Table 2
Influence of carbon and nitrogen sources on GUS expression during co-cultivation of TR22-2 with *F. oxysporum*
Influence was determined on Cove agar containing different carbon and nitrogen sources as indicated. GUS activity was estimated within the TR22-2 mycelium (symbols: +++: strong expression; ++: clear expression) and at the border between TR22-2 and *F. oxysporum* (symbols: +++: strong enhancement; ++: clear enhancement; +: weak enhancement; ∅: no influence)

Medium composition	GUS activity within the colony	GUS activity at the border
1% glucose 1% nitrate	++	∅
1% glucose 0.1% peptone 2% malt extract	++	∅
1% galactose 0.1% peptone 2% malt extract	++	∅
1% lactose 0.1% peptone 2% malt extract	+++	∅
1% glucose 1% peptone 2% malt extract	++	+++
1% galactose 1% peptone 2% malt extract	++	+
1% lactose 1% peptone 2% malt extract	+++	++

on low peptone content (0.1%) and growth on nitrate resulted in a neutral interaction, indicating that high peptone concentrations enhance the inductive influence of *F. oxysporum*.

An *afp::uidA* fusion gene was used to examine the influence of various pro- and eukaryotes on *afp* expression at the level of transcription. Remarkably, transcription is not exclusively affected by some filamentous ascomycetes but also by bacteria or yeast. Interactions range from neutral to strongly inductive or strongly suppressive. However, it is difficult to determine the compounds, which stimulate or inhibit *afp* expression. The observed influence of bacteria and yeast on *afp* expression poses the question whether these effects can be explained by a specific induction or repression signal of the co-cultivant. From the ecological point of view, it does not make sense for *A. giganteus* to secrete more AFP when competing with bacteria or yeast for nutrients, as AFP does not inhibit the growth of these microorganisms (LACADENA *et al.* 1995). As it was shown that *afp* transcription is subject to sophisticated control by environmental conditions, e.g. nutritional factors, ambient pH, and different stress conditions (MEYER *et al.* 2002, MEYER and STAHL 2002), it seems more likely that dual cultures with bacteria and yeast cause unspecific responses of *afp* transcription. For example, the pH of the mutual medium might be changed by the co-cultivant or nutrient limitation and different types of stress, provoked by the co-cultivant result in signals, which enhance or repress *afp* transcription.

Co-cultivation with filamentous fungi, however, can result in specific fungal-fungal interactions. This might be the case for *F. oxysporum*, which is highly sensitive to AFP (THEIS, WEDDE, MEYER, STAHL, unpublished) and triggers *afp* transcription. This induction was not observed when the culture supernatant of *F. oxysporum* was used or when the mycelium of *F. oxysporum* was autoclaved prior to incubation with *A. giganteus*. These results suggest that the influence of *F. oxysporum* on *afp* expression is dependent on cell-to-cell contacts of vital cells. If *A. giganteus* senses the presence of *F. oxysporum* and AFP expression is induced it gains a growth advantage.

Notably, the influence of *F. oxysporum* on *afp* expression is dependent on the medium composition. An increase in peptone concentration (0.1% to 1%) was found to strengthen the inductive influence of *F. oxysporum* on *afp* expression. DA SILVA *et al.* (2001) reported that the metabolism of *F. oxysporum* is mainly regulated by the level of structural complexity of the nitrogen source. Biomass production and secretion of hydrolytic enzymes is very high in media containing peptone. Therefore, it can be speculated that only in the presence of high peptone concentrations, *F. oxysporum* produces a so far unknown signal, which can be sensed by *A. giganteus*. This signal has to be transmitted to the nucleus to activate *afp* transcription by factors binding to regulatory sequences within the promoter. The *afp* promoter shows three stretches of 10, 11 and 13 nucleotides in length (ATGATTACCA, TTTTGGAGAGA, GGAGATCATTTCC) which are identical to the promoter of the *paf* gene encoding the related antifungal protein (PAF) in *P. chrysogenum* (MARX *et al.* 1995). These stretches might be a potential target for such activation. Thus, it would be interesting to test whether these sequences are involved in induction of *afp* transcription in further experiments.

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