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Integration of Bioinformatics and Omics Technologies in Crop Improvement

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Bioinformatics-based technologies play a vital role in agricultural research by providing means to generate improved cultivars with superior traits, which could help meet the rising global demands for food and fuel. In our lab, we are pursuing next-generation sequencing (NGS) and phenotyping technologies to enhance the crop stress tolerance and yields without compromising its beneficial agronomic traits, in response to various abiotic and biotic stresses affecting the productivity of crops. We are implementing and developing a combination of omics-based approaches, including comparative genomics, transcriptomics, phenotyping and gene network analysis in potato, tomato, sugarcane, energycane, and citrus to identify resistance genes, gene interaction, and molecular markers in response to various environmental stresses. These resources will be important for crop improvement using advanced biotechnology and plant breeding techniques. In addition to molecular level discovery, we are developing and implementing new Bioinformatics software and web resources to provide an innovative way to interpret large-scale datasets generated from omics-based research.

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Developing Sugarcane as a Highly Productive Biofactory for Therapeutic Proteins

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Sugarcane is an ideal platform for the production of protein-based therapeutics at commercial levels. It is one of the fastest growing species with a highly efficient carbon fixation pathway, which allows the production of a large biomass and hence a higher yield of recombinant proteins at a cost-effective scale. The specific goal of this project is to develop an efficient expression system in sugarcane to produce large quantities of a recombinant protein with potent antiviral and antitumor activities. Initially, we have recovered protein expression levels up to 0.1% of total soluble protein (TSP) (equivalent to 0.72 mg/kg fresh weight) in sugarcane lines expressing the therapeutic protein under the control of the constitutive *maize ubiquitin 1* (*Ubi1*) promoter. To optimize the expression system, we transformed sugarcane varieties CP72-1210 and CP89-2143 with a combination of constructs carrying the therapeutic protein under the control of multiple stalk-regulated promoters; *dirigent5-1* (*SHDIR5-1*) and *dirigent16* (*SHDIR16*) developed in our laboratory, and constitutive promoters; proline rich protein (*SHPRP*), elongation factor1□(*SHEF1*□) and *Sugarcane bacilliform virus* (*SCBV21*). Protein yields of the lines generated with the multiple promoter expression system increased from 0.1% to 1.3% TSP (9.4 mg/kg stalk fresh weight tissue) using the combination of *Ubi1*, *SCBV21*, *SHDIR5-1* and *SHDIR16* promoters, that is over 10x more protein yield than the one obtained with a single promoter.