

NOTES

Opposite Patterns of Expression of Two *Aspergillus nidulans* Xylanase Genes with Respect to Ambient pH

A. P. MACCABE, M. OREJAS, J. A. PÉREZ-GONZÁLEZ,† AND D. RAMÓN*

Departamento de Biotecnología, Instituto de Agroquímica y Tecnología de Alimentos,
Consejo Superior de Investigaciones Científicas (CSIC),
46100 Burjassot, Valencia, Spain

Received 26 November 1997/Accepted 15 December 1997

The *Aspergillus nidulans* xylanase genes *xlnA* and *xlnB* are subject to regulation by ambient pH via the zinc finger transcription factor PacC. In the presence of D-xylose, *xlnA* is expressed under conditions of alkaline ambient pH while *xlnB* is expressed at acidic ambient pH. These data have been confirmed for acidity- and alkalinity-mimicking *A. nidulans* mutants.

In nature, many microbes are exposed to large variations in ambient pH and thus require both an efficient pH homeostatic system and a regulatory mechanism which ensures that those molecules exposed to the environment (such as certain permeases, small metabolites, and extracellular enzymes) are only produced under appropriate pH conditions. The ascomycete *Aspergillus nidulans* is able to grow over a wide pH range (14). The regulatory circuit controlling pH regulation in this microorganism has been analyzed both genetically and molecularly. As an example, this system regulates the secretion of alkaline phosphatase in alkaline growth conditions and acid phosphatase in acidic environments (2).

pH regulation of gene expression in *A. nidulans* is mediated by the wide-domain zinc finger transcription factor PacC (16). In alkaline culture conditions, this factor is converted to its truncated functional form in response to the ambient pH signal transduced by the products of six genes (*palA*, *-B*, *-C*, *-F*, *-H*, and *-I*) and is able to activate the expression of those genes whose products are appropriate at alkaline ambient pH and repress those whose expression is suited to acidic pH (1, 3, 10, 11, 16). Activation is exercised by binding to the consensus target sequence 5'-GCCARG-3' (5). We have previously shown that *A. nidulans* produces three xylanases when grown on D-xylose as the sole carbon source: one minor xylanase (X_{24}), encoded by *xlnB*, and two major xylanases (X_{22} and X_{34}), encoded by *xlnA* and *xlnC*, respectively (6, 7, 9, 12). In this article we demonstrate pH regulation of the expression of the *xlnA* and *xlnB* genes.

The nucleotide sequences of the upstream regions of the *xlnA* and *xlnB* genes have been determined and reveal the presence of two and one consensus PacC binding sites, respectively (Fig. 1). The occurrence of such binding targets suggests that the transcription of these genes might, at least in part, be regulated by this transcription factor.

Transcription of the xylanase genes was analyzed in mycelia

grown under acidic (pH ~4.5), neutral (pH ~6.5), and alkaline (pH ~7.5) growth conditions. Wild-type conidia were inoculated in minimal medium (MM) (13) supplemented with 0.5% (wt/vol) Casamino Acids and 1% (wt/vol) D-fructose as the sole

xlnA promoter:

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-661 TCCTGGAAGTGCCTGATCATTATTCCTCCGAAAATGTAGTACCCAGTAAGTGGCTAGCG  
-601 GTGGCTATGGTAGGACATCTATGCTAAGCTGGAGTTCTCATTGAACGTGTACCGGCCGA  
-541 TTGCCCTAAACTCTGATTGAGAGCCGGAACCTCATCTACCTGATGCTCAGGGGCCATCC  
-481 AATAGCTTCCGATAGCATTACAGACAGATGGACTCGTCTTGGCCCAACGGGTCTAGAACAG  
-421 TCGCCGGAGCTGCCTCTATTGAAACGGAGCTGAACCATGATACCTTAAGCGTCCCAAGCG  
-361 GCGCCGTTTCCCACTGGAACAAGGAGCAATAGAAATTCGACAGATTCTTCATTGAGGCT  
-301 ATTGAGCAATTCGGTTTGTGGAGCGGATCGGGTCCACTGGTATTAGTCTGGGGTTTTTC  
-241 TTTGCCCGATGGGCTCTAGACATGCACAGCTTCAGTGTGCTACGCTATCTGGGAA  
-181 AACGAATGGCTATTTCAGGATTTATAACCAAAAGAGCCGGAACAGGCTGATTGCCCTCT  
-121 CACGGGGAGAGCTGTACTTCTGATCCAGAGSCTATTAACCCGACACTACCTATAAAGGA  
-61 GGTAGCATCTCTTCTGTCCGGCTCCAGATTCCAACAACCAACTGACAGGATCAGCAC  
-1 AATG
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xlnB promoter:

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-640 CTTGTGAGTAGAAGCATCGTGCCAGACATCACACGCAATACAGCTCCCTCAGCATTTTT  
-590 TCGATACCCAAAACCTCAGTTAACAACCTGCAGCCTAGAGTTGATCAGGACTTCTGCCGGA  
-530 GATATCTCCATACGTACCGGAGGCCACTGTTCAGGCCAATTTTCCCGCAGAGATCGCT  
-470 GATCTTCCACCGCAATCTTCAAGCTTCTACTCAGCCAACTCAGATCGACGGCCCTGCC  
-410 TATTCTGTATCTACCGGTGGTTTACGCTATATTTCTGACAGCATATTTGGATTGGCGGC  
-350 ACGATATTGAAGCTTCTGGCAAAGCTTAAACGTATATGCCAAGACTGTCAATATACTTGA  
-290 GACACAACCCAAATTAGCCTATTACCGGTGGGAACAAGACTTCTCACTTGACACCCGT  
-230 CTATGTTTCACTCGACACATGCGTGGATTCAAATTCGCCATCGAAAGATGGTAGCCAT  
-170 TCAAAGGCTTCTGGATTAAACCGGAGCCTAAAGAAATATAACCTCAAACACTCCGTCC  
-110 CCACAGTCAGCAGTACCCCGAGTATCATATGATGGAGCTGACTATAAAGCAACGTCGCC  
-50 GCACGCTCAACACGTCCTGCTGCTCAACACTTCAACAACCGGCAACATG
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FIG. 1. DNA sequences of the *xlnA* and *xlnB* gene promoters (EMBL accession no. Z49892 and Z49893, respectively). The translational initiation codon is shown in bold, and consensus PacC binding sites are shown in bold and underlined.

* Corresponding author. Mailing address: Departamento de Biotecnología, Instituto de Agroquímica y Tecnología de Alimentos, Consejo Superior de Investigaciones Científicas, Apartado de Correos 73, 46100 Burjassot, Valencia, Spain. Phone: (34) 6 3900022. Fax: (34) 6 3636301. E-mail: dramon@iata.csic.es.

† Deceased 9 August 1997.

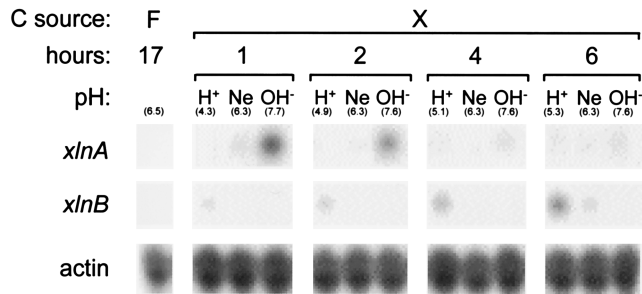


FIG. 2. Expression of *xlnA* and *xlnB* genes in *A. nidulans* wild-type mycelium in response to external pH. Carbon (C) sources present were D-fructose (F) and D-xylose (X). pH conditions are indicated as follows: H⁺, acidic; Ne, neutral; and OH⁻, alkaline. The actual pHs of the culture media at the time of recovery of mycelia for RNA isolation are indicated in parentheses. Actin gene expression is shown as a loading control.

carbon source. Incubation was done for 17 h at 37°C with orbital shaking, and the mycelia were subsequently transferred to buffered media containing 1% (wt/vol) D-xylose as the sole carbon source for 1, 2, 4, and 6 h. Total RNA was prepared and analyzed by Northern blotting. Figure 2 shows that the *xlnA* transcript appears shortly after transfer and only in alkaline growth conditions. In contrast, the *xlnB* transcript is detected after 4 h and mainly in acidic growth conditions. These data suggest pH regulation of the expression of *xlnA* and *xlnB*.

In order to investigate whether this response to ambient pH is mediated by PacC, we examined the transcript levels of the two genes in different pH mutant genetic backgrounds. Wild type, *pacC*^{C14} (an extreme alkalinity-mimicking mutant) (2, 16), *pacC*^{+/-20205} (an acidity-mimicking *pacC* mutant [17]), and *palA1* (a mutant in the signal transduction pathway mimicking acidic conditions) (1, 2, 10) mycelia were grown in D-fructose MM as noted above and transferred to MM (pH 6.5) containing 1% (wt/vol) D-xylose as the sole carbon source. At different time points after transfer (1, 2, 4, and 6 h) total RNA was isolated and analyzed by Northern blotting. Figure 3 shows that the alkalinity-mimicking *pacC*^{C14} mutation simultaneously results in elevated levels of the *xlnA* transcript and reduced levels of the *xlnB* messenger. In contrast, the acidity-mimicking *pacC*^{+/-20205} and *palA1* mutations yield the opposite pattern of expression. The highest level of expression of *xlnA* occurs in the *pacC*^{C14} mutant background, whereas that of *xlnB* occurs in the *palA* background.

The analyses described above show an absolute correspondence between the patterns of transcription of the xylanase genes under different ambient pH conditions and those observed in the pH mutant backgrounds. Specific transcription of

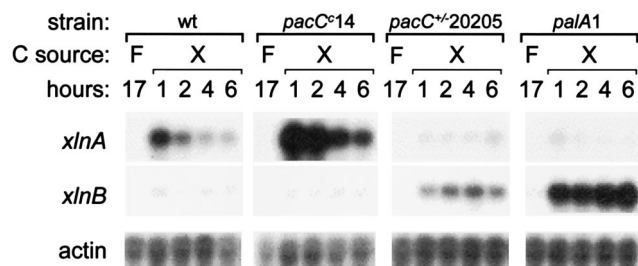


FIG. 3. *xlnA* and *xlnB* expression in *A. nidulans* pH-regulatory mutants. Carbon (C) sources present were D-fructose (F) and D-xylose (X). Measurements at the time of recovery of mycelia for RNA isolation showed that the pH of all culture fluids fell within the range of 5.9 to 6.5. Actin gene expression is shown as a loading control.

the *xlnA* and *xlnB* genes requires both the presence of an inducer (D-xylose) and optimal ambient pH. In *Aspergillus niger* the regulation by pH of the two major acidic extracellular proteases was investigated by Northern analysis (8). Due to the absence of pH-regulatory mutants of *A. niger*, this study was carried out by varying the pH of the culture medium. In the present study, pH regulation of the expression of two *A. nidulans* xylanase-encoding genes was investigated under different conditions of ambient pH and for different alkalinity- and acidity-mimicking mutants. This constitutes the first demonstration of the control of xylanase gene expression by ambient pH via the wide-domain pH regulator PacC. It is interesting to note the noncoincident, reversed patterns of expression of *xlnA* and *xlnB* with respect to pH and the time course of induction. The former might be related to the fact that *xlnB* codes for an acidic xylanase stable at acidic pH and *xlnA* encodes a neutral xylanase that is less stable at acidic pH (6, 7).

Including the data presented in this report, four *A. nidulans* alkaline-expressed genes, *ipnA*, *pacC*, *prtA*, and *xlnA*, have been studied with respect to pH expression (4, 16). In agreement with the proposed model for PacC as a transcriptional activator (11, 16), each of these genes contains several consensus PacC binding sites in the promoter. Only in the case of *ipnA* has the physiological relevance of the PacC sites been determined (5). The mechanism for the negative action of PacC in the regulation of acid-expressed genes is poorly understood. Interestingly, *pacA*, the only acid-expressed *A. nidulans* gene studied so far, contains an upstream PacC site, but it lies well within the transcribed region and quite close to the putative initiator codon (15, 15a). In contrast, the PacC site in *xlnB* lies much more nearly in the region where PacC sites occur in alkaline-expressed promoters.

This work was supported by the EC-BIOTECH project BIO2-CT93-0174. A.P.M. was the recipient of EC Biotechnology Programme fellowship BIO2-CT94-8136, and M.O. is the recipient of a CSIC post-doctoral contract.

Thanks are due to Herb N. Arst, Jr., for kindly providing us with the *A. nidulans* mutants used in this work.

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