

new hot papers - 2010

March 2010



Andrew H. Paterson talks with *ScienceWatch.com* and answers a few questions about this month's New Hot Paper in the field of Plant & Animal Science. The author has also sent along an image of his work.



Article Title: The Sorghum bicolor genome and the diversification of grasses

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SW: Why do you think your paper is highly cited?

As the second fully sequenced cereal genome (rice being the first), sorghum permitted us to compare these divergent lineages in the flowering plant group (grasses) that provides humanity with most of its food and feed, and a growing share of its fiber and fuel.

Sorghum also added new dimensions to our ability to compare monocots (including the cereals) to eudicots such as the other flowering plant genomes sequenced to date. The importance of sorghum as a botanical model for food/feed/fodder/biomass production makes this work important to the transition to a more bio-based economy.

Better understanding of its drought tolerance may help in adapting to a future in which agriculture has access to a smaller portion of the world's water supply. Unique physiological mechanisms (i.e., traits) underpinning its high nitrogen use efficiency (NUE) may benefit other crops, and reduce nitrate runoff into the world's waterways.

SW: Does it describe a new discovery, methodology, or synthesis of knowledge?

We described the largest and most complex plant genome that had been sequenced using the whole-genome shotgun approach, at that time.

In addition to the value of sorghum itself for comparative biology (detailed above), this work illustrates

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the high level of sequence contiguity and accuracy that may be achieved by using the whole-genome shotgun sequencing approach to clothe a backbone of detailed genetic and physical maps.

Our work suggests that hundreds of additional plant genomes (including most of the crops that sustain humanity) may be amenable to this sequencing approach, despite high levels of gene duplication and repetitive DNA.

A surprise regarding the organization of this relatively large genome appears to be true of many additional plant genomes. Remarkably, about 985 of the recombinations in this genome and the vast majority of gene-like sequences are contained in about one-third of the total chromosomal DNA.

This suggests various strategies to more affordably generate very informative partial sequences of complex genomes of many other grasses and other plant species, and should help us to reduce our reliance on a very small number of crops as sources of our food, feed, fuel, and fiber.

Figure 1



Sorghum stands tall.

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SW: Would you summarize the significance of your paper in layman's terms?

Initial analysis of the sorghum genome sequence provides insights into the "parts list" of plants that are well-adapted to converting sunlight and carbon dioxide into usable products (grain and biomass) at high temperatures and with a minimum of water.

This knowledge will help to accelerate improvement of the relatively small and simple genome of sorghum to meet human needs for food and biomass/biofuel, and also will accelerate improvement of its close relatives with much larger and more complex genomes, such as sugarcane and "giant Chinese silver grass" (*Miscanthus*), which reaches 12 feet in height and has silvery plumes that are well-separated above the cornstalk-like foliage in late summer.

SW: How did you become involved in this research, and were there any problems along the way?

When I started down this road in 1992, plant genomics was in its infancy. Funding for plant genomics research was modest, and the importance of sorghum was appreciated by only a small community of scientists and stakeholders.

Improved genomics technology and heightened awareness of what genomics could offer, the resurgence of interest in biofuels, increased awareness of the need to produce crops with less water, and invigorated international efforts to enhance the quality and stability of the food supply in Africa (where sorghum is native, and a staple) all helped to bring the sequence to fruition.

SW: Where do you see your research leading in the future?

The reference genome of sorghum opens many new doors to better utilize the intrinsic genetic potential of plants to meet human needs. We are working to learn about functions of specific genes that differentiate sorghum from other botanical models and/or major crops.

Also, the sequence reveals that different regions of the genome of sorghum and other grasses have evolved by very different mechanisms and at very different rates. We would like to learn the causes of

this phenomenon and the reasons for it.

SW: Do you foresee any social or political implications for your research?

Sorghum is well-suited to several niches in the global agro-ecosystem that are likely to be of growing importance. Already, it is an essential staple in much of Africa, especially in the Sahel region where episodic drought is frequent and challenges to development are great.

Improved yield stability (especially drought tolerance and resistance to insect pests and hemi-parasitic weeds from the genus *Striga*) and nutritional quality of food/feed produced from sorghum grain is one important dimension needed in an integrated effort to better meet the basic needs of some of the world's poorest people in some of the world's most difficult agricultural environments.

The drought tolerance of sorghum makes it of growing interest well outside its native region in Africa. Presently, agriculture enjoys access to a large share of the world's water supplies, but population growth and climatic changes suggest that many parts of the world will face a "water crisis" in the next few decades.

Expanded production of sorghum itself may contribute to an agricultural system that can better sustain humanity while using less water. Furthermore, identifying the genetic determinants of sorghum's intrinsic drought tolerance may contribute to the improvement of other crop plants (such as maize) to be more drought tolerant and/or water-use efficient.

Increased production of sorghum and its close relatives may reduce dependence on fossil fuels. Sorghum is the #2 source of seed-based biofuel (after maize) in the USA, and it shows much promise as a source of "next-generation" biofuel from lignocellulosic tissues.

Perennial forms of sorghum offer the means to breed genotypes that can be produced on marginal soils that are not well-suited to food production, with a minimum of cultivation to mitigate erosion.

Rapid progress envisioned in learning about the functions of sorghum genes is expected to translate well to its close relatives, sugarcane (arguably the leading biofuel crop worldwide), and *Miscanthus* (a singularly promising biofuel crop for temperate regions).

Recent studies have also shown that sorghum appears to be unique among cultivated cereals in having the ability to protect its nitrogen supply from nitrification by soil microbes. This "biological nitrification inhibition" capacity of sorghum has tremendous potential to improve NUE of crop production and reduce nitrate pollution of waterways associated with intensive crop production.

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Figure 1:



Figure 1:

Sorghum stands tall. Comparison of the completed genome sequences of rice (foreground) and sorghum (background) provides insight into the ~70-million year evolutionary history of *Poaceae* grasses that provide much of our food, animal feed, and fodder, as well as a growing share of our fuel. These two grasses, together with the more recently sequenced *Brachypodium distachyon*, are attractive models for determining the functions of genes that are important to the productivity and quality of a wide range of seed/grain, turf, forage, and biomass crops, as well as the spread and persistence of many weedy/invasive grasses. Ongoing studies are expected to provide insights into productivity under favorable conditions, drought and disease resistance under unfavorable conditions, reproductive biology, nutritional value, compositional properties related to biofuel uses, and many other dimensions of grass biology. Photo credit Dr. C. T. Hash, ICRISAT.

KEYWORDS: MAIZE GENOME; RICE GENOME; WIDE ANALYSIS; CELL-WALLS; EVOLUTION; SEQUENCE; GENES; IDENTIFICATION; RECOMBINATION; DUPLICATION.

