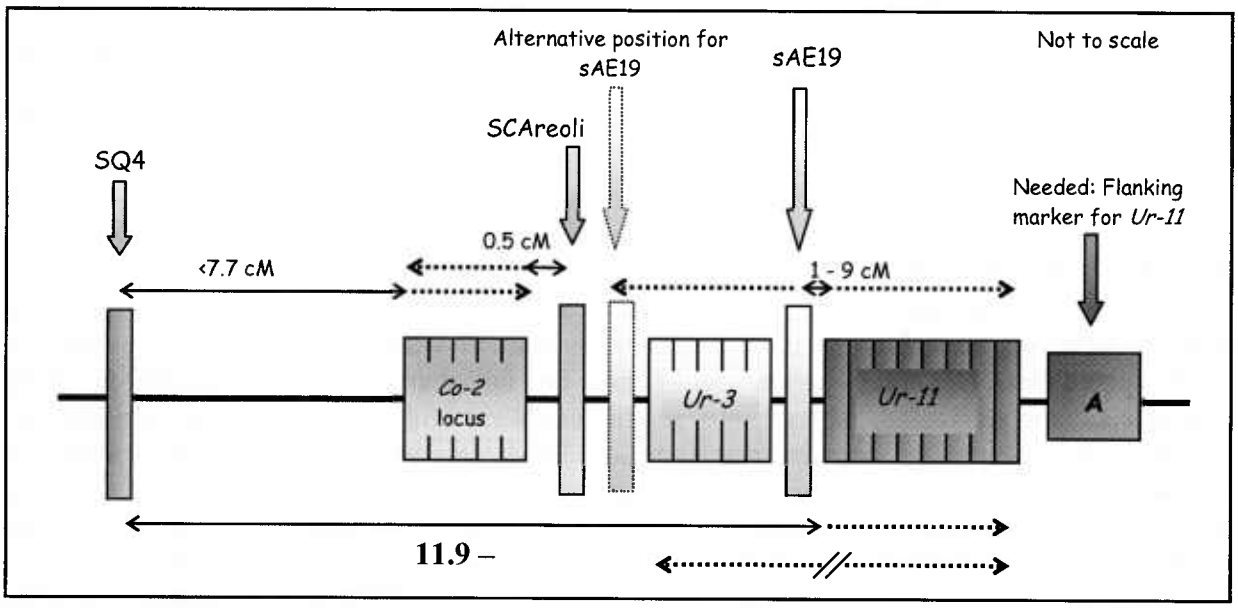

Fig. 1. Postulated positions of some of the resistance genes and existing linked markers for the resistance gene cluster on common bean chromosome 11.

REFERENCES

Awale *et al.*, 2008. Annu. Rep. Bean Improv. Coop. 51:174-175.
De Queiroz *et al.*, 2004. Annu. Rep. Bean Improv. Coop. 47:271-272.
Freyre *et al.*, 1998. Theor. Appl. Genet. 97, 847-856.
Geffroy *et al.*, 1998. Theor. Appl. Genet. 96: 494-502.
Johnson *et al.*, 1995.Theor.Appl.Genet 90:659-664.
Liebenberg. 2003. PhD Thesis, Univ. of the Free State, SA.
Liebenberg *et al.*, 2008. Annu. Rep. Bean Improv. Coop. 51:90-91.
Liebenberg & Pretorius, 2004. S.A. J. Plant and Soil 21(4):245-250
Madubanya et al., 2009. Annu. Rep. Bean Improv. Coop. 52:78-79.
Miklas *et al.*, 2006. Euphytica 147:105-131.
Saghai-Marrof *et al.*, 1984. Proceedings of the National Academy Sciences USA 81:8014-8019.
Stavely, J.R. 1990. Phytopathology 80:1056.
Stavely, JR. 1998. Annu. Rep. Bean Improv. Coop. 41:17-18.