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An acidic pH is a determinant factor for *TRI* genes expression and trichothecenes B biosynthesis in *Fusarium graminearum*

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Abstract

Reducing production of type B trichothecenes by *Fusarium graminearum* on cereals is necessary to avoid contamination leading to yield reduction and harmful impacts on human and animal health. Understanding how trichothecenes biosynthesis is induced is essential. The effect of ambient pH on fungal growth, toxin biosynthesis and TRI genes expression was studied during in vitro liquid culture of F. graminearum on minimal medium. Fungal development stopped at day 3 after a sharp pH drop in the medium. At the same time, induction of TRI genes expression was observed and toxin started to accumulate one day later. Acidification seems a determinant factor for induction, as neither the toxin nor the TRI genes were detected when the pH was maintained neutral. Shifting from neutral to acidic pH by mycelium transfer induced TRI genes expression and toxin accumulation. The regulation of toxin production by the ambient pH seemed to be specific to some TRI genes since TRI5, located in the core FgTRI5 cluster, showed an immediate induction while TR1101, located elsewhere in the genome, showed a more progressive response. The regulation of trichothecene biosynthesis by the ambient pH seems to be a general mechanism, independent from strains or chemotype as all tested strains, including F. graminearum and F. *culmorum* species, showed a regulation of toxin production in response to the ambient pH. We conclude that *in vitro*, external acidification is required for induction of *TRI* genes expression.

Keywords: Fusarium, trichothecenes, TRI genes, pH.

Introduction

Fusarium graminearum (Teleomorph: Gibberella zeae Shwabe) is one of the causal agents of Fusarium diseases which infect many crop plants (Goswami and Kistler, 2004). Fusarium Head Blight and Fusarium Ear Rot, the most common Fusarium diseases on wheat and maize respectively cause yield losses and reduction in grain quality due to the accumulation of trichothecenes mycotoxins (Bhatnagar et al., 2002, Bennett and Klich, 2003). F. graminearum produces type B trichothecenes (TCT B) including deoxynivalenol (DON), nivalenol (NIV), and their acetylated derivates (3ADON, 15ADON, 4ANIV) (Xu and Berrie, 2005). The trichothecene biosynthesis pathway was established and nearly all TRI genes that are implicated have been described in Fusarium sporotrichioides and F. graminearum (Desjardins et al., 1993, Lee et al., 2002, Kimura et al., 2003, Kimura et al., 2007). Most of them localize in one genomic locus which is now referred as the "FgTRI5 cluster" (Hohn et al., 1993, Brown et al., 2004). Among the clustered genes, TRI5 encodes the trichodiene synthase responsible for the first step in the pathway (Hohn and Beremand, 1989), TRI4 encodes a multifunctional oxygenase which catalyses all the steps leading from trichodiene to isotrichotriol (Hohn et al., 1995, Tokai et al., 2007), TRI6 gene encodes a Zinc finger transcription factor, it was found to be a positif regulator of other TRI genes (Proctor et al., 1995), TRI6 itself is regulated by another regulatory protein encoded by TRI10 (Tag et al., 2001). Two other TRI genes have been found in a two-gene minicluster, the TRI1 cluster (Brown et al., 2003, McCormick et al., 2004) and another gene TRI101 encoding a 3-Oacetyltransferase which catalyses the acetylation of trichothecenes resides outside the TRI gene clusters. Although this gene encodes an enzyme essential in the progression of the biosynthetic steps it has been described to have a key role in self-protection (Kimura et al., 1998).

Since the publication of the regulatory role of TRI6 and TRI10, quite little is known about the induction of trichothecene production. A recent report showed that TRI6 and TRI10 controlled many fungal genes expression *in planta* (Seong et al., 2009). Thus, significant progress has to be made towards understanding the essential steps in the regulation of *TRI* genes induction. Some reports described a profound effects on trichothecenes production *in vitro* of carbon and nitrogen sources (Miller and Greenhalgh, 1985, Jiao et al., 2008) or fungicides (Covarelli et al., 2004). It

was also shown that magnesium (Pinson-Gadais et al., 2008), hydrogen peroxide (Ponts et al., 2007), temperature (Schmidt-Heydt et al., 2008) and ferulic acids (Boutigny et al., 2009) modulated *TRI* genes expression and trichothences production by *F. graminearum* in liquid cultures. Very recently, it has been reported that a low extracellular pH is determinant for toxin production in *F. graminearum* (Gardiner et al., 2009). It has been demonstrated that the production of aflatoxin, sterigmatocystin in *Aspergillus spp*. (Keller et al., 1997), fumonisin in *Fusarium verticillioides* (Flaherty et al., 2003) and a large spectrum of secondary metabolites including some antibiotics and mycotoxins are influenced by the ambient pH.

Filamentous fungi and yeasts are capable of growing over a wide range of pH due to an efficient pH homeostatic mechanism which tailors the gene expression to the environmental pH (Penalva et al., 2008). This pH regulatory system, well described in *Aspergillus nidulans*, involves six known components encoded by *palA*, *palB*, *palC*, *palF*, *palI* (Arst and Penalva, 2003) that mediates the proteolytic activation of the zinc finger transcription factor PacC in response to the alkaline ambient pH (Diez et al., 2002), which induces the alkaline-expressed genes and represses the acidic-expressed genes (Tilburn et al., 1995). More recent studies report that the pathways responsible for many secondary metabolites biosynthesis are controlled by PacC factor in various fungi suggesting an essential role for this transcriptional regulator (Espeso and Penalva, 1996, Keller et al., 1997, Flaherty et al., 2003).

In this study we analyzed pH variation during development of *F. graminearum in vitro* and the kinetic of toxin production using the minimal synthetic medium (MS) described by Boutigny et al. (Boutigny et al., 2009). Effect of pH on toxin induction was analyzed for four different *Fusarium* strains. In order to investigate the role of the ambient pH in the regulation of trichothecenes biosynthesis, we analyzed the expression of four *FgTRI5* cluster genes *TRI5*, *TRI4*, *TRI6*, *TRI10* and *TRI101* non cluster gene in addition to the probable pH response transcription factor *PAC1*, in different pH conditions. The results suggest a determinant role of acidic growth conditions on "*FgTRI5* cluster" genes expression.

Materials and methods

Strain, spores preparation, culture media and culture conditions

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The *F. graminearum* strain CBS185.32 (Centraalbureau voor Schimmelcultures, The Netherlands) was used throughout this work. It is a producer of DON and its acetylated form 15ADON. In our culture conditions, the 15ADON form was predominantly produced.. Potato Dextrose Agar (PDA) medium was used for propagating the fungus. For spores suspension preparation, fungal strains were grown in the CMC sporulation liquid medium (Cappelini ans Peterson, 1965) at 25°C and 150 rpm into darkness for 3 days, then filtered through mira-cloth (100 μ m). The filtrate was used as a spore suspension to inoculate the media during this study.

All liquid-culture experiments were performed in Petri plates (Ø 55mm) containing 8 ml of the appropriate culture medium inoculated with the appropriate spore suspension to reach a final concentration of 10⁴ spores/ml. The culture media used in this study were: a minimal low buffered Mycotoxins Synthetic medium (MS medium) containing KH₂PO₄ 0.5 g l⁻¹, K₂HPO₄ 0.6 g l⁻¹, MgSO₄ 0.017 g l⁻¹, (NH₄)₂SO₄ 1 g l⁻¹, glucose 20 g l⁻¹ and 0.1 ml l⁻¹ Vogel's trace elements stock solution (Vogel, 1956). This medium was already used in previous works (Boutigny et al., 2009). Its initial pH is 6.5 and quickly decreases during growth of the fungus. To obtain the buffered media, exactly the same components than the MS medium were used and buffered with a mixture of 50 mM of 3-(N-morpholino) propanesulfonic acid (MOPS) and 55 mM of 2-(N-morpholino) ethanesulfonic acid (MES) to obtain the BMS6.5 medium (MS buffered to pH6.5) or with citric acid 40 mM and Na₂HPO₄ 20 mM to obtain the BMS3 (MS buffered to pH3). Incubation was performed at 25°C in darkness conditions without shaking. For transfer experiments, the mycelia were incubated for 3 days in the BMS6.5 medium, then collected, washed with BMS3 medium and transferred to Petri dishes containing BMS3 medium. The cultures were collected by centrifugation in sterile conditions; the liquid medium was stored at -20°C until extraction of the toxin and the mycelium was used to perform total RNA extraction or lyophilized for fungal biomass quantification either directly or after storage at -80°C. All cultures were done in triplicate.

Toxin analyses and pH measurements

Ethyl acetate extractions of liquid culture samples were performed as previously described (Boutigny et al. 2009). Quantification was done by comparing the samples to the standard solutions of DON and 15ADON prepared from commercial pure powder samples (Sigma-Aldrich Co.) using HPLC as previously described (Bily et al., 2004). The pH of the cultures was measured

directly from the supernatants using "InoLab pH 720" pH meter following the manufacturer's instructions (WTW GmbH, Weilheim, Germany).

Total RNA extraction and cDNA preparation

To perform total RNA extraction, 100 mg of mycelium was ground for 1 min in 1 mL of TRIzol® reagent (Invitrogen) with the TissueLyser System® (Qiagen). Total RNA was extracted according to the manufacturer's instructions. The quality of the RNA preparation was verified by agarose gel electrophoresis and the RNA concentration was measured using a nanodrop® ND 1000 spectrophotometer (Labtech International LTD[®]). The reverse transcription reactions were performed on 5 μ g of total RNA using the SuperScriptTM II First-Strand Synthesis System for RT-PCR (Invitrogen), the thermal cycling conditions were programmed using an iCyclerTM (Bio-Rad) following the manufacturer's instructions (Invitrogen).

Expression analysis by real-time PCR

Abundances of the transcripts of TRI5, TRI4, TRI6, TRI10, TRI101 and PAC1 were evaluated using a LightCycler® LC2.0 system and the LightCycler® Software 3.5.3 (Roche), with 1 µL of diluted cDNA in a 10 µL PCR reaction, using the QuantiTectTM SYBR® Green PCR Kit (Qiagen) according to the manufacturer's instructions. Expression of GAPDH (Glyceraldehyde phosphate dehydrogenase) was used as endogenous control. PCR reactions were carried out at 94°C for 15 min, followed by 50 cycles of 94°C for 10 s, 15 s at appropriate hybridization temperature for each primer pairs (Table 1), and 72°C for 25 s. Results were obtained from three replicate assays. Primer pairs for amplifying the TRI genes have been previously described (Boutigny et al., 2009) and are listed in table 1. The GAPDH primer pair was designed based on the sequence of F. graminearum PH-1 strain GAPDH (Table 1). Primers for PAC1 were designed using the sequence of the probable pН response transcription factor *pacC* FGSG 12970.3 (www.broadinstitute.org/annotation/genome/fusarium_graminearum/). The absence of nonspecific PCR amplification was checked by running melting curve and agarose gel analyses of the final PCR product.

PCR efficiencies (*E*) were determined as previously described (Ponts et al., 2007) using a standard curve generated from five log dilutions of a standard cDNA mixture prepared by mixing a fraction of each cDNA samples.

Real-time PCR data analysis

In order to verify the stability of *GAPDH* expression throughout the culture time course, we proceeded to the comparison of the crossing point values (*Cp*). The *Cp* values experimentally measured for the target *TRI* genes were compared in the different pH conditions of culture and normalized to the *Cp* values obtained for the reference gene *GAPDH*. Then, the expression levels of the target genes, normalized by the reference gene expression were compared at different pH values using the REST® software (Relative expression Software Tool) (Pfaffl, 2001, 2002). Expression of the target genes in the neutral pH medium BMS6.5 has been always chosen as control condition and the results were given as values relative to the control in each experiment.

Results

Pattern of fungal development, toxin production and pH variation in MS medium

The main objective of this experiment was to determine the pattern of pH evolution and the kinetic of type B trichothecenes accumulation during the development of *F. graminearum*. Cultures were performed in liquid conditions without shaking in MS medium which is a low buffered poor minimal medium specifically adapted for B trichothecenes production by *Fusarium* (Boutigny et al. 2009). During the culture the *F. graminearum* CBS 185.32 strain, the growth begins to be visually detectable two days after inoculation (Figure 1). The full development stopped at day 3 with a dried mycelium mass weighting around 45 mg per 8 ml of culture medium. The production of trichothecenes starts to be detected at day 3 of culture, increases rapidly the two following days and the toxin continues to accumulate until day 16. Only the sum of DON and 15ADON is reported as the two forms followed the same pattern of toxin production. pH measurement, performed throughout the culture, shows a prompt acidification two days after inoculation. The initial pH of the medium is 6.5 at inoculation and drops to 3 after only 3 days of culture. This acidification coincides with the initiation of trichothecene B production.

Effect of pH change on fungal development and TCT B production

In order to study in details the effect of pH variation on toxin production and fungal development, culture were carried out in three pH conditions: First, a culture in the MS medium as above serves as the control. Secondly, a culture in the BMS6.5 "neutral" medium in which buffering capacity was increased in order to maintain the pH to 6.5. For the third condition, the fungal development was achieved for three days in the BMS6.5 medium and the mycelia were transferred to the BMS3 medium buffered to maintain pH3. The pattern of the pH variation in different culture media was followed. In the control in MS medium, natural acidification occurred during the growth of mycelium leading quickly to pH 3. As expected, in the BMS6.5 medium, the pH was maintained close to neutrality throughout the 7 days of culture. The BMS3 medium buffered at pH 3 maintained this very acidic pH starting with the transfer of mycelium and throughout the duration of the culture. In the buffered media, the pH maintained a value in the expected range (initial pH \pm 0.2 pH units) which confirms the reliability of the buffers used during this study.

The dry fungal biomass was determined (Figure 2A). The overall development of the mycelium in the three conditions was maximal at day 3 of culture. In the MS medium, where the acidification occurred naturally during the fungal development, the biomass accumulation is lower than in the BMS6.5 in which the natural acidification is prevented by the buffer. In the third culture condition, where the mycelium accumulated until 3 days at pH 6.5 and was then transferred to medium buffered at pH 3, the biomass did not increase after the transfer.

The type B trichothecenes accumulating in the culture medium were quantified by HPLC-DAD (Figure 2B). In the MS medium, the toxin production starts to be detectable at day 4 and accumulates the following days. In the BMS6.5 medium, no toxin at all is detected throughout the culture course. However, in the third culture condition (transfer to the acidic condition), the toxin production is induced but it begins to be detectable only at day 5 and significantly increase at day 7.

TRI genes expression is induced by acidic pH

In order to investigate whether or not the regulation of toxin biosynthesis by the ambient pH is due to a molecular regulation of the "FgTRI5" cluster, expression of TR15, TR14, TR16, TR110, TR1101 and PAC1 genes was analyzed by Q-RT-PCR. Using the three pH conditions detailed

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above, the expression levels were compared at day five. As *GAPDH* gene maintains a relatively stable expression during the culture and in the different conditions, it level of expression served as control and was used to normalize *TRI* genes expression (Figure 3). *TRI5* and *TRI4* encoding the enzymes implicated in the first steps of the biosynthetic pathway are highly expressed in the acidic media (MS and BMS3 media) compared to "neutral" medium (BMS6.5) in which their expression is residual. The expression of *TRI6* and *TRI10*, encoding the regulators of the other *TRI* genes, are also induced and their level of expression in the "acidic" media can be largely sufficient to explain the strong activation of *TRI5* and *TRI4*. The *TRI101* gene is interesting because it encodes an enzyme involved in an intermediate step of the biosynthesis pathway but it is located outside the "*FgTRI5* cluster" (Kimura et al. 2007). As other *TRI* genes, this gene also shows an activation of expression. However, its differential of expression between acidic and neutral pH seems less important than what is observed for the genes located in the "*FgTRI5* cluster". In contrary to *TRI* genes, the quantification of *PAC1* expression shows that as expected, this gene is highly expressed under neutral pH, and the acidification clearly represses its expression.

TRI5 and TRI101 respond differentially to the pH variation

The expression kinetic of *TR15* and *TR1101* was compared from the third day to the seventh day of culture. Histograms (Figure 4) show their relative expression in the "acidic" media compared to their expression in the "neutral" medium (BMS6.5). Expression of *PAC1* was also investigated. In both media where acidification occurred either naturally or by transfer of the culture, expression of *PAC1* gene was repressed immediately in response to acidification. This repression is maintained at any time of the culture (Figure 4A,B). Similarly, *TR15* expression showed an immediate response to the acidification. At day 3, *TR15* was highly expressed in the MS medium in which the pH already dropped to 3 at that time (Figure 4A); its expression conserved the same level in the following days. In opposite, the *TR1101* gene responded more progressively to the pH variation and still increased at the seventh day of culture. Similarly, when the mycelium was transferred from neutral to acidic pH (BMS6.5 \rightarrow BMS3) at day 3, *TR15* showed an immediate response to the response to the acidic pH (BMS6.5 \rightarrow BMS3) at day 4 with progressive increase the following days (Figure 4B). This suggests that the two *TR1* genes respond differentially to the induction by acidic pH.

Trichothecene B induction by acidic pH is common to different Fusarium strains and species

In order to verify whether the effect of pH change observed here is not a particularity of the *F*. *graminearum* CBS 185.32 strain chosen for this study, the effect of pH variation on other strains of *Fusarium* was analyzed. Strains of different chemotype (i.e. producing different type B trichothecene) were selected in our laboratory collection. The same three culture conditions as used above were applied to four *Fusarium* strains either from the *graminearum* or the *culmorum* species. Toxin measurements at day 7 showed results very similar to the one observed for *F*. *graminearum* CBS185.32 strain since all the four tested strains produced high amount of trichothecenes under acidic but never produced any toxin under the neutral pH growth conditions (Figure 5 in supplementary section).

Discussion

The minimal synthetic medium used during this study is low buffered, thus the observed acidification is suspected to be the result of ammonium consumption during fungal development (Jernejc and Legisa, 2001). The shutdown in the fungal development, concomitant with the acidification, can be explained by the stressing conditions due to the extreme pH although the exhaustion of one of the nutriment sources (ammonium or glucose) cannot be excluded. Control cultures in GYEP medium which contains low ammonium concentration also showed an acidification during fungal development. However, the extent of the pH drop was always greater in the MS medium where the level of toxin production was largely higher (data not shown). This may suggest that the strong acidification promotes the high level of toxin production, although, the fungal development is optimal only under neutral pH. Also, the results presented here clearly demonstrate that preventing acidification by maintaining a neutral pH in the medium prevents the induction of toxin biosynthesis. An artificial acidification conducted by transferring the mycelium from neutral (BMS6.5) to acidic pH (BMS3), leads finally to accumulation of the toxin, suggesting that low pH is necessary for the induction of trichothecenes biosynthesis *in vitro*.

Our results showed that the expression of *TR15* gene seems to be directly induced by acidic pH meanwhile *TR1101* expression seems to be more related to the level of trichothecene accumulation.

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This is coherent with the fact that TRI101 gene is not located in the "*FgTRI5* cluster" and with the role of self-protection assigned to the TRI101 gene product (Kimura et al. 1998) whose expression could be related to the quantity of toxin produced and suggests a feedback regulation. However TRI101 expression has recently been shown to strongly depend of TRI6 gene expression in *F. graminearum* and was not increased by trichodiene supplementation in a TRI5 deletion mutant (Seong et al. 2009). Thus, TRI5 and TRI101 expression levels are regulated differently one another while both are under TRI6 control (Peplow et al. 2003). This observation may indicate that TRI6 and TRI10 are not the only factors that control the TRI genes expression. Our results suggest that the mechanism of regulation by the ambient pH mediating the regulation of TCT B production acts through the strong modulation of various TRI genes expression, especially those located in the core "*FgTRI5* cluster".

Taken together, the data presented here are in agreement with the recently published study (Gardiner *et al.* 2009) where it has been showed that the highest level of *TRI5* expression and DON accumulation is reached under pH 3 and it reduces drastically as far as the pH progress to neutrality. Although the induction of *TRI5* in response to low pH was previously reported (Gardiner *et al.* 2009), this study elucidate for the first time, the differential pattern of *TRI* genes expression in response to the ambient pH. Also, it brings forward that the regulation of trichothecenes B production by the ambient pH is a general mechanism in *Fusarium species* producing trichothecenes, independently from strains and toxin chemotype.

Acidification seems to be mandatory for toxin production and *TRI* genes expression *in vitro* in *F*. *graminearum*. This main conclusion supports the hypothesis that trichothecene biosynthesis could be negatively regulated by the general pH regulatory system. In *Aspergillus*, the dissection of the pH regulatory system common for most fungi revealed the presence of PacC, a zinc finger transcription factor able to activate alkaline expressed genes and repress acidic expressed genes by binding to "GCCARG" consensus sequences located in their promoters. PacC itself is activated under neutral or alkaline pH by the Pal signalling pathway (Arst and Peňalva, 2003). Orthologues of all these components of the pH regulatory system are present in the genome of *F. graminearum* and the "GCCARG" consensus binding sequences is detected in various genes promoters of the "*FgTRI5* cluster" (data not shown). In addition we showed that expression of the probable

FgPAC1 gene is high when *TRI* genes are not expressed and is always repressed when *TRI* genes are induced. Whether this *F. graminearum* potential homologue of PacC really represses *TRI* genes expression in this fungus is now under investigation in our laboratory using molecular approaches.

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Table 1. Primer pairs used to amplify *GAPDH*, *TRI5*, *TRI4*, *TRI6*, *TRI10*,*TRI101* and *PAC1* cDNA by Real-Time PCR and PCR efficiencies obtained for five log dilutions of the cDNA mix.

| Gene A | Accession No. | Forward primer sequence (5' to 3') | Reverse primer sequence (5' to 3') | Tm | PCR |
|--------|---------------|------------------------------------|------------------------------------|------|------------|
| | | | | (°C) | efficiency |
| | | | | | |
| GAPDH | FG06257 | CCTTTCATTGAGCCTCAC | CGTACATGGGAGCGTC | 59 | 2 |
| TRI5 | FG03537 | GACCCTAAGCGACTACAG | GTGCTACGGATAAGGTTC | 58 | 1,99 |
| TRI4 | FG03535 | TATTGTTGGCTACCCCAAGG | TGTCAGATGCGCCTTACAAA | 58 | 1,96 |
| TRI6 | FG03536 | AGCGCCTTGCCCCTCTTTG | AGCCTTTGGTGCCGACTTCTTG | 58 | 1,96 |
| TRI10 | FG03538 | TCTGAACAGGCGATGGTATGGA | CTGCGGCGAGTGAGTTTGACA | 58 | 1,93 |
| TRI101 | AB011417 | AGGGCATTAGCGAGGGAAACACA | ACGGCACGCCTTGGAGAGTAGAC | 59 | 1,97 |
| PAC1 | FGSG12970.3 | GAGCCAGGCATGCGAAGAATG | CTCTGGAGGTATGCTTCAGCGG | 66 | 1.94 |

Figure 1. Kinetics of *F. graminearum* CBS185.32 growth, toxin production and pH change in MS liquid medium. Inoculation was done at day 0 and cultures were stopped at nine different times (One, two, three, four, six, eight, 10, 13, 16 days after inoculation). Fungal biomass (mg per culture) and toxin measurements (sum of DON + 15ADON) are the result of three biological replicates. Error bars are the standard error of the mean.

Figure 2. Effect of pH on toxin production and fungal growth. Kinetic of fungal biomass (A) and trichothecenes B production (DON + 15ADON) (B) during culture in three different culture conditions: (i) MSM: MS medium (low buffered); (ii) BMS6.5: MS medium buffered to pH6.5 using MOPS/MES buffer and (iii) BMS6.5 \rightarrow BMS3: Culture was done in BMS6.5 medium then

transferred at day 3 to BMS3 medium buffered at pH3. The cultures were stopped at day 3, 4, 5 and 7 days after inoculation. nd: non detectable. Values are the result of three biological replicates. Error bars are the standard error of the mean.

Figure 3. Effect of acidic pH on *PAC1* and *TRI* genes expression. The histograms represent (in logarithmic (log2) scale) the expression ratio of *TRI5*, *TRI4*, *TRI6*, *TRI10*,*TRI101* and *PAC1* at day 5 in the MS medium (white bars) and in the BMS3 medium two days after transfer from BMS6.5 (dashed bars) compared to their expression in BMS6.5 medium.

Figure 4. Kinetic of *TRI5*, *TRI101* and *PAC1* expression in response to pH change. Histograms represent the expression ratio of *TRI5* (white bars), *TRI101* (dashed bars) and *PAC1* (black bars) in MS medium (A) and BMS3 medium (B) relative to the expression in BMS6.5 medium after three, four, five and seven days of culture. For the BMS3 medium (B), the transfer from BMS6.5 was done at day three, so genes expression for the two compared conditions was considered similar (ratio=1) for this day, thus the value is zero in the logarithmic scale.

Figure 5. The behaviour of TCTB production in different *Fusarium spp.* strains after pH change. Type B trichothecenes (DON + ADON or NIV + 4ANIV) accumulation after 7 days of culture in three different culture conditions: MSM: (i) MS medium (low buffered); (ii) BMS6.5: MS medium buffered to pH6.5 using MOPS/MES buffer (toxin not detected) and (iii) BMS6.5 \rightarrow BMS3: Culture was done in BMS6.5 medium than transferred at day 3 to BMS3 medium buffered at pH3. The tested strains are *F. culmorum* INRA 233 (DON/15ADON), *F. culmorum* INRA 117 (DON/3ADON), *F. graminearum* INRA 155 (DON) and *F. culmorum* INRA 319 (NIV/4ANIV). nd: non detectable.



80x49mm (600 x 600 DPI)





80x92mm (600 x 600 DPI)

Pac1



7

L





Supplementary section: The behaviour of TCTB production in different Fusarium spp. strains after pH change. Type B trichothecenes (DON + ADON or NIV + 4ANIV) accumulation after 7 days of culture in three different culture conditions: MSM: (i) MS medium (low buffered); (ii) BMS6.5: MS medium buffered to pH6.5 using MOPS/MES buffer (toxin not detected) and (iii) BMS6.5→BMS3: Culture was done in BMS6.5 medium than transferred at day 3 to BMS3 medium buffered at pH3. The tested strains are F. culmorum INRA 233 (DON/15ADON), F. culmorum INRA 117

(DON/3ADON), F. graminearum INRA 155 (DON) and F. culmorum INRA 319 (NIV/4ANIV). nd: non detectable.

80x40mm (600 x 600 DPI)