

Winged Bean: How to Take Off?

Understanding Winged Bean Development and Plant Architecture for Future Improvements

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Winged bean is considered self-pollinating, but bees might promote outcrossing.

As Crop winged bean (*psophocarpus tetragonolobus*) is a legume mainly cultivated in equatorial areas. Almost the entire plant is **edible**: green pods and tubers are widely used for consumption, and raw seeds could be a potential **higher source of vegetable proteins and fats** compared to other major legumes like chickpeas, lentils or kidney beans.

Growth and Development demand thorough investigations in crops. Winged bean grows indeterminately, with stems over 3.5-4m high and more than 30 branches per plant. These characteristics, or “**traits**”, make the crop **difficult to manage**, especially on a large scale, and is considered as one of the main reasons why this crop has been neglected, despite its potential.

Past Efforts investigated such traits. Results have so far described variability within and between varieties, while a deeper understanding of their genetic architecture remains unrevealed. **Twenty-four varieties of winged bean have been so far described here in CFF-UNMC** (Wong Q.N., 2013), providing data about their vegetative growth, development and physiological characteristics: such data are used for selecting varieties for controlled crosses, in order to investigate the genetic bases of selected traits linked with plant architecture and development.



HOW TO APPROACH THE ANALYSIS OF A TRAIT?

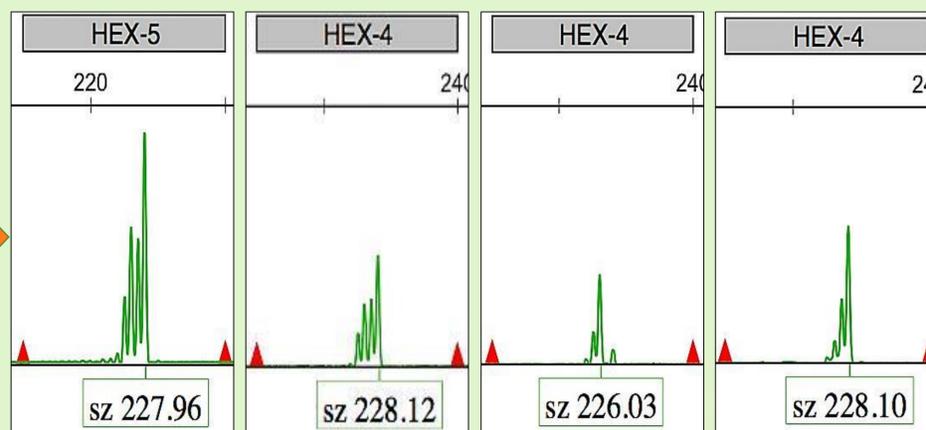
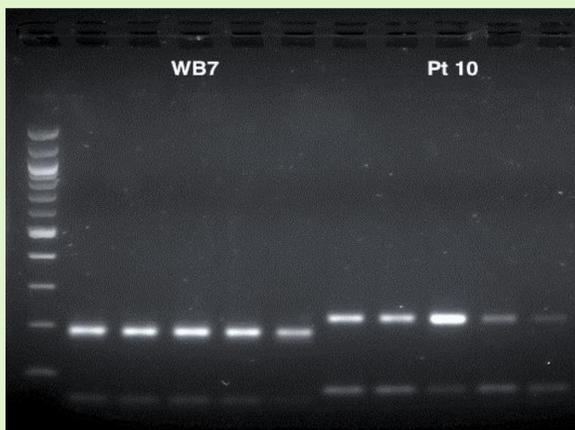


Fig. 1: a) Temperature gradient PCR with primers targeting the SSRs WB7 and Pt10; b) Capillary electrophoresis for Pt10 with 4 kind of WB from Malaysia, Papua New Guinea, Indonesia, and Sri Lanka (M4, T10, T17, and 319).

Molecular Markers: “flags”

Simple Sequence Repeats (SSRs) are used as molecular markers. These are DNA sequences that act as “**flags**” representing each one a DNA region. Each has different dimension (polymorphism) between **different plants** (Fig 1a,b), such that in an individual, generated from a cross, we can always identify whether a specific DNA region is inherited from one parent or the other.

Controlled Crosses

Multiple varieties of winged bean with diverging origins will be crossed with a **single Malaysian** one (Fig. 2). The analysis of the generated progenies (**F₁** and **F₂**) should allow to understand the **genetic bases** (how are they inherited, and which is dominant?) of traits like time to flowering, stem length, number of branches, leaf area and internode length. Progenies will also be used for linkage analysis: find the “**flag**” associated with a specific trait.

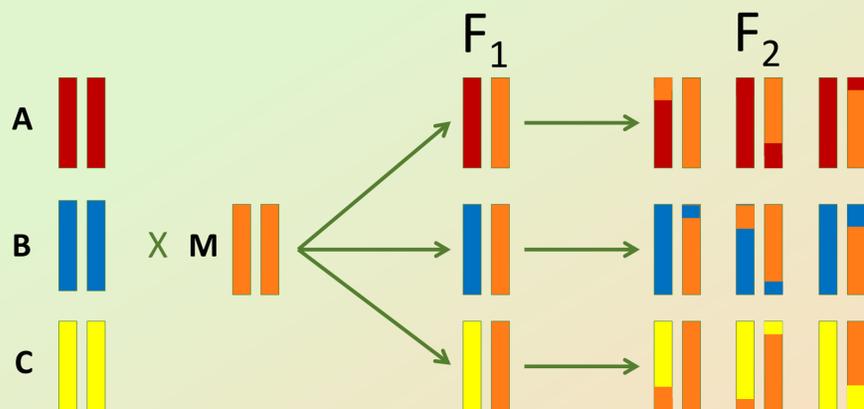


Fig. 2: Controlled Crosses Scheme. Genotypes from Nigeria, Bangladesh, Sri Lanka, Papua New Guinea and Indonesia (here simplified with A,B,C) will be crossed to a single Malaysian line (M). Hybrids (F₁s) will be left free to self-pollinate to obtain the respective F₂s.

Eventually: knowing how a trait is regulated and inherited, and having the tool to identify the DNA regions controlling it, are critical steps to plan future **improvement programmes**. Therefore, the information that could be acquired from these analyses, about the plant development and its architecture, can provide the bases for combining favorable traits into **new improved varieties of winged bean**, to fully exploit its potential.

Ref.: USDA Food Search; Erskine & Khan, 1977; Erskine 1981; National Academic Press, 1981; Eagleton, 2002