Strain Improvement in Biocontrol Fungi
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INTRODUCTION

Antagonistic and hyperparasitic fungi could be our useful allies in integrated pest management technologies allowing us to reduce the amount of pesticides released into the environment. Ampelomyces quisqualis, Coniothyrium minitans, Peniophora gigantea, Pythium oligandrum, as well as several species of Gliocladium and Trichoderma are the most potent biocontrol agents efficient against either leaf or soil inhabiting plant pathogens. The antagonistic activity of these fungi is attributed to various mechanisms including antibiosis, parasitism, competition and induced resistance (Goldman et al., 1994). There are many examples of the successful experimental use of hyperparasitic fungi, their application on a commercial scale is, however, limited to a few cases.

IMPROVEMENT OF BIOCONTROL EFFICACY BY USING BIOTECHNOLOGICAL METHODS

Species of the genus Trichoderma are by far the most intensely studied organisms in this field of research. These fungi produce extracellular cell-wall degrading enzymes, including chitinases, cellulases, β-1,3-glucanases and proteases. The mycolytic activity of these enzymes has long been recognized as a major factor in the hyperparasitic mechanism exerted by Trichoderma (Elad et al., 1982).

Different strategies have been tried to increase the chitinase activity of one of the most potent biocontrol species, T. harzianum. Haran et al. (1993) introduced the chitinase gene of Serratia marcescens into the genome of T. harzianum under the control of the
constitutive 35S promoter and obtained two transformants which expressed higher levels of chitinase activity in the presence of glucose. However, when these transformants were grown on chitin, the transgenic strains expressed lower chitinase activity than the parental wild-type strain. The authors explained this phenomenon by cleavage of the heterologous enzyme by host proteases and the interference of the resulting protein fragments with host chitinases during the secretory process. Margolles-Clark et al. (1996) used a transformation construct that contained the coding region of the 42 kDa endochitinase gene (ThEn-42) of T. harzianum under the control of the cellulase promoter, cbhl from Trichoderma reesei and could achieve a ten-fold increase of the chitinase activity in most of the 20 transformants tested. This was an elegant approach to the chitinase overproduction under in vitro conditions, but the behavior of these transformants under natural conditions is difficult to predict, as their increased chitinase production was elicited by cellulase-inducing components (owing to the cbhl promoter) and no specific induction occurred in the presence of chitin, the real substrate of the overproduced enzyme.

In our laboratory, another evolutionary variant of the 42 kDa endochitinase encoding genes, named Tam-ch was cloned by screening the genomic library of Trichoderma hamatum, strain Tam-61 with a PCR-amplified chitinase sequence from the same fungus (Giczey et al., 1998). A 3.5 kb genomic DNA fragment containing the coding region, as well as the 5' and 3' regulatory sequences was reintroduced into the host strain by PEG-mediated homologous transformation under selection pressure provided by hygromycin B. The integration and the stability of the transforming construct was demonstrated by Southern blotting in 10 transformants. The integration of the transforming vector was stable only in one copy and occurred through homologous recombination in 9 of 10 transformants, while random integration was detected in one transformant. All but one transformant expressed higher levels of chitinase activity in comparison to the wild type recipient strain; the maximum level of increase rose 5-fold. Duplicating the copy number of the entire endochitinase gene under its own regulatory sequences is especially suitable for improving the biocontrol capability of Trichoderma as the highly conserved 42-kDa endochitinase-encoding gene, present in all mycophagous species of Trichoderma (Fekete et al., 1996) has been shown to be specifically triggered in mycoparasitic interactions (Carsolio et al., 1994). Triggering occurs when a specific “mycoparasitic” protein complex binds to the promoter sequences of the gene and displaces the binding of a catabolite repressor protein (Lorito et al., 1996). The transformation strategy we used was thus based on the molecular regulation of the Trichoderma endochitinase gene and RNA-blot analysis confirmed the rationality of this decision: when fungal cell wall preparation was added as a sole carbon source, significantly higher levels of Tam-ch mRNA were detected in all the transformants compared to the wild-type recipient. Another advantage of the 42-kDa endochitinase gene is that its overexpression causes no adverse effects on the transformants as described for the first time by Margolles-Clark et al. (1996) in T. harzianum. The disadvantage of our method is, however, that a bacterial antibiotic resistance gene was introduced into the transformants, precluding thus their outdoor testing.

Genes encoding lytic enzymes others than chitinases has also been used for the genetic improvement of Trichoderma strains. Co-transformation of T. longibrachiatum with the hygromycin resistance gene and the egll gene, encoding β-(1,4)-endoglucanase resulted in a significant increase of the extracellular endoglucanase activity (Sánchez-Torres et al. 1994). In a more recent study (Migheli et al., 1998) these transformants were found to show enhanced biocontrol activity against Pythium ultimum on cucumber. The biocontrol ability of T. harzianum has successfully been improved by increasing the copy number of a basic proteinase gene (Flores et al. 1997); in greenhouse tests...
these transformants proved to be superior in reducing Rhizoctonia infection of cotton.

Should we encourage research to uncover the secondary metabolite profiles of lesser known biocontrol fungus species?

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REFERENCES


