Improving smallholder farmers' food security through disease resistant common beans

SFIAR PhD Award 2020 Application

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Introduction

Common bean (*Phaseolus vulgaris* L.) is the most important grain legume for human consumption and an important food security crop. Because of the high protein content and affordable price, beans are also known as "meat of the poor". Highest per capita consumptions of bean are found in Latin America and eastern Africa, with consumptions of up to 66kg annually (Broughton et al. 2003). In these regions, common beans are often cultivated by smallholder farmers as a subsistence crop under sub-optimal conditions. Consequently, on-farm yields throughout the tropics realize only a fraction (around 20%) of the yields that are usually achieved under experimental conditions (Beebe, 2012). One of the most limiting factors to bean production are plant diseases, with the fungal bean disease angular leaf spot (ALS) responsible for yield losses of up to 80% (Schwartz et al. 1981). Although pesticides offer means for disease control, they are often out of reach for many smallholder farmers because they are expensive and rarely available. Resistance breeding can offer a more sustainable and feasible solution for ALS control on smallholder farms.

Description of my research

One of the major challenges in breeding for ALS resistance is the high diversity of the pathogen and the recurrent appearance of new, highly virulent strains. Since ALS resistance is usually strain-specific, the so far known ALS resistant bean varieties are only protected against one or few particular pathogen strains. To ensure bean varieties are resistant against the prevalent pathogen strains in an area, knowledge on the resistance loci contained in a variety and the effectiveness of these loci against local pathogen strains is crucial. However, for the five ALS resistance loci known in common bean (reviewed in Nay et al. 2019a), little is known about the range of their effectiveness. In addition, they were all discovered using pathogen strains from Latin America and it was not clear whether the same resistance loci are effective against strains from Africa.

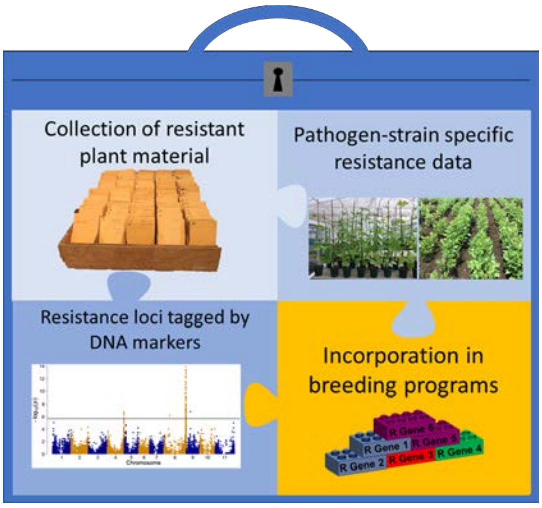

Figure 1: Toolbox to facilitate ALS resistance breeding

During my doctoral studies, I investigated the effectiveness of resistance loci against diverse ALS pathogen strains from two continents. Based on the results, I developed a toolbox that facilitates the breeding for pathogen strain-specific resistance. The ALS breeding toolbox established in this research is shown in Figure 1 and consists of a collection of the most resistant bean germplasm (top left), information about the resistance of the collection in glasshouse and field trials (top right) and molecular markers linked to resistance loci (bottom left). Taken together, this information will help breeders selecting and pyramiding the most effective resistance loci into their varieties (bottom right).

Achievements

ALS resistant common bean collection. During my project, a collection of 316 common bean varieties, representing the best available ALS resistance sources as well as susceptible checks has been assembled. The collection consists of 124 large seeded Andean beans, 129 small seeded Mesoamerican and 63 crosses between the two genepools. The varieties contained in the collection represent several grain types, climbing and bush beans, and dry and snap beans. The varieties are available to interested breeders and researchers from the CIAT gene bank or the breeding program.

ALS pathogen strain-specific resistance data. To study the effectiveness of resistance in varieties against different pathogen strains, the assembled collection was tested in important bean producing regions on two continents. The experiments were conducted in the glasshouse to detect strain-specific resistance and in the field to detect resistance against a mixture of strains under natural conditions. Twenty-seven varieties were found resistant (ALS score ≤3 on a 1 – resistant to 9 – susceptible scale) in the four greenhouse and the two field trials conducted in Colombia, 43 were resistant in the greenhouse and the field trial conducted in Uganda. Two varieties were resistant in all experiments. We observed a notable difference of resistance between the continents and of the 46 most resistant varieties in Colombia (average ALS leaf score over all experiments ≤3), only 15 had an average score of ≤3 against the Ugandan pathotypes tested.

Molecular markers associated with ALS resistance. To make my findings useful for breeders and the bean community, molecular marker co-segregating with resistance loci were developed to efficiently track resistance in breeding material (Figure 2). Genetic data for the 316 common bean varieties was obtained and the association of

DNA polymorphisms to ALS resistance was tested in each trial separately. In all field and greenhouse trials, ALS resistance was associated to the *Phg-2* locus on chromosome 8. Furthermore, in one greenhouse trial, the resistance locus *Phg-4* on chromosome 4 was also effective. Further dissection of the predominant *Phg-2* locus uncovered an unprecedented diversity of functional haplotypes for a resistance locus in common bean. Of the eleven haplotype groups identified by DNA based clustering, one haplotype group conferred broad-spectrum ALS resistance, six showed pathotype-specific effects, and the remaining seven did not exhibit clear resistance patterns. Molecular markers co-segregating with the resistance locus *Phg-4* and with specific haplotypes of *Phg-2* were discovered. Important for breeding purposes is, that the broad-spectrum resistance haplotype (Figure 2, Marker M1) was not showing resistance in the greenhouse trial in Uganda (UG 61-63), while another haplotype did (Nay et al. 2019b).

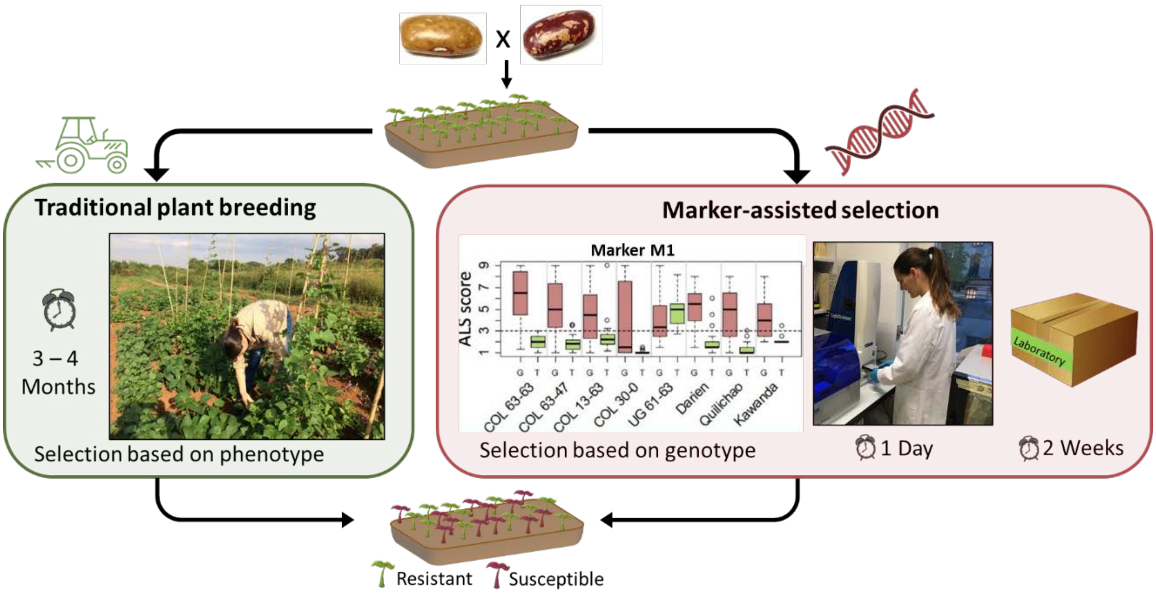

Figure 2: Molecular markers co-segregating with resistance loci or haplotypes greatly facilitate breeding for ALS resistance. While it takes 3-4 months to know which progeny of a cross is resistant in the traditional approach, it only takes a day in the lab if a molecular marker is known to co-segregate with resistance. The molecular marker M1 shown here co-segregates with the ALS broad spectrum resistance haplotype and bean varieties that have a T nucleotide at this position are highly resistant against all but the UG 61-63 pathogen isolate. If no lab facilities are available, the marker testing can be outsourced cost efficiently at less than 0.20 CHF per marker test and plant.

Incorporation in breeding programs. To ensure the translation of our research results into the farmer's fields, this project was conducted in close collaboration with the International Center of Tropical Agriculture (CIAT). The CIAT bean breeding focuses on low-input systems as encountered on smallholder farms throughout the tropics and runs large breeding programs in Colombia and Uganda. My toolbox supports CIAT breeders to include ALS resistance in their new varieties and is available to interested breeders. To release new varieties, CIAT works with national agricultural programs, and in Africa it coordinates the Pan African Bean Alliance (PABRA), a network of 31 African countries, that is responsible for the dissemination of seeds on the ground.

Relevance

Despite the known importance of pathotype-specificity in ALS resistance, this is the first time ALS resistance was studied in such a diverse panel of common beans and tested with an extensive diversity of pathogen isolates on two continents. While I expected to find the five previously described resistance loci being effective against different isolates, my research has shown that different haplotypes within one genetic region are responsible for a large part of the observed differential reaction to tested ALS pathogen strains. Furthermore, this research highlights the importance of conducting ALS research in the target area to ensure effective disease resistance. The ALS resistance toolbox established in my research will make it easier, cheaper and faster for breeders to include ALS resistance as a trait in their breeding programs.

For me personally, it made a deep impression to see how many smallholder farmers in Uganda are struggling to produce enough food for their families, even though Uganda has one of the most favorable climates for agriculture. This climate is however not only favorable for agriculture but also for pathogens that attack the crops. Because of limited other options to protect their plants, resistance breeding is the most feasible solution to ensure stable yields for the people that most depend on their harvest for food security.

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