REGULATION OF PECTINOLYTIC GENE EXPRESSION IN *ASPERGILLUS*

R.P. DE VRIES\(^1\) AND L. PAŘENICOVÁ\(^2\)

\(^1\)Molecular Genetics of Industrial Microorganisms, Wageningen University, Dreijenlaan 2, 6703 HA Wageningen, The Netherlands

Current address: Microbiology, Utrecht University, Padualaan 8, 3584 CH Utrecht, The Netherlands, e-mail: r.p.devries@bio.uu.nl

\(^2\) Dipartimento di Biologia, Università degli studi di Milano, Via Celoria 26, 20133 Milano, Italy

Abstract

This chapter discusses the current knowledge of the regulation of pectinolytic genes in *Aspergillus* and presents a summary of recent data obtained on this topic. So far, little is known about regulatory factors involved in pectin degradation. It appears that the pectinolytic regulatory system is more complex than the xylanolytic regulatory system, in which a general activating factor (XlnR) plays a central role. Some pectinolytic genes are expressed in response to the presence of pectin or pectin derived compounds, but constitutively expressed pectinolytic genes have also been reported. Indications for the involvement of general regulatory factors such as carbon catabolite repression and pH regulation have also been reported. Specific regulatory systems have been proposed for the regulation of genes encoding pectinolytic enzymes acting on the side chains of pectin.

1. Introduction

Due to the complex structure of the pectic polysaccharides, biodegradation of these compounds requires a wide range of enzymes. These enzymes can be divided into two groups: those acting on the pectin main chain (endo-and exopolygalacturonases, pectin and pectate lyases, rhamnogalacturonan hydrolases and lyases, pectin methyl and acetyl esterases, and rhamnogalacturonan acetyl esterase) and those acting on side chains of the pectic hairy regions (arabinofuranosidases, endoarabinanase, β-galactosidase, endogalactanases, and feruloyl esterases). The production of such a large number of enzymes is a significant energetic burden for microorganisms. Therefore, many microorganisms have developed complex regulatory systems for the production of these enzymes. In this chapter the regulatory factors affecting the production of pectinolytic enzymes by species of the filamentous fungus *Aspergillus* will be discussed. These fungi are widely studied as a source of pectinolytic enzymes and serve as a model system for phytopathogenic fungi such as *Botrytis cinerea*.

The genus *Aspergillus* can be divided into several subgroups, some of which consist of pathogenic fungi (e.g. *A. fumigatus*, *A. flavus* and *A. parasiticus*). Most important for industrial applications are members of the group of black aspergilli. This group has been
classified in detail over the last 10 years, which resulted in the clear distinction of eight groups of black aspergilli (A. niger, A. tubingensis, A. foetidus var., A. carbonarius, A. japonicus, A. aculeatus, A. heteromorphus, and A. ellipticus) (67) and to the classification of two new species represented by the isolates A. brasiliensis IMI381727 and A. aculeatus CBS114.80 (68). Products of several of these species have obtained a GRAS (Generally Regarded As Safe) status, which allows them to be used in food and feed applications. The black aspergilli have good fermentation capabilities and secrete high levels of protein making them interesting organisms for industrial applications.

The expression of genes encoding polysaccharide degrading enzymes is usually induced by a monomeric or dimeric degradation product of the polymeric substrate. In aspergilli the regulatory systems involved in (hemi-)cellulose degradation are among the best studied. In A. niger it has been shown that the xylanolytic system is induced in the presence of D-xylose (84) and the regulation of the expression occurs at the transcriptional level via the activator XlnR (86). Recently, a model was suggested for the role of XlnR in the regulation of (hemi-)cellulose degradation by A. niger (Fig. 1) (23).

During growth of A. niger in the presence of arabinoxylan XlnR is activated by monomeric xylose which is already present in the substrate. Alternatively, xylose can be released by endoxylanase B and β-xylosidase, both of which are present at low constitutive levels. The expression of (hemi-) cellulolytic genes is then activated by XlnR (29, 41, 85).

FIG. 1. Model for the role of XlnR and CreA in the regulation of the genes encoding (hemi-) cellulose degrading enzymes by Aspergillus niger. UAS, upstream activating sequence; URS, upstream repressing sequence; → activation; —— repression; —— released by corresponding enzyme. Reprinted from de Vries et al. (23) with permission from the publisher.