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Scientists Complete Genome Sequence of Castor Bean **Beans also produce highly toxic protein ricin, a biosecurity threat**

A team of researchers from the Institute for Genome Sciences (IGS) at the University of Maryland School of Medicine and the J. Craig Venter Institute (JCVI) have sequenced and analyzed the genome of the Castor bean (*Ricinus communis*). The castor bean is the source of the highly valuable castor oil, and their findings will be published in the September issue of ***Nature Biotechnology* (published online on 8/22/10)**.

Castor bean also produces the highly toxic protein ricin, which has been reportedly used for bioterror threats. The availability of the castor bean genome sequence will allow engineering of improved castor bean plants that produce high levels of castor oil without the complications of ricin. The castor bean genome sequence that will be featured on the ***Nature Biotechnology*** cover is the first genome sequence published in the Euphorbiaceae family that includes cassava, rubber tree, physic nut, the invasive weed leafy spurge and ornamental poinsettias.

Dr. Pablo Rabinowicz, lead author and a scientist specializing in plant genomics at IGS, explained, "A better understanding of the biology of ricin accumulation may permit the development of less toxic varieties and may improve public safety by helping the development of improved diagnostic and forensic methods for ricin detection and tracing the origins of samples from potential bioterror attacks."

The castor bean plant is a tropical perennial shrub that originated in Africa, but is now cultivated in many tropical and subtropical regions around the world. It can be self- and cross-pollinated and worldwide studies reveal low genetic diversity among castor bean germplasm. Because of the nearly uniform ricinoleic acid content of castor oil and the unique chemical properties that this fatty acid confers to the oil, castor bean is a highly valued oilseed crop for lubricant, cosmetic, medical and specialty chemical applications. Castor bean is also of economic interest as a potential source of biodiesel.

The high oil content of its seeds and the ease with which it can be cultivated in unfavorable environments, contribute to its appeal as a crop in tropical developing countries.

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An important obstacle to widespread cultivation of castor bean is the high content of ricin, an extremely toxic protein, in its seeds. Ricin is considered one of the deadliest natural poisons when administered intravenously or inhaled as fine particles.

The relative ease with which ricin can be purified has raised questions about its possible use in bioterrorism. Knowledge of the genetics and enzymology of fatty acid metabolism in castor bean seeds is important in efforts to ensure a sustained supply of hydroxy fatty acids without the complications posed by the toxicity of ricin.

“The castor bean genome will allow comparative genomic studies in the Euphorbiaceae, furthering our understanding of genome evolution in this family, particularly of cassava, which is an important food source in poor, tropical countries,” said Dr. Rabinowicz.

The research was supported by the National Institute of Allergy and Infectious Diseases (NIAID), National Institutes of Health, Department of Health and Human Services and the Federal Bureau of Investigation (FBI).

Future research may explore the implications of the castor bean genome for the production of biofuels. Furthermore, because it is a close relative of cassava, castor bean research will contribute to the advancement of cassava breeding of lines with higher stress resistance and nutritional content.

About IGS

The Institute for Genome Sciences (IGS) at the University of Maryland School of Medicine is an international research center dedicated to advancing the use of genomics to improve health and the environment. Led by Dr. Claire Fraser-Liggett, a preeminent genome scientist and microbiologist, IGS is located in a BioPark in downtown Baltimore. IGS scientists are pioneers in the expanding fields of genomics, bioinformatics and metagenomics. For more information, see www.igs.umaryland.edu.