

Scientists do groundwork for genetic mapping of algae biofuel species

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Using green algae to produce hydrocarbon oil for biofuel production is nothing new; nature has been doing so for hundreds of millions of years, according a Texas AgriLife Research scientist.

"Oils from the green algae *Botryococcus braunii* can be readily detected in petroleum deposits and [coal deposits](#) suggesting that *B. braunii* has been a contributor to developing these deposits and may be the major contributor," said Dr. Timothy Devarenne, AgriLife Research scientist with the Texas A&M University department of biochemistry and biophysics. "This means that we are already using these oils to produce gasoline from petroleum."

It's not just a gee-whiz science trivia, Devarenne said. *B. braunii* is a prime candidate for biofuel production because some races of the green algae typically "accumulate hydrocarbons from to 30 percent to 40 percent of their dry weight, and are capable of obtaining hydrocarbon contents up to 86 percent of their dry weight.

"As a group, algae may be the only photosynthetic organism capable of producing enough biofuel to meet transportation fuel demands."

Devarenne is part of a team comprised of other scientists with AgriLife Research, the University of Kentucky and the University of Tokyo trying to understand more about *B. braunii*, including its genetic sequence and its family history.

"Without understanding how the cellular machinery of a given algae works on the molecular level, it won't be possible to improve characteristics such as oil production, faster growth rates or increased photosynthesis," Devarenne said.

Like most green algae, *B. braunii* is capable of producing great amounts of hydrocarbon oils in a very small land area.

B. braunii algae show particular promise not just because of their high production of oil but also because of the type of oil they produce, Devarenne said. While many high-oil-producing algae create vegetable-type oils, the oil from *B. braunii*, known as botryococcones, are similar to petroleum.

"The fuels derived from *B. braunii* hydrocarbons are chemically identical to gasoline, diesel and kerosene," Devarenne said. "Thus, we do not call them biodiesel or bio-gasoline; they are simply diesel and gasoline. To produce these fuels from *B. braunii*, the hydrocarbons are processed exactly the same as petroleum is processed and thus generates the exact same fuels. Remember, these *B. braunii* hydrocarbons are a main constituent of petroleum. So there is no difference other than the millions of years petroleum spent underground."

But, a shortcoming of *B. braunii* is its relatively slow growth rate. While the algae that produce 'vegetable-type' oils may double their growth every six to 12 hours, *B. braunii*'s doubling rate is about four days, he said.

"Thus, getting large amounts of oil from *B. braunii* is more time consuming and thus more costly," Devarenne said. "So, by knowing the genome sequence we can possibly identify genes involved in cell division and manipulate them to reduce the doubling rate."

Despite these characteristics and economic potential of algae, only six species of algae have had their genomes fully sequenced and annotated, Devarenne said. And *B. braunii* is not one of the six.

Devarenne and his colleagues have done some of the groundwork in better understanding *B. braunii* and sequencing its genome.

They are working the Berkeley strain of the B race of *B. braunii*, so named because it was first isolated

at the University of California at Berkeley. The team has determined the genome size and an estimate of the B race's guanine-cytosine content, both of which are essential to mapping the full genome, he said. There are also races A and L of *B. braunii*, but they were not looked at by the team.

Guanine-cytosine bonds are one of base pairs composing DNA structure. Adenine-thymine is the other possible base pair.

"Genomes with high guanine-cytosine content can be difficult to sequence and knowing the guanine-cytosine content can help to assess the amount of resources needed for genome sequencing," Devarenne said.

The team determined *B. braunii*'s genome size to be 166.2 ± 2.2 million base pairs, Devarenne said. The size of the human genome is about 3.1 billion base pairs. That of the house mouse is also about 3 billion base pairs. But the *B. braunii* genome size is larger than any of the other six previously sequenced [green algae](#) genomes.

The team also looked at the phylogenetic placement of *B. braunii* - where it belongs in the family tree of similar algae species. Though they knew from the work of other scientists that the B race of *B. braunii* was distinct from other races of *B. braunii*, there was some question that the genetic samples of the B race used in a previous study by other scientists might be contaminated by another algal species.

To check this, they used a process called reverse transcription to isolate genes from a pure culture of the B race of *B. braunii*, and then mapped those genes to confirm the relationship of the B race to other races of *B. braunii*.

"Our results support the original Berkeley DNA sequence used for phylogenetic placement was from a contaminating algae," Devarenne said. "And our study places the B race of *B. braunii* in the correct location on the 'algal family tree'."

The actual genome sequencing and mapping will be performed by DOE's Joint Genome Institute.

"We've submitted genomic DNA from *B. braunii* for JGI to use in sequencing, but that hasn't begun yet," he said.

More information: The results and methods of their study will be published online in the *Journal of Phycology*, an international journal of algae research, this summer.

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