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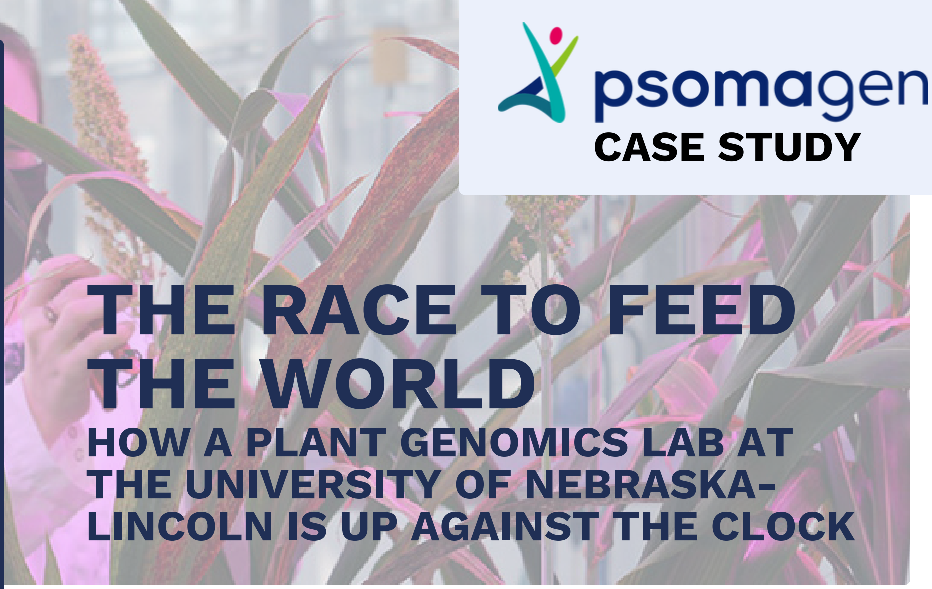
CASE STUDY



THE RACE TO FEED THE WORLD

HOW A PLANT GENOMICS LAB AT THE UNIVERSITY OF NEBRASKA-LINCOLN IS UP AGAINST THE CLOCK

DR. JAMES SCHNABLE

Gardner Professor of Maize Quantitative Genetics
University of Nebraska–Lincoln

By the year 2050, our current crop yields will likely not be enough to meet the world's food needs. The United Nations (UN) is estimating an increase of two billion people worldwide within the next 30 years. Today's crops are produced in quantities that meet the global demand for food — not exceed it. In this case study, Psomagen worked with the Schnable Lab to research plant resilience and develop new crops.

Despite continued work toward the UN's Department of Economic and Social Affairs' Sustainable Development Goal 2 (SDG2), food security challenges have risen in recent years. To worsen the situation, the Food and Agriculture Organization of the United Nations has stated that "The COVID-19 pandemic made the pathway toward SDG2 even steeper." The rise in COVID-19 cases led key decision-makers to enforce county-by-county lockdowns, delaying experiments for laboratories across the country. However, the lockdown did not put all research to a halt. The bench was off-limits, but for the Schnable lab at the University of Nebraska-Lincoln (UNL) — there was data to analyze.

> *"When the coronavirus was just starting to spread, UNL was going through a phased shutdown. During this time, I was in contact with Psomagen about doing these thousand-sample projects. I mentioned that I had a lot of samples sitting in the freezer and asked if it was possible to send them over for sequencing. Psomagen was able to get a large sorghum dataset generated for us. This meant that there was still work for people to do while at home, something to make progress during the lockdown."*
>
> *-Prof. James Schnable, Gardner Professor of Maize Quantitative Genetics*
> *University of Nebraska-Lincoln (UNL)*

Our Current State of Science

Plant breeders aren't able to adapt their crops to changing environments fast enough. It takes seven to ten years for plant geneticists to develop new varieties that maintain or improve productivity in our planet's ever-changing climate. UNL scientists studying plant genomics are trying to predict how plants will thrive in a specific environment without actually testing them in that environment. "Our long-term goal is to understand why different varieties of corn and sorghum do well in different environments across the US, said Professor James Schnable. "If we better understand what determines a plant's survivability, it will help us develop better varieties of corn and sorghum for individual environments."

A key stage in this work is measuring naturally occurring genetic variation (or DNA differences) between hundreds or thousands of different varieties of corn and sorghum. The collection of high-quality samples is necessary to obtain good sequencing data. Providing ample high-quality samples is challenging, and this was intensified during the pandemic shutdown. The Schnable lab was unsure if they would be able to have a field season and therefore, unsure of the type of data they would have. "During the pandemic we had people who were working from their apartments all across the state," said Professor Schnable. "If we hadn't been able to keep them fed with new data, progress in my lab would have ground to a halt."

Research Hurdles

The current availability of environment-specific plant genomic data is too small.

Breeders have data for how their specific strain will do in the environment they are working in, not on how their strain will do in other environments. Collaborative data comparing a strain's genotype, phenotype, and viability in different environments is the type of larger genomic data sets that scientists at UNL need. "We're often doing things on a scale not traditionally done in academia. When we are trying to generate information on genetic markers for QTL mapping or GWAS, that can mean generating and tracking thousands of unique samples."

It takes nearly a decade for plant geneticists to develop a new crop variety.
Gathering the data needed for plant hybrid development is a long process of sampling, analyzing, and testing. Efficiency and the ability to accrue as much data as possible in as few attempts as possible is key.

Due to the pandemic, a rising population, and compromised food security, every second for plant genomics research, development, and application counts. Samples need to be analyzed and data extrapolated as quickly as possible to determine subsequent project steps.

> *"Often we wait on data that we need to analyze in order to make decisions about what new varieties are going to go into the field the next year. The turnaround times with Psomagen are exceptional, which is one of the things we really value. We can send ten, one hundred, or one thousand samples — Psomagen processes it and gives us our data back rapidly."*
>
> *-Prof. James Schnable*

The Psomagen Solution

Through Psomagen's sequencing services, UNL is able to gather gene-expression data to help predict a plant's survivability and productivity and to identify a phenotype that displays viability across a variety of environments.

UNL received the proper services and support to get quality data in the quantities they wanted — all within a timeframe that satisfied them.

> *"Psomagen is able to accommodate the size and scope of our projects, generating data faster. We trust Psomagen and that's why we choose them."*
>
> *-Jon Turkus*
> *Schnable Lab Technician, University of Nebraska-Lincoln*

> *"After the sequencing is done, Psomagen's data delivery is very efficient. The turnaround time is weeks - it's fast."*
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> *-Dr. Guangchao Sun, Schnable Lab Postdoctoral Scholar*
> *University of Nebraska-Lincoln*

The Schnable Lab in Action

In a recent publication, the Schnable Lab used comparative functional genomics to assess the genome of the stress-tolerant Paspalum vaginatum, a wild relative of sorghum. They investigated what specific traits might lead to increased biomass productivity (crop yield) in corn (Zea mays) and hope to use this information to create high-quality and resilient crops.

"We want to understand the mechanisms underlying the resilience of our crop's wild relatives," said Dr. Guangchao Sun, Postdoctoral Scholar at the Schnable Lab. "We want to be able to transfer this resilience to our crops so that we can improve the yield of our crop."

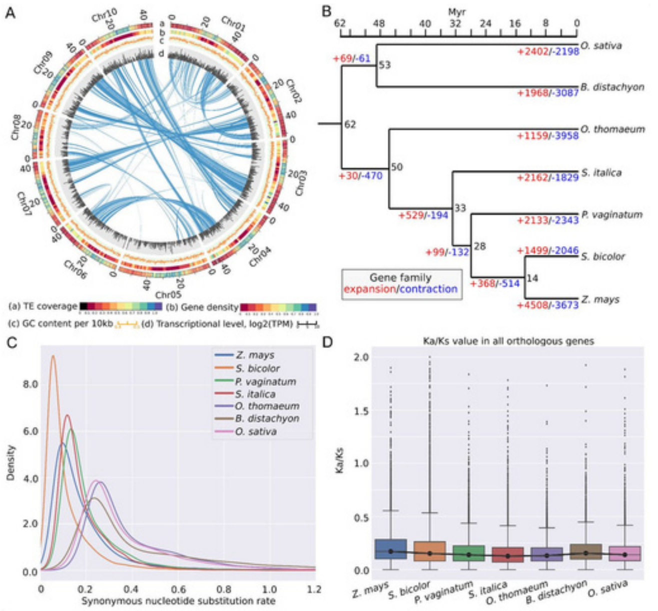
One Plant's Phenotype Leads to Resilience When Produced in Another

Dr. Schnable and his team sequenced a reference genome of Paspalum vaginatum, the wild crop known to withstand abiotic stresses. When subjected to nutrient-deficit stress, the crop showed an increase in trehalose, a naturally occurring sugar.

Comparative evolutionary analyses of P. vaginatum pinpointed a protein sequence that led to an evolution of particular genes. The resilience of present-day P. vaginatum is associated with the genes that affect trehalose metabolism. Dr. Schnable wanted to produce this same phenotype in maize and sorghum by slowing down a key step in trehalose metabolism and then subjecting the crops to nutrient-deficit stress.

The crops showed a mitigated decrease in overall biomass and a greater allocation of biomass to the plant shoots. This is a prime example of the plant genomic data needed in larger quantities, from different labs, and acquisition at quicker rates.

Paspalum (Paspalum vaginatum) genome and evolution. Figure 1 (Sun, G., et al.)



(A) Circos plot for the paspalum genome. a: TE coverage per 100 Kb, b:GC content per 10 kb region, c: gene density (generic region coverage) per 1 Mb, d: transcription represented by log2(TPM) per 100 kb and e: inter- and intra- chromosomal synteny. (B) Phylogeny and estimated divergence times among maize (Zea mays), sorghum, paspalum, foxtail millet (Setaria italica), Oropetium (Oropetium thomaeum), Brachypodium (Brachypodium distachyon), and rice (Oryza sativa). Numbers in black indicate the estimated divergence time (in millions of years before present) for each node. Numbers in blue and red indicate the number of gene families predicted to have experienced copy number expansion or contraction along each branch of the phylogeny, respectively. (C) Distribution of the estimated lineage-specific synonymous substitution rates for syntenically conserved genes in each of the seven species shown in panel A. (D) Distribution of the estimated lineage-specific ratios of nonsynonymous substitution rates to synonymous substitution rates for syntenically conserved genes among each of the seven species shown in panel A.

The Big Picture

Faster identification of the DNA differences between greater and greater numbers of crop varieties means a faster turnaround in crop development. This will not only sustain current crop needs but also provides the prolific foundation to meet the world's future food needs. Dedicated labs and sequencing service providers are working to ensure greater food security for the future.

> *"The thing I've really valued about our relationship with Psomagen is that I have never requested a project and have been told 'That's too large, we'd have to do it in stages or stretch it out over months'. However big the project gets, it seems like Psomagen is able to take it in stride. This is really powerful."*
>
> *- Professor James Schnable, Gardner Professor of Maize Quantitative Genetics, UN*

References

United Nations, Department of Economic and Social Affairs. https://www.un.org/development/desa/en/news/population/world-population-prospects-2019.html

The Schnable Lab's manuscript on the Paspalum genome: Sun, G., Wase, N., Shu, S., Jenkins, J., Zhou, B., Chen, C., Sandor, L., Plott, C., Yoshinga, Y., Daum, C., Qi, P., Barry, K., Lipzen, A., Berry, L., Gottilla, T., Foltz A., Yu, H., O'Malley, R., Zhang, C., Devos, K.M., Sigmon, B., Yu, B., Obata, T., Schmutz, J., Schnable, J.C. (2021). The genome of stress-tolerant crop wild relative Paspalum vaginatum leads to increased biomass productivity in the crop Zea mays. BioRxiv. https://doi.org/10.1101/2021.08.18.456832