



Universiteit
Leiden
The Netherlands

Transcriptional control of pectin degrading enzymes in *Aspergillus niger*

Niu, J.; Niu J.

Citation

Niu, J. (2017, October 18). *Transcriptional control of pectin degrading enzymes in Aspergillus niger*. Retrieved from <https://hdl.handle.net/1887/54939>

Version: Not Applicable (or Unknown)

License: [Licence agreement concerning inclusion of doctoral thesis in the Institutional Repository of the University of Leiden](#)

Downloaded from: <https://hdl.handle.net/1887/54939>

Note: To cite this publication please use the final published version (if applicable).

Cover Page



Universiteit Leiden



The handle <http://hdl.handle.net/1887/54939> holds various files of this Leiden University dissertation.

Author: Niu, J.

Title: Transcriptional control of pectin degrading enzymes in *Aspergillus niger*

Issue Date: 2017-10-18

Stellingen

Behorende bij het proefschrift

Transcriptional control of pectin degrading enzymes in *Aspergillus niger*

- With the development of next generation sequencing techniques, forward genetic screens in combination with genome sequencing has become a powerful and affordable approach to identify novel elements of regulatory pathways.
This thesis
- The fact that in a forward genetic screen mutations in both *gaaR* and *gaaX* were identified that caused constitutive expression of pectin degrading enzymes could be explained by a physical interaction between these regulatory factors.
This thesis
- Different approaches to study the regulation of galacturonic acid-dependent gene expression identified only partially overlapped collection of genes, indicating that besides GaaR and GaaX, also other yet unknown (transcription) factors are involved in the regulation of galacturonic acid utilization.
(Martens-Uzunova and Schaap 2008; Chapter 5 and Chapter 6)
- Structural similarity between 2-keto-3-deoxy-L-galactonate and dehydroquinate, suggests that for the galacturonic acid pathway the inducer binds to the “dehydroquinase-like” domain of the GaaX repressor protein as was found for QutR in quinate pathway.
(<http://www.ebi.ac.uk/chebi/init.do>; Giles *et al.* 2000; Levett *et al.* 2000; Chapter 6)
- Carbon catabolite repression in filamentous fungi is normally mediated by the wide domain regulator CreA. However, our results show that the *pgxC* promoter is still repressed by glucose in the *creA* null background suggesting the presence of a role for an alternative repression mechanism.
(Chapter 4)

- Based on results for *A. niger*, LaeA is not only a regulator of classical secondary metabolism but also of the production of organic acids.
(Bok and Keller 2004; Niu *et al.* 2016)
- The CRISPR-Cas9 system is an adaptive immune system in bacteria protecting them from naturally occurring genome modifications caused by viral infections. Bacteria would be surprised to find that this natural system has evolved into a powerful tool for modifying their genome and the genome of many other species.
- The current set-up of CRISPR-Cas9 system for gene targeting provides little benefit over the split marker approach combined with NHEJ mutants.
(Weyda *et al.* 2017; Chapter 2)
- Given the Dutch climate experience from a foreigners eye, the English expression for heavy rains perfectly explains why so many cats and dogs are seen everywhere in the Netherlands.
- Experiencing the deadlines in the final stages of doing a PhD study gives a better understanding of the Chinese saying “an inch of gold will not buy an inch of time (寸金难买寸光阴)”.