

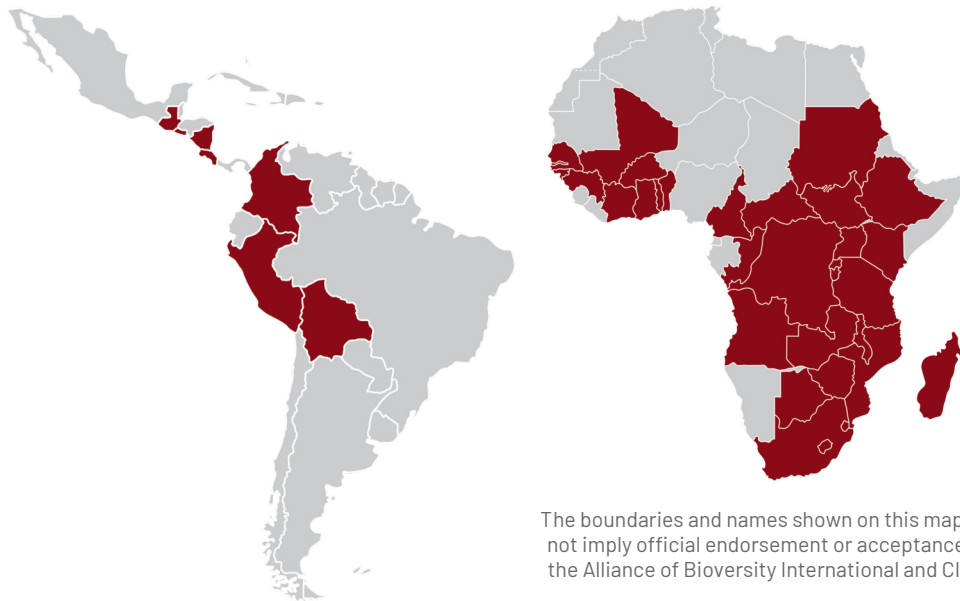
Goal

The Bean Molecular Genetics team supports the breeding program by discovering and deploying powerful molecular markers. We map critical traits and integrate state-of-the-art strategies to boost the development of new bean varieties with enhanced biotic and abiotic stress tolerance as well as improving key nutritional and processing qualities. By identifying valuable genes in wild relatives and landraces, we use marker-assisted selection to precisely transfer them into elite lines to accelerate the creation of superior genotypes.



Where we work

We provide solutions for bean breeding and research programs in Africa (PABRA), Latin America (Kolfaci), and the Caribbean.



The boundaries and names shown on this map do not imply official endorsement or acceptance by the Alliance of Bioversity International and CIAT.

How we do it

- **Gene discovery and marker deployment:** We have established effective processes that begin with the discovery of genes and novel variants within our germplasm, as well as those reported in scientific literature. This workflow has allowed us to develop markers and validate them using phenotypic data for their successful implementation in our bean breeding program.
- **DNA sequencing:** Implementation of high-throughput genotyping techniques for gene and marker identification and use of third-generation sequencing strategies to increase efficiency and reduce the cost for the assembly of whole genomes.
- **Bioinformatics:** By utilizing advanced bioinformatics tools, we have tapped into the immense potential of genotypic data from over 5,000 genotypes generated in our program, sourced from various genotyping platforms. This has enabled us to generate molecular markers for assisted selection programs, conduct trait mapping analyses, and identify introgressions that are agronomically significant.

The impact



Expand understanding of common bean genetics: Through our gene-discovery projects, we develop and share cutting-edge resources (diverse genetic populations, high-resolution sequencing datasets, genome-wide association studies, and validated molecular markers) that collectively deepen our knowledge of *Phaseolus vulgaris* genetics. These tools also empower our breeding partners to make faster and more informed decisions.



Accelerate common bean breeding efficiency: We provide end-to-end genotyping procedures from selecting the most promising parental lines and verifying true F₁ hybrids to deploying marker-assisted selection. By identifying non-redundant genetic diversity, elimination of self-pollinations and rapidly fixing key traits, breeding cycles are reduced which translates into resource saving.



Deliver open bioinformatics pipelines: To foster reproducible science, we openly release the pipelines that power our discoveries. Each workflow is designed to be scalable, reusable, and fully documented, meeting FAIR standards so that researchers everywhere can run, inspect, and adapt our tools.

**FAIR (Findable, Accesible, Interoperable, Reusable).*

Actions for innovation

- Optimization of the in-house genotyping and sequencing systems through the application of cutting-edge technologies.
- Leveraging de-novo-assembled genomes for mapping studies and marker development.
- Assist in parental selection through molecular markers.

Technologies



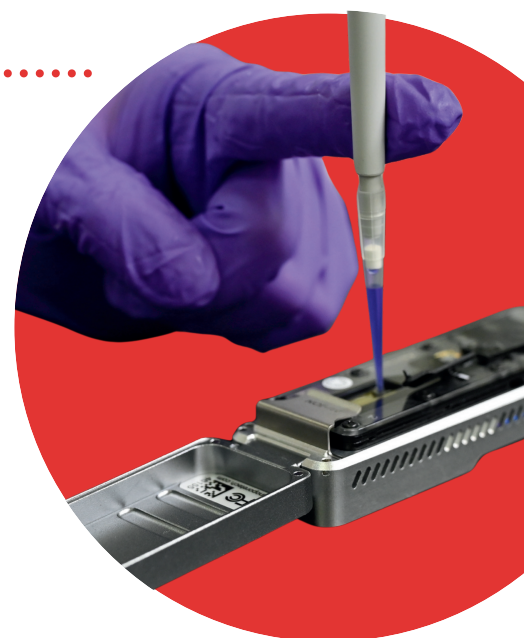
Powderbot is a tool to automatize seed powder collection in plates for DNA isolation.



Allele-specific genotyping technologies (i.e. KASP, Tm-shift, PACE) are implemented for marker assisted selection.



Genome-wide genotyping systems (DArTSeq, GBS) are utilized for trait mapping studies.



To know more about the program, visit us:



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