m PESS 1.7 Understanding Genetic Regulation of Photosynthetic Mechanisms to Enhance Plant Productivity

Measuring and monitoring gene expression provides fundamental insights for plant photosynthesis Food security for a burgeoning global population, facing the threat of a changing climate, will require a paradigm shift in crop production and stress resilience. Major efforts are being directed at understanding how we might turbocharge crop productivity;

perhaps by augmenting photosynthesis with a carbon concentrating mechanism (CCM). Current approaches range from incorporating elements of maize photosynthesis into rice, but in a collaboration between Cambridge and NIPGR, New



OF CCM GENE OPERATION

"Recommendations to funders and policy makers: support for individuals is crucial in order to conduct high quality research, and to train upcoming aenerations that are the future researchers in a developing country"

Prof Nvovani Madise Director of Research for Sustainable Development Policies AFIDEP UNIVERSITY OF CAMBRIDGE



environmental stress.



The Microbial Carbon Concentration Mechanism could enhance Agricultural Production The key enzyme driving

carbon uptake by plants (RubisCO) is slow and rather

inefficient. Algae have evolved a CCM which helps to

turbocharge photosynthesis. Using the model green alga.

Chlamydomonas reinhardtii, a partnership between

Cambridge and NIPGR has been investigating the molecular basis of the mechanism which allows RubisCO to

aggregate within a subcellular microcompartment, the

pyrenoid. We have been characterising how a specific

protein, EPYC1, acts as a molecular glue to facilitate

pyrenoid assembly, and using outputs from the GRN

analysis to identify key molecular factors which coordinate CCM operation. In future, these carbon capture

mechanisms (CCMs) could be transferred to higher crops to increase photosynthetic efficiency and resilience to

Delhi, we have defined novel highly productive algal traits prior to transfer into higher plants.



Revolutionising genomics though modelling and empirical studies Tremendous advances in the availability of high throughput Omics- datasets demand new analytical protocols for sifting and sorting genes related to specific traits. Colleagues at NIPGR are pioneering new algorithms and computational methods to find the proverbial needle (key regulators) in the haystack of hundreds of millions of transcriptional reads. Spatio-temporal mapping of changing relationships between genes allows key regulatory hubs to be identified at important stages of plant or algal development, using Gene Regulatory Networks (GRN) and graph embedding methods for transforming nodes and edges into numerical representations.

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