**Advance in the use of interspecific crosses to improve common bean through introgression of tepary bean**

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**Background and significance**

The common bean (*Phaseolus vulgaris* L.), one of the most consumed legumes in the world, is negatively impacted by abiotic and biotic constraints due to the increase of climate change. Heat and drought limit the grain yield and quality significantly in several bean production regions in Central America, Brazil, East, and Southern Africa (Beebe et al., 2012). In fact, by 2050 It is projected a reduction in half of the suited areas where beans are currently grown due to an increase in heat and drought (Beebe et al., 2012). The bean productivity is also significantly reduced by biotic constraints such as bean rust, caused by *Uromyces appendiculatus* (Pers.: Pers), which is considered one of the main diseases in the dry and snap bean production (Acevedo et al., 2012), and common bacterial blight (CBB), caused by *Xanthomonas campestris* pv. phaseoli Smith (Dye) and *Xanthomonas fuscans* *subsp.* fuscans sp, which is a severe worldwide bacterial disease in the common bean (Duncan et al., 2012).

Solutions for abiotic and biotic constraints in the common bean can be found in a related species called tepary bean (*Phaseolus acutifolius*). Tepary bean has a unique array of traits, including heat tolerance (Porch & Hall, 2013) and water use efficiency (Markhart, 1985; Rao et al., 2013) and can handle higher heat and drought than common beans. Moreover, some accessions of tepary beans are broadly resistant to bean rust(Miklas & Stavely, 1998) and common bacterial blight (Mhlaba et al., 2018). Although previous studies have successfully used tepary bean to transfer disease and insect resistance into common bean (Kusolwa & Myers, 2005; Vargas et al., 2014; Yu et al., 2000), the introgression of complex quantitative traits, such as heat and drought tolerance, have remained elusive. There is also no report of introgression of rust-resistance genes from tepary to common bean.

Challenging hybridization between common bean and tepary bean reduces the possibilities to move highly complex traits since crossing both species typically require numerous pollinations, embryo rescue, tissue culture, and consecutive backcrosses to obtain viable plants (Mejía-Jiménez et al., 1994). Embryo rescue minimizes the hybridization to individual plants rather than segregated recombinant populations (Waines et al., 1988), and consecutive backcrosses limit the possibilities to introduce significant tepary variation on common beans (Mejía-Jiménez et al., 1994).

To transfer quantitative genetic traits, such as heat and drought tolerance, as well as disease resistance, from tepary to common bean, it is necessary to enhance the cross efficiency between both species. Therefore, we developed three interspecific genotypes that increase the crossability between common bean and tepary bean without embryo rescue. These genotypes are currently used as bridge parents for introgression of highly complex tepary traits into the common bean.

To deep understand the genomic structure of the bridge parents and elucidate the reasons why these genotypes are suitable for hybridization without embryo rescue, several genomic features, such as genetic diversity, introgression regions, single nucleotide variants (SNVs), and genomic regions with copy number variation (CNVs), will be analyzed in the three bridge genotypes, and their parents, using common and tepary bean genome references.

**Experimental Design**

A whole-genome sequence of nine samples (bridge genotypes and their parents), and two reference genomes (common bean and tepary bean) will be used in this project. The first step will be to verify the quality of the sequence using the program FastQC High Throughput Sequence QC report version 0.11.9 (<https://www.bioinformatics.babraham.ac.uk/projects/fastqc/>). The second step will be to map the nine samples with both reference genomes. Finally, the main goal will be to find the copy number of variations (CNV) and the introgression regions using an integrated framework tool called NESEP ([git@github.com:NGSEP/NGSEPcore.git](mailto:git@github.com:NGSEP/NGSEPcore.git)) and following the procedure reported by Lobaton et al., (2018).

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