Improving plant genetic engineering by manipulating the host

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Agrobacterium-mediated transformation is a major technique for the genetic engineering of plants. However, there are many economically important crop and tree species that remain highly recalcitrant to Agrobacterium infection. Although attempts have been made to ‘improve’ transformation by altering the bacterium, future successes might come from manipulation of the plant. Recent studies that identified several plant genes involved in Agrobacterium-mediated transformation, and their over-expression in currently transformable species, suggest that this approach holds great promise for improving the transformation of recalcitrant, but agronomically important, crops.

The genetic transformation of plants by the Gram-negative soil bacterium Agrobacterium tumefaciens is the only known example of natural inter-kingdom genetic exchange. During the course of infection, Agrobacterium processes a region of DNA, the T-(transferred) DNA, from a resident Ti-(tumor inducing) plasmid and transfers T-DNA and several virulence (Vir) proteins to plant cells. These Vir proteins include VirD2 (an endonuclease that is involved in T-DNA processing and that is covalently attached to the 5′ end of the processed single-stranded T-strand), VirE2 (a sequence-independent single-stranded DNA binding protein that probably coats T-strands) and VirF. It has been proposed that VirD2, VirE2 and the T-strand form a complex, the T-complex, which is the probable molecular form that is transported through the plant cytoplasm into the nucleus [1]. The site of assembly of this complex (within the bacterium or within the plant cell) remains somewhat controversial (reviewed in [2]).

In nature, the result of this genetic transformation process is the generation of crown gall tumors on infected plant tissues. However, scientists can delete T-DNA-encoded oncogenes and replace them with genes of agronomic value that are subsequently transferred to and expressed within plant cells in a procedure known as Agrobacterium-mediated genetic transformation. This process is considered preferable to genetic transformation by artificial approaches (e.g., electroporation, microinjection, or ‘biolistic’ bombardment of cells with highly accelerated naked DNA molecules) because of the ease and low cost of the procedure and because of the relatively low complexity of intact transgenes integrated into the plant genome. Thus, Agrobacterium-mediated transformation has been used not only to generate a wide variety of transgenic plants [3] but also for the genetic transformation of fungi [4–6] and even human cells [7].

Although Agrobacterium-mediated transformation would appear to be the method of choice for plant genetic engineering, many economically important plant species, and elite cultivars of particular species, are highly recalcitrant to the method. In particular, the efficient genetic transformation of soybeans, cotton, cereal grains, many legumes and tree species of horticultural and industrial importance remains problematic. Scientists have attempted to increase the efficiency of plant transformation by identifying or manipulating more highly virulent Agrobacterium strains (e.g., [8]) or by improving plant culture conditions [9]. Although the use of ‘super-virulent’ strains and ‘super-binary vectors’ containing additional copies of various vir genes have increased the transformation of many plants, including cereals, limits might have been reached in these efforts [2]. An alternative approach to increasing plant transformation might lie in manipulation of the plant itself. To accomplish this, it is first necessary to identify plant genes and their respective encoded proteins that are involved in the transformation process. Several publications within the past two years suggest that this approach could be fruitful.

Plant genes involved in Agrobacterium-mediated transformation: histones and T-DNA integration

Several years ago my laboratory embarked on a series of experiments to identify plant genes involved in Agrobacterium-mediated transformation using a classical genetic approach. We developed a screening protocol [10] to identify mutants that were ‘resistant to Agrobacterium transformation’ (rat mutants) in a population of T-DNA-mutagenized Arabidopsis plants [11]. To date, we have screened >16 000 mutagenized plants and identified (using forward and reverse genetic methods) >100 rat mutants. Of particular interest is rat5, a mutant containing a T-DNA insertion in the 3′ untranslated region of the histone H2A-1 (HTA1) gene [12]. rat5 mutant plants could be transiently but not stably transformed by Agrobacterium, suggesting that the block to transformation resides at the T-DNA integration step (T-DNA molecules do not necessarily need to integrate into the plant genome to express transiently [13,14]). Over-expression of wild-type copies of the HTA1 gene in rat5 mutant plants could restore transformation proficiency. More importantly, over-expression of the HTA1 gene in wild-type Arabidopsis plants significantly increased

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susceptibility to Agrobacterium-mediated root transformation [12] and slightly increased the transformation frequency by the ‘flower dip’ method, initially suggesting that histone H2A expression, and hence T-DNA integration, might be limiting in the transformation of target cells (Fig. 1a). Yi et al. [15] recently demonstrated that Arabidopsis elongation zone root cells that express the HTA1 gene are most highly susceptible to Agrobacterium-mediated transformation. Alteration of the expression pattern of HTA1 in roots by wounding, phytohormone treatment or Agrobacterium infection changed the pattern of transformation susceptibility in a corresponding manner, suggesting that HTA1 expression might serve as a molecular ‘marker’ for predicting cells most prone to Agrobacterium infection.

Improving nuclear transport of the T-complex

Another approach has been used by Vitaly Citovsky’s laboratory to identify plant proteins involved in the Agrobacterium transformation process. Using a yeast two-hybrid interaction approach, Ballas and Citovsky [16] identified an importin-α (AtKapo) that interacted specifically with a nuclear localization signal (NLS) sequence within VirD2. Nuclear localization of the T-complex is an essential step in Agrobacterium-mediated transformation, and both VirD2 and VirE2 contain NLS sequences. Mutation of the VirD2 NLS impairs T-complex nuclear translocation and transformation to various extents [12,17,18]. However, Citovsky’s group was not able to show, using a yeast two-hybrid system, interaction of VirE2 with AtKapo [16,19]. Rather, they showed that VirE2 interacted with the Arabidopsis protein VIP1 [20]. VIP1 could mediate VirE2 nuclear translocation and tobacco plants expressing an anti-sense construction of the VIP1 gene were recalcitrant to subsequent Agrobacterium transformation [20].

Recently, Tzfira et al. [19] demonstrated that over-expression of VIP1 in transgenic tobacco plants could substantially increase the efficiency of Agrobacterium-mediated transformation (Fig. 1b). Not only were VIP1 transgenic plants more susceptible to stable transformation (as evidenced by an increase in efficiency in generating hygromycin-resistant shoots) but they were additionally more receptive to transient transformation (as evidenced by an increase in transient GUS activity expressed from a T-DNA-encoded gusA-intron gene). VIP1 transgenic plants also expressed processed mRNA from a T-DNA-encoded gusA-intron gene more quickly after infection than did wild-type plants (4 hr compared with 12 hr), suggesting more rapid and/or efficient T-strand nuclear targeting. Thus, over-expression of a gene involved in the nuclear targeting step of Agrobacterium-mediated transformation, as well as genes such as HTA1 involved in the T-DNA integration process, can potentially increase the transformation efficiency of plants.

Future prospects

Various steps in the Agrobacterium-mediated transformation of plant cells are indicated in Figure 2. Events occurring within the bacterium, including signal perception, vir gene induction, T-strand processing, and T-DNA/Vir protein transport, are reasonably well understood, although the formation and functioning of the Type IV secretion apparatus necessary for T-DNA and Vir protein export remain an active area of research. We currently understand considerably less about events that take place on or within the plant cell, including bacterial attachment, T-DNA and Vir protein transfer, cytoplasmic trafficking, nuclear targeting, and T-DNA integration. Each of these steps might be considered a target for
manipulation. Considering the recent successes in overexpression of several plant genes involved in transformation, what can we expect in the future? Genetic and protein interaction approaches mentioned above, combined with genomic methods (Veena, H. Jiang, R.W. Doerge, and S.B. Gelvin, unpublished observations), have identified >100 Arabidopsis genes involved in Agrobacterium-mediated transformation. These genes encode proteins involved in bacterial attachment (an arabinogalactan protein), T-DNA transfer (a xylan synthase), nuclear targeting (importins and actins, perhaps indicating the use of the actin cytoskeleton as a ‘track’; P. Rao and S.B. Gelvin, unpublished observations), and T-DNA integration (histones and chromatin modifying proteins). It seems likely that some of these genes could serve as targets for genetic manipulation to increase transformation. However, there are probably many surprises in store for us. For example, although mutation of the histone H2A-1 gene HTA1 results in decreased T-DNA integration, over-expression of HTA1 might affect transformation by another mechanism. Recent results from my laboratory indicate that over-expression of HTA1 in many different rat mutant lines can restore transformation-susceptibility to these otherwise highly recalcitrant mutants (L.-Y. Lee, S. Davis, X. Sui, and S.B. Gelvin; unpublished observations). Many of these mutations are in genes not known to be involved in T-DNA integration. Thus, HTA1 over-expression could generally ‘sensitize’ plant cells to Agrobacterium-mediated transformation in an as yet unknown way. Detailed investigation of plant gene function and expression patterns in the future will probably lead to novel methods for improving the genetic engineering of plant cells.

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Molecular computing revisited: a Moore’s Law?

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Moore’s Law states that the processing power of microchips doubles every one to two years. This observation might apply to the nascent field of molecular computing, in which biomolecules carry out logical operations. Incorporation of new technologies that improve sensitivity and throughput has increased the complexity of problems that can be addressed. It is an ultimate goal for molecular computers to use the full potential of massive parallelism.

In 1994, Leonard Adleman performed the first successful experiment that solved a mathematical problem using DNA [1]. In doing so, he provided a concrete demonstration of what many biologists had long believed: that the components that encode the building blocks of life are, at their core, a complex computer that can process information in many different ways. Since then, the field of ‘molecular computing’ including DNA, RNA and other information-bearing biopolymers, has been the subject of numerous scientific articles, books, international conferences and even a posthumously published novel by Robert Ludlum [2]. Two factors drive progress in molecular computing: the use of the inherent massive parallelism of nucleic acid interactions to perform many computations simultaneously and the incorporation of new technologies into nascent ‘computers’ to improve automation and sensitivity. Here, we examine the nature of this parallelism and the technologies that have been applied to molecular computing (see Box 1).

Representative molecular computing problems

Important considerations in molecular computation include the methods of encoding information, generating potential solutions and selecting and identifying correct solutions. As a framework, we discuss two NP-complete problems that have been approached by researchers, Hamiltonian path (HP) and Satisfiability (SAT).

Adleman’s original problem was an instance of HP, which asks: ‘Given a set of cities, a starting point, an ending point, and the (one-way) routes connecting them, is it possible to visit every city exactly once?’ One algorithm generates all potential solutions and selecting and identifying correct cities. He generated all potential solutions by intermediates. Adleman’s approach[1] (reviewed in[5]) was to encode the cities as unique 20-nucleotide (nt) sequences of single-stranded DNA and the paths between them as 20-nt sequences complementary to half the sequence of each of the cities they connect. He generated all potential solutions by combining the sequences representing cities and routes in a test tube and isolated the unique correct solution using a three-step process. First, routes that begin and end in the correct cities were selected by PCR with specific primers. Next, routes of the correct length, 140 base pairs, were gel-isolated. Finally, he sequentially purified those molecules that hybridized with each of the five intervening ‘cities’. Including verification, the process took approximately one week of bench time.

The most difficult problem solved on a molecular computer to date [6] is a 20-variable, 24-clause instance

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