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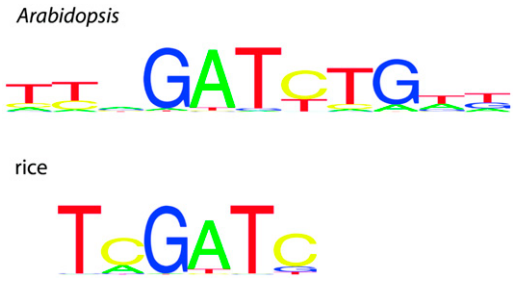
IN BRIEF

The IMEter Predicts an Intron's Ability to Boost Gene Expression

Most eukaryotic genes are interrupted by one or more introns that are transcribed and then removed by splicing before the mRNA exits the nucleus. Some intron-containing genes have much higher expression levels than intronless versions of the same gene (reviewed in Le Hir et al., 2003). The first intron of the *shrunken-1* gene from maize produced a 91-fold increase in expression of a reporter gene construct (Vasil et al., 1989). Enhancing introns must fall within 1 kb of the transcription start site to have a positive effect on mRNA accumulation (Rose, 2004). However, the mechanism underlying intron-mediated enhancement (IME) in plants is largely unknown.

Rose et al. (pages 543–551) adopted a bioinformatics approach to identify introns that stimulate gene expression in *Arabidopsis* and rice. The authors reason that introns near the start of transcription would be enriched in IME signals and that distal introns, which do not seem to affect gene expression, would be depleted in IME signals. They designed a word-based discriminator, the IMEter (http://korflab.ucdavis.edu/cgi-bin/web-imeter.pl), that assigns a positive score to input sequences that are similar to proximal introns and a negative score to sequences that resemble distal introns. After training the IMEter on more than 40,000 introns from *Arabidopsis*, they found that the calculated IMEter scores strongly correlate with the enhancing ability of experimentally tested introns. Thus, the degree to which an individual intron matches the proximal intron profile strongly predicts its ability to augment gene expression. Analysis of the top-scoring introns revealed a motif (see figure) that is dispersed throughout enhancing introns but is scarce in nonenhancing introns. By inserting a series of hybrid introns into a reporter gene construct, the authors further demonstrate that the sequences responsible for elevating gene expression are distributed throughout the enhancing intron.

To determine if IME signals are conserved across plant species, the researchers trained the IMEter on more than 30,000 introns from rice and again tested its ability to detect expression-enhancing introns in *Arabidopsis*. Once more, the calculated IMEter scores were in good agreement with the observed expression-enhancing abilities of the introns. This suggests that the signals responsible for IME are conserved between *Arabidopsis* and rice. The rice-trained IMEter also predicted enhancing introns from maize and rice, and further analysis identified an IME signal in rice that is similar to the enhancing motif of *Arabidiopsis* (see figure). Because addition of an intron from the host species can often enhance transgene expression, the authors suggest that the IMEter may be a useful tool for optimizing expression in transgenic plants.



Sequence motifs that may be responsible for IME in *Arabidopsis* and rice.

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