

Unraveling the historic journey of the mung bean: A tale of evolution, migration and climate adaptation

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World Vegetable Center in Taiwan tests different genetic materials to cultivate and breed mung beans. The new USC Dornsife research will enlighten what genetic materials to use for optimal breeding and cultivation. Credit: World Vegetable Center, Taiwan

The mung bean, commonly known as green gram, has played a pivotal role as a cheap protein source in regions where access to meat is limited. Spanning over 4,500 years, the cultivation of this humble legume has



sustained civilizations throughout its history. While its migration routes and cultivation expansion have been a mystery, a new study by researchers at USC Dornsife College of Letters, Arts and Sciences that was published in *eLife* reveals insights into the circuitous odyssey of this resilient crop.

The study, co-led by Sergey Nuzhdin, professor of biological sciences at USC Dornsife, employed cutting-edge genomic techniques to trace the evolutionary trajectory of the mung bean. The team analyzed mung bean seeds from three global seed banks, including the Australian Diversity Panel, the World Vegetable Center in Taiwan and the Vavilov Institute of Plant Industry in Russia.

The research unveiled a distinctive path of cultivation and shed light on the factors influencing its expansion. Contrary to previous assumptions—based on the geographical proximity between South and Central Asia—genetic evidence suggests that the mung bean first spread from South Asia to Southeast Asia, and then finally reached Central Asia, including Western China, Mongolia, Afghanistan, Iran and Russia.

Adapting to climate

Nuzhdin and his team of international scientists used an interdisciplinary approach that looked at population information, <u>environmental</u> <u>conditions</u>, empirical field and laboratory investigation, and <u>historical</u> <u>records</u> from ancient Chinese sources. Through this analysis, they discovered that divergent climatic conditions and farming practices across Asia shaped the mung bean's unique trajectory, not deliberate human cultivation choices.





Vavílov Institute of Plant Industry in Russia. Credit: Eric J. Von Wettberg

Nuzhdin was surprised that the evolution was not solely driven by human activity through domestication but instead was intricately intertwined with the mung bean's adaptation to diverse climates encountered throughout its journey.

What the research unraveled was the existence of two distinct adaptations of the mung bean, each favored in specific geographic locations. The southern variant, originating in South Asia before



1068-1077 CE, is characterized by larger seeds, favoring higher yields in regions with scorching climates. In contrast, the northern variant, originating in northern China around 544 CE exhibited drought tolerance and a short vegetative period during the summer planting season. The mung bean later spread to the rest of China and Southeast Asia including Cambodia, Indonesia, the Philippines, Thailand, Vietnam and Taiwan.

Genetic variations

While the study's historical revelations are compelling in their own right, their implications have relevance to new ways of breeding crops. The mung bean's genetic makeup, including its short growing season and resilience to <u>extreme heat</u>, hold significant potential for mitigating the impact of climate change on agriculture. Particularly in Southeast Asia, where prolonged heat waves and the severity and impact of flooding threaten valuable agricultural areas, these genetic variants could prove to be a game-changer in the face of climate change.

"Our findings offer a critical roadmap for breeders aiming to enhance mung bean production in the face of climate change predictions, especially in the southern regions. This fundamental research holds immense importance in guiding the selection of genetic materials for breeding programs," Nuzhdin said.

More information: Pei-Wen Ong et al, Environment as a limiting factor of the historical global spread of mungbean, *eLife* (2023). <u>DOI:</u> <u>10.7554/eLife.85725</u>

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