

Better genes for better beans

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Some of the most underappreciated crops could soon become the most valuable tools in agriculture with new research from the Centre for Underutilised Crops at the University of Southampton. Coordinator Mark Chapman has created a resource of new genetic data that will enable scientists to uncover why certain legume crops succeed where others fail. Ultimately, the new data will prepare the world for future pressures on agriculture.

Thousands of species belong to the legume family, the Fabaceae, yet only a few of them are used in mainstream agriculture. Dozens more are underutilized. Unlike soybean, peanut, chickpea, and other chart toppers, the underutilized species can grow in areas of very poor soil with limited water availability. This is because they are equipped with unique variations in plant growth genes that have been lost from mainstream [crops](#) through years of breeding.

Chapman's work will enable researchers to identify these valuable genes. He has sequenced and annotated the transcriptomes of four underutilized [legumes](#) that are native to Africa and grown today on small-scale farms in parts of Asia and Africa. Hyacinth bean, grasspea, winged bean, and Bambara groundnut all exhibit different stress-tolerant traits.

"These legumes were selected because of their extreme tolerances, but so far only limited research has been carried out," explains Chapman, who also teaches evolutionary biology at the University of Southampton. "Hyacinth bean is one of the most drought-tolerant legumes, often used as forage for livestock, and grasspea is so resilient to drought that it is

grown as an insurance crop. Winged bean expresses strong disease tolerance, and Bambara groundnut grows on marginal soils where even other legumes struggle."

Across these beans, Chapman identified between 32,446 and 34,401 total genes. He also identified nearly 3,000 genetic markers that will help researchers investigate the [genetic variation](#) within and between different species. These markers will be essential for linking genetic sequences to the traits demonstrated by the legumes that thrive in harsh environmental conditions.

Chapman says, "These markers mean that genetic diversity within and between these (and other) legume species can be rapidly assayed, allowing for identification of regions of the genome, or even specific genes, that play a role in stress tolerances, aiding future breeding to increase stress tolerance in legumes."

This study marks the first attempt to produce genetic data of this kind for these crops and will serve as a valuable resource for gene discovery across the legume family. Chapman is the sole author of the work, which published in a recent issue of [Applications in Plant Sciences](#). All sequence data are publicly available to the research community via the National Center for Biotechnology Information (NCBI) Sequence Read Archive and the Dryad Digital Repository.

Legumes are nutritionally vital plants because they are rich in protein and heavily relied upon in areas where meat is scarce. In some areas of Africa, they are known as the "meat of the poor." When combined with grains, legumes can provide the full complement of essential amino acids needed in the human diet.

"As coordinator of the Centre for Underutilised Crops (at the University of Southampton) one of my aims is to bring mainstream genetic and

genomic technologies to the study of previously undervalued, yet very important crops," says Chapman. "Investigations into less-studied crops have the potential to reveal new varieties and unique alleles that could be applied in future [agriculture](#) and crop breeding. This particular study of legumes is a necessary first step for the identification of stress-tolerant lines of all crops, and it is hoped that more investigations into other underutilized crops can be carried out in this way."

Provided by Botanical Society of America

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