trations of other intracellular metabolites change to compensate for the primary lesion[5]. The same probably applies to the ionome (and, in some cases, may explain coincident changes in the levels of several mineral elements in many of the mutants identified).

Second, the results from numerous expressed sequence tag (EST) and genome sequencing projects demonstrate that most plant transporters are encoded by multigene families, the members of which exhibit overlapping, but nonidentical, expression patterns. Seldom is it obvious which members (if any) of a family are crucial, or are at least major contributors, to the homeostasis of a specific ion without knowledge of the mineral element profiles of the appropriate mutants.

Third, many inorganic nutrients are transported by more than one transporter family and many plant transporter families transport more than one nutrient. For instance, in *Arabidopsis,* K^+ uptake can be mediated by members of the KUP/HAK/KT transporter family, as well as by members of the KAT and AKT channel families, if not also by other uncharacterized transporters such as those belonging to the KEA family[6]. Likewise, although the CAX and NHX transporter families were originally defined on the basis of the capacity of their prototypes for Ca^{2+}/H^+ and Na^+/H^+ antiport, respectively, it is becoming increasingly clear that this is not what all members of these families do.

Fourth, there are some plant transporter families (*e.g.*, the MATE family) or subfamilies (*e.g.*, the ATH ABC transporter subfamily) whose transport substrates are completely unknown. These cannot be second-guessed using homology arguments but are nonetheless implicated in ionic homeostasis by the results from systematic cDNA microarray analyses[6].

Fifth, as if this is not enough in the way of deliverables for the plant community, it should be appreciated that ionic profiling will provide strong clues not only to the functional capabilities of transporters or at least to the functional networks in which they participate, but also to the components or upstream or downstream processes that modulate the expression, activity, or the membranes (compartments) to which the transporters localize to exert their effects. Indeed, this next phase of research in ionomics should clarify which genes play key roles in ion regulation, providing a wealth of biological information, which in turn should open the door to an exciting array of possibilities for improving human nutrition and engineering plants for phytoremediation.

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Bacterial batteries

Fritz Scholz & Uwe Schröder

Long-lived fuel cells lacking diffusional electron mediators have been created that convert simple and abundant sugars into electricity with >80% efficiency.

Energy generation and waste disposal are two key challenges in the quest for sustainable societies. Electrochemical fuel cells may, in principle, provide an elegant solution by linking both tasks. On page 1229 of this issue, Chaudhury and Lovley[1] show that *Rhodoferax ferrireducens*, a metal-reducing bacterium recently isolated from subsurface sediments in Oyster Bay, Virginia, USA[2], provides a constant flow of electrons to simple graphite electrodes in a fuel cell while oxidizing glucose or other simple sugars. This is a notable achievement for several reasons: first, glucose has never before been shown to be microbially oxidized in a fuel cell at 80% electron efficiency; second, unlike most other heterotrophic microbial systems, the culture in the anodic fuel cell compartment requires no dissolved electron-shuttling mediators; and third, the bacteria can generate a steady electron flow over extended periods of time while growing on a variety of simple substrates, such as lactate, acetate, glucose, fructose, sucrose or xylose.

A microbial fuel cell is, in essence, a system that harvests electrons produced during microbial metabolism and channels them for electric current generation. Three different microbial fuel cell designs (types A, B and C) have been implemented, with varying degrees of success. In type A fuel cells, artificial redox mediators capable of penetrating bacterial cells are added to the culture solution within the anodic fuel cell compartment, enabling electrons produced during fermentation or other metabolic processes to be shuttled to the anode[3]. Type B fuel cells incorporate metal-reducing bacteria (*e.g.*, members of the Geobacteraceae and Shewanellaceae) that partly exhibit special membrane-bound cytochromes capable of transferring electrons directly to the electrodes (rather than dissolved or solid iron(III) or manganese(IV/III) species)[4]. And type C fuel cells oxidize fermentation products, such as hydrogen and methanol, on electrocatalytic electrodes (that is, chemically modified electrodes capable of efficiently oxidizing such metabolites)[5]; these latter reactions are often inhibited on the surface of gold, platinum or carbon electrodes.

All three designs have their share of advantages and disadvantages. Type A fuel cells show rather good current densities but suffer from a need to use synthetic and often toxic redox mediators that have to be added to the cell culture and are nonrecoverable. Type B fuel cells can work in natural environments (*e.g.*, sediments); however, the growth rate of the bacteria and thus the current densities generated are very low. And although type C fuel cells produce the highest current densities and work with simple and easily available microorganisms (*e.g.*, *Escherichia coli*), electrocatalytic electrodes require rather expensive surface modifiers that make implementation harder[6].

Chaudhury and Lovley have now found in *Rhodoferax ferrireducens* a microorganism that is, compared with *Geobacter* or *Shewanella* species, superior in its glucose-catabolizing efficiency (**Fig. 1**). Bearing in mind that the organism itself needs some of the glucose for its own biomass production, an 80% electron yield is indeed a very surprising and impressive result. In addition, electrons generated by *R. ferrireducens* are easily transferred to the anode without the assistance of electron-shuttling mediators, and the cells

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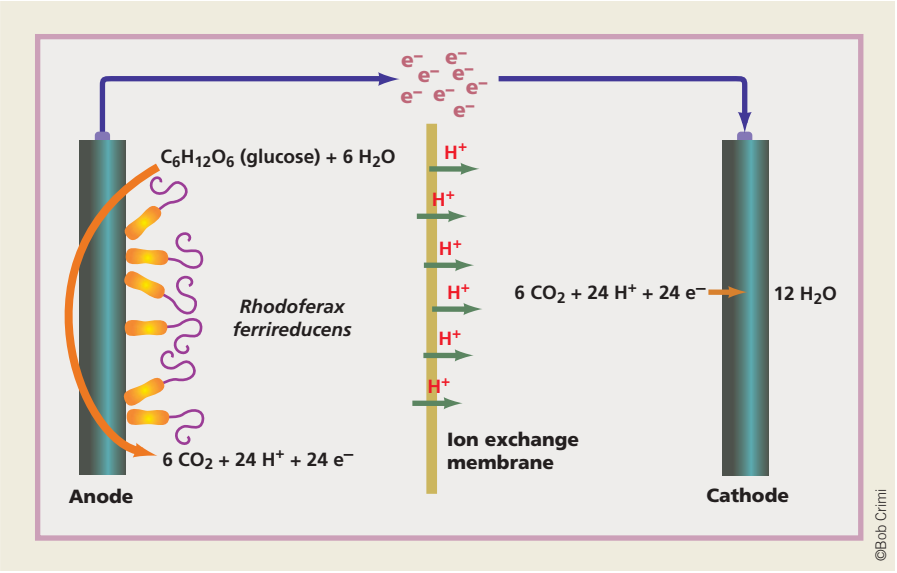

Figure 1 *Rhodoferax ferrireducens* microbial fuel cell. *R. ferrireducens* burns carbohydrates to CO_2 in the anodic compartment, a process that produces free electrons which are directly captured by the anode. From there, the electrons are channeled to the cathode, where they reduce oxygen to water. The transfer of electrons from the anode to the cathode results in the generation of an electrical current.

grow at a steady rate, which guarantees a steady supply of electrons and therefore a consistent current density.

Whereas microbial fuel cells have a long to go before they compete with more established physico-chemical electrical batteries, several factors provide added impetus to research into microbial electricity production. First, bacteria are omnipresent in the environment and are thus adapted to feeding on virtually all available carbon sources, which makes them into potential catalysts for electron flow generation in biofuel cells—extending the range of possible substrates for electricity generation from low molecular fuels (*e.g.*, hydrogen or methanol) used in conventional fuel cells to carbohydrates or more complex organic matter present in sewage, sludge[7] or even marine sediments[8]. A further argument relates to the increasing cost of precious metals. These constitute the catalytic core of conventional fuel cells, and thus one may envision that in the future biocatalysts like bacteria may become a serious cost-reducing alternative. Finally, it is worth noting that bacteria can be described as self-reproducing, self-renewing catalysts, and in an ideal case where a simple initial inoculation of a suitable strain could be cultured continuously in a fuel cell, long-term fuel cell operation could be initiated and maintained. This also represents the major advantage of microbial-based fuel cells over the closely related immobilized enzyme–based fuel cell systems in which catalysis happens on surface-immobilized enzymes of microbial origin. In these systems, the enzymatic activity diminishes quickly over time.

Taking advantage of using simple monosaccharides from waste or other detritus as substrates for electricity generation is an important achievement, which leaves one wondering about possible applications of this system. As an example, biotechnological hydrolysis of the di-, oligo-, and polysaccharides in molasses could be effectively coupled to a *R. ferrireducens*–driven fuel cell, thus creating a power plant virtually limitless with respect to fuel resources. It is very hard to guess now what the economy of such systems would be, but the development of efficient microbial fuel cells, such as the one described here, is the first step towards this goal.

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Breathing new life into insect-resistant plants

William J Moar

Expressing insecticidal proteins from sources other than *Bacillus thuringiensis* in crop plants should reduce the likelihood for development of insect resistance to toxins.

Development of pest resistance to insecticidal transgenic crops remains a major concern worldwide[1]. Although the use of *Bt* (*Bacillus thuringiensis*) cotton and corn in the United States alone constitutes 20–30% of all cotton and corn grown there (totaling over 20 million acres), almost all of these crops contain only one of two *Bt* proteins for Lepidoptera control (Cry1Ab for *Bt* corn and Cry1Ac for *Bt* cotton). As a result, development of insect resistance to toxins is a major concern, and scientists continue to search for additional genes to express along with either *Bt* gene described above (gene pyramiding), or alone in plant cultivars that can be planted either in a mosaic or sequential fashion with current *Bt* crops (**Fig. 1**). In this issue, Liu and coworkers report the successful expression of a non-*Bt* insecticidal protein in plants at high levels, conferring activity against two different orders of insects (Lepidoptera and Coleoptera)[2]. These results have the potential to help decrease the rate of insect resistance development to toxins expressed by commercially available insect-resistant transgenic plants, such as *Bt* cotton and corn. In addition, expressing one protein with activity against insects from two dif-

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