

A genome may reduce your carbon footprint

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With the costs of genome sequencing rapidly decreasing, and with the infrastructure now developed for almost anyone with access to a computer to cheaply store, access, and analyze sequence information, emphasis is increasingly being placed on ways to apply genome data to real world problems, including reducing dependency on fossil fuel. For the efficient production of bioenergy, this may be accomplished through development of improved feedstocks.

A recently published study examined the impact of very cheap sequence data (approximately 1USD per genome) on improvement of switchgrass, a perennial grass well suited to biomass production. Results were published in the current issue of *The [Plant Genome](#)*.

Acquiring the [genetic component](#) of natural variation is or will soon become cheap enough that it will soon be able to be incorporated through marker-assisted selection into almost all breeding programs. With availability of cheap sequencing capacity, neither complete sequence assembly nor gene annotation is required to apply these techniques.

In a species such as switchgrass there exists a great deal of phenotypic variation derived from latitudinal adaptation across its natural range and local adaptation to soil, temperature, and moisture conditions. It is still largely undomesticated and thus large gains might be realized through fixation of beneficial alleles in breeding populations. There are likely to be a few genes with large effects that will dramatically impact yields once incorporated into breeding programs. This has occurred during the

[domestication](#) of all our grain crops, but it may take just a fraction of the time now.

The development of a dollar genome sequence could provide information highways that would cut across several disciplines and drive the development of next generation biomass feedstocks, [bioproducts](#), and processes for replacing [fossil fuels](#). New feedstocks could produce sustainable high yields with minimal inputs in regions where competition with food is minimized, as well as provide ancillary environmental benefits associated with carbon sequestration and environmental remediation.

Another result of inexpensive sequencing would be an increased use of comparative genomics. A comprehensive survey of genetic diversity would help guide conservation efforts to preserve germplasm diversity and allow reconstruction of past speciation events at a more detailed level.

As a result of access to multiple related genomes, similarities between closely related species would allow inference of missing data. For example, if a draft switchgrass genome assembly does not provide a complete assembly as judged by comparison to an inbred [genome](#) or more closely related grass, it will be possible to infer unresolved regions, including retrotransposon family composition and composition of other abundant repetitive elements. Comparative approaches would be applied to better understand the molecular basis for differences between species that result in higher or lower yields in different environments.

More information: The full article is available for no charge for 30 days following the date of this summary. View the abstract at plantgenome.scijournals.org/content/2/1/5.full .

Source: Crop Science Society of America ([news](#) : [web](#))

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