

resulted in a further drop in forward voltage to about 5 V, and an increase in the efficiency to about 1% (photons per electron injected). These devices are believed to operate by double charge injection of electrons and holes from the negative and positive electrodes, respectively. These singly charged excitations combine to form excitons which can then decay by photoemission. Changing the band-gap of these conjugated polymers, by appropriate chemical modification, can result in a change in the wavelength of the photoemission: red-shifted upon reduction of band-gap and blue-shifted upon increasing the band-gap. Enhancement of the photoemission efficiency and further lowering of forward operating voltage are two of the primary areas of current activity that is expected to

lead to improved devices of greater technological relevance.

The use of organic molecule-based systems for development of micro-electronic devices can lead to a greater control over their functional parameters due to better fine tunability of the molecular structure of these molecules. Organic polymers, in addition, have a further advantage that they are easier to fabricate into various device structures. This realization has led to the search for new polymeric structures that can replace active components in micro-electronic devices. Conjugated polymers exhibit a variety of interesting properties and form an important class of materials that is destined to make a significant contribution toward development of new and novel devices in the area of

microelectronics, data storage and optical signal processing.

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S. Ramakrishnan is in the Department of Inorganic and Physical Chemistry, Indian Institute of Science, Bangalore 560 012, India

How to reap what you did not sow — II

T. Ramakrishnan

The spectacular advances in recent times in genetic engineering and biotechnology owe their origin to the epoch-making discoveries in bacterial genetics and molecular biology in the forties and fifties of this century. The application of bacterial genetics to increasing the yield of plant products is at present engaging the attention of a number of plant molecular biologists all over the world. This development is not surprising since bacteria have been classified under plant kingdom and the discoveries in bacterial genetics should logically be extendable to plants.

One of the striking illustrations of this logic has been the discovery¹ that the amount of starch in plants like potato can be increased by the introduction of the ADP glucose pyrophosphorylase gene from the bacterium *Escherichia coli*.

Starch is the main storage carbohydrate in practically all plants and in several crops it is a major component of the harvest. During this decade the demand for starch has increased tremendously, mainly as a result of the development of high fructose syrup and ethanol in place of petrol for use in automobiles.

The enzymes involved in the synthesis of starch include adenosine diphosphate glucose pyrophosphorylase (ADPGPP) and starch synthase. ADPGPP has been proposed to play a central role in both plant starch synthesis as well as bacterial glycogen synthesis.

In *E. coli*, ADPGPP is encoded by the *glgC* gene. It is activated by fructose 1,6-biphosphate (FbP), and inhibited by adenosine monophosphate (AMP) and inorganic phosphate (P_i). An *E. coli* K12 strain, 618, is available with a point mutation in the *glgC* gene (Gly₃₃₆-Asp). This gene is termed *glgC16*, and the gene product is less dependent on FbP and less inhibited by AMP and P_i . As a result, this strain accumulates about 33% more glycogen than the wild-type.

The plant ADPGPP is regulated positively by 3-phosphoglyceric acid (3PGA) and negatively by P_i , and shows homology to the *E. coli* enzyme. In this study the *E. coli glgC* gene was used to examine ADPGPP regulation; in order to minimize allosteric interactions, the *glgC16* gene was used.

First, since starch biosynthesis occurs in plastids, the *glgC16* gene product was fused to a modified chloroplast transit peptide (CTP), and targeted to plastids,

by incubating the radio-labelled protein with intact lettuce chloroplast preparations. Both uptake as well as processing of the fusion protein was confirmed.

The enzymatic activity of the CTP-*glgC16* gene product was examined in a transient assay. The gene, under control of the cauliflower mosaic virus-enhanced 35S (e35S) promoter and the polyadenylation signal derived from the nopaline synthase in plasmid pMON999 was electroporated into tobacco protoplasts. Activity specific to the bacterial enzyme was demonstrated, which was P_i -resistant.

Stable transformants were produced by mating the above plasmid containing a neomycin phosphotransferase gene as marker into *Agrobacterium tumefaciens* strain ASE, and subsequently transforming into tobacco, tomato and potato. An increase in starch content from an average of 3 to a maximum of 9-fold was detected.

However, it was found that constitutive expression of the CTP-*glgC16* gene under the 35S promoter inhibited plant growth and development, possibly by reducing sucrose availability for normal plant activities. It was possible to reverse this effect by growing a transgenic

potato plant in sucrose-containing medium.

To overcome the observed inhibitory effects, the CTP-*glgC16* gene was placed under the control of a tuber-specific patatin promoter, and transferred to potato plants. An increase of 35% to 60% in starch content was observed in tubers. A small-scale field trial gave similar results.

It was observed, however, that the degree of starch increase was not absolutely proportional to the amount of expression of enzyme, i.e. the expression of low levels of the CTP-*glgC16* gene resulted in high levels of starch production. One possible explanation is that the rate-limiting step in starch

synthesis is not ADPGPP, but starch synthase. In this case, allosteric regulation of ADPGPP may be involved in the synthesis of starch. In order to study the relevance of allosteric influences on ADPGPP activity, the wild-type ADPGPP gene from *E. coli* was subsequently used for further plant studies.

The wild type CTP-*glgC* gene was used to transform potato and tomato plants. In both instances, a high level of enzyme expression was observed, but only a slight increase in starch content. This implies that the ADPGPP enzyme activity, and not enzyme amount, is rate limiting in the starch biosynthesis pathway.

In conclusion, it is very striking that a single enzymatic step regulates end-product levels in a complex multicellular organism. It is possible that the same principle can be used to study and possibly manipulate the levels of lipids, amino acids and carbohydrates.

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T. Ramakrishnan is in the Microbiology and Cell Biology Department, Indian Institute of Science, Bangalore 560 012, India

COMMENTARY

Invasive alien weeds in the Western Ghats

R. Muniappan and C. A. Viraktamath

The invasion of alien species has been a neglected subject until the General Assembly of the Scientific Committee on Problems of the Environment (SCOPE) came up with the need to address the ecology of biological invasions in 1982 (ref. 1). In 1986, an international workshop was held in Hawaii which identified the need for information on biological invasions in the tropics. In support of this recommendation, SCOPE sponsored an international workshop on 'Ecology of Biological Invasions in the Tropics' in September 1989 in India².

The term 'biological invasion' used by ecologists includes exotic plants and animals that are introduced and established. Agronomists identify the introduced pestiferous plants as 'exotic weeds' and entomologists and plant pathologists target them for classical biological control by introducing host specific natural enemies.

The nature of invasive plants and the characteristic features and properties that assist them in invading the tropical regions is given by Saxena³. Most invasive alien weeds in India are of neotropical origin. Weeds such as *Lan-*

tana camara (lantana), *Chromolaena odorata* (Siam weed) and *Eichhornia crassipes* (Water hyacinth) were introduced into India as ornamental plants. They escaped cultivation and became wild. The absence of their natural enemies in the new and the favourable environment has led to their successful establishment and to become dominant species.

The seriousness of invasive alien weeds was recognized in the early 1900s by the Government of India. In 1916, Ramachandra Rao was detailed to study the distribution and natural enemies of the exotic weed, *L. camara*, throughout India and Burma⁴. He reported about 148 local herbivores recruited by this invasive weed and also gave a detailed account of the menace caused by other invasive weeds such as *C. odorata*, *Opuntia dillenii* (prickly pear), *Mimosa pudica* (sensitive plant), *E. crassipes*, *Lippia geminata* and *Jatropha grossipifolia*.

The Western Ghats constitute the region between Dangs district (21° N), Gujarat in the North to Kanyakumari district (8° N), Tamil Nadu in the South, traversing through the states of Maharashtra, Goa, Karnataka and Kerala.

The Western Ghats play an important role in the maintenance of ecological balance and cultural and economic developments in South India.

This region has luxuriant vegetation comprising evergreen rain forests, mixed deciduous or monsoon forests and subtropical or temperate forests⁵. Invasive alien weeds have contributed to the deterioration of the Western Ghats by invading disturbed areas, vacant lands, pastures, farm lands, forests, and plantations, interfering in afforestation programmes, suppressing native vegetation, and possibly causing the extinction of some species, interfering in wildlife management, poisoning domestic and wildlife, increasing fire hazards, preventing recruitment of native species, reducing the aesthetic value of parks and reserves and affecting the socio-economic development. In the invasive alien weed-infested areas biotic diversity has been considerably reduced and single species dominance is noted.

Most of the invasive alien weeds were introduced intentionally for agricultural, forestry, pasture, ornamental and/or for other purposes. A few were accidentally introduced through transportation of