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RESEARCH HIGHLIGHT

Progress for the pea of prosperity

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This issue of *The Plant Journal* features the release of a high-quality reference genome for cowpea (*Vigna unguiculata* L. Walp), one of the most widely cultivated legumes in the world. Built using state-of-the-art technologies and an innovative assembly approach, this reference genome promises to be a valuable resource to both scientists and breeders.

Cowpea originated in Africa, although the exact region where it was domesticated is still a contested topic (Lush and Evans, 1981). There are two main cultivated forms, *unguiculata* and *sesquipedialis*. The dominant subspecies *V. unguiculata* is widely cultivated in Africa, India, the Middle East, and the Americas, mainly for dry grain. It is particularly important in sub-Saharan Africa, where it serves as the main source of protein in the human diet. Millions of sub-Saharan Africans depend on cowpea production for food, animal feed, and cash income (FAO, 2004). Cultivated in Eastern and Southern Asia, *V. sesquipedialis* is known as asparagus bean or ‘yard-long’ bean. It features strikingly long pods (up to 1 meter) that are harvested at an immature stage, quite popular in Chinese and other Asian cuisines.

One of the most ancient crops known to humankind, cowpea has a rich history that spans across continents. Perhaps for this reason, it has many common names in English: cowpea, black-eyed pea, southern pea, bachapin bean, crowder pea, china pea, and cowgram (FAO, 2004). In the southern U.S., legend has it that eating black-eyed peas on New Year’s Eve brings a prosperous new year. The crop arrived in the country in the early 1700s with the transatlantic slave trade and was planted in the Carolinas, the largest producers of rice in the U.S. at the time (Harris, 2010). Enslaved West Africans were brought there because of their knowledge of rice production, and along came their native crop, the cowpea. As in Africa, it was often planted at the borders of the fields to control weeds and enrich the soil, and cattle grazed on it (hence the name cowpea). Cowpea was also introduced to Northern Mexico in the late 1600s by the Italian Jesuit missionary Eusebio Francisco Kino (Castetter and Bell, 1942). It spread into what is now California, where landraces that resemble those of modern-day Iberian Peninsula can still be found. Other cultures also associate black-eyed peas (i.e., cowpeas) with luck. Sephardic Jews eat them during the Jewish New Year to bring fertility and good fortune. In a little known but fascinating bit of ancient history, black-eyed peas found their way to the Jewish New Year meal by accident: according to historian Gil Marks, a list of five foods mentioned in the Talmud to eat on New Year included fenugreek (*rubia*), but Sephardim may have confused that with *lubia*, the word for black-eyed peas (Marks, 2010).

Cowpea is more than just a lucky pea: it also offers exceptional nutritional qualities and is remarkably resilient to harsh environments. Cowpea grains have high contents of protein, carbohydrates, essential amino acids and minerals, along with a relatively low content of fat (Iqbal *et al.*, 2006; Jayathilake *et al.*, 2018). In addition, the crop is highly resistant to high temperatures and drought stress (Ehlers and Hall, 1997), the most resilient among the major crop legumes. With this unique combination of qualities, cowpea is a key crop for food and nutritional security in the face of climate change. The availability of a high-quality genome sequence will support progress in cowpea research and breeding.

The publication of the reference genome sequence (see Figure) is the product of a large collaborative effort led by Stefano Lonardi, María Muñoz-Amatriaín, and Timothy Close. Lonardi is a Professor of Computer Science and Engineering at the University of California Riverside (UCR), and Muñoz-Amatriaín, who was a Project Scientist at UCR, is now an Assistant Professor at Colorado State University. Timothy Close is a Professor of Botany and Plant Sciences at UCR. Contributions from scientists in several institutions in the U.S. and other countries rounded out the team effort. Cowpea research at UCR began with now-retired Professor Anthony Hall in the mid-70s. Hall led the cowpea effort at UCR for over 25 years and established partnerships with African researchers that laid the foundation of collaborations that continue to this day. Funding from the Feed the Future Innovation Lab for Climate-Resilient Cowpea (USAID) and the Tropical Legumes project of the Generation Challenge Program (CGIAR) enabled the group at UCR to start developing genomic resources with colleagues in West Africa, including short-read sequences and a SNP genotyping assay (Muñoz-Amatriaín *et al.*, 2017). The reference genome was funded mainly through the National Science Foundation BREAD program.

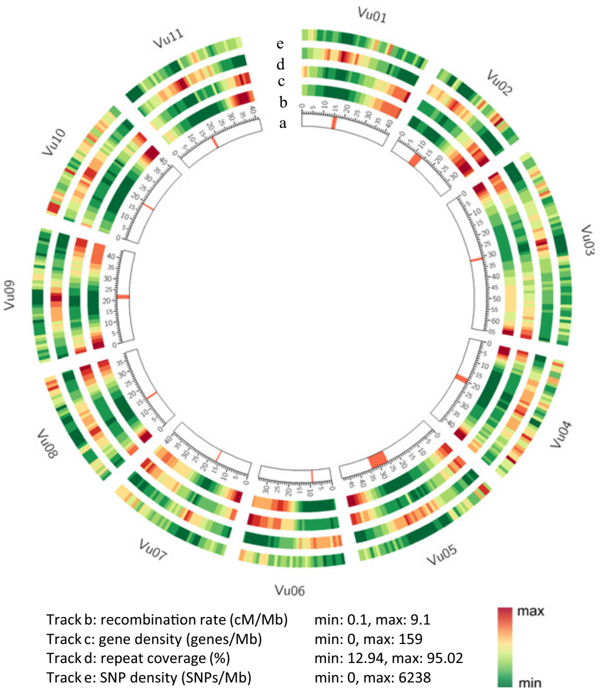

Figure. Landscape of the cowpea genome. (a) Cowpea chromosomes in Mb, with red lines representing centromeric regions; (b) Recombination rate at each 1 Mb; (c) Gene density in 1 Mb windows; (d) Repeat coverage in 1 Mb windows; (e) SNP density in 1 Mb windows.

According to the authors, the project brought a few interesting surprises that required problem solving and innovation to keep the work moving forward. To assemble the genome, they experimented with different assembly tools and parameter settings and noticed that each provided somewhat different results. Noting the strengths and weaknesses of each assembly tool, they came up with an innovative algorithmic solution that 'merges' multiple assemblies with the help of two optical maps and a high-density genetic linkage map, to generate the most contiguous, least error-prone assembly.

Another surprise was a large chromosomal inversion identified when comparing the reference cultivar to other cowpea accessions. Confirming its presence was a long and laborious process, requiring many PCR amplifications to define the region, which were especially challenging due to the abundance of repetitive sequences around the breakpoints.

Although this reference genome is key to enabling progress in cowpea research and breeding, the authors point out that it does not capture the full genetic variability of the species. Their next objectives include generating *de novo* assemblies for a set of diverse cowpea varieties to gain insights into the cowpea pan-genome. This will enable further investigation of the genetic diversity of this important crop plant.

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