**PanFaba: The Pangenome of faba bean**

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Faba bean (*Vicia faba* L.) is one of the first domesticated plants at the dawn of agriculture. Its high yield potential and higher grain protein content hold promises for sustainable regional protein supply worldwide. The giga-size chromosomes (~13 Gb) bloated by repetitive sequences had hampered its study and crop improvement. Recently, with international collaborative effort, a high-quality reference genome was released [1]. With a revolutionary new low-cost high accurate long-read sequencing and a chromosome-scale physical map in hand, it is now possible to undertake investigations into the pangenome of faba bean. We characterized the faba bean germplasm collections (> 2000 accessions) representing global diversity using genotyping-by-sequencing (GBS). We selected a representative set of over 45 genomes to develop chromosome-scale genome assemblies. The faba pan-genome will contain a more accurate and diverse representation of global genomic variation, improve trait mapping and serve as the permanent genomic resource for sustainable breeding and research.

***References:***

[1] Jayakodi M. et al, The giant diploid faba genome unlocks variation in a global protein crop, Nature, 615, 2023, 652-659.