



VeA, a Global Regulator of Secondary Metabolism, Can Increase Production of Secondary Metabolites

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Technology description

Microorganisms, such as fungi, produce a variety of secondary metabolites. These secondary metabolites display a broad range of activities, including antibiotic, immunosuppressant, phytotoxic and mycotoxic activities, and are useful for drug or technological development. For example, the antibiotic penicillin and the cholesterol-lowering drug lovastatin are secondary metabolites.

However, producing large amounts of secondary metabolites is difficult, and available techniques often provide unpredictable results. Because they are formed from a relatively small number of metabolic pathways, identifying the genes that control these pathways may provide an alternative method of generating secondary metabolites.

The inventors previously identified a global regulator of secondary metabolism, called LaeA, in fungi (see WARF reference number P02379US). Overexpression of the laeA gene upregulates production of secondary metabolites, greatly increasing penicillin production in *Aspergillus nidulans* and lovastatin production in *A. terreus*. On the other hand, deletion of laeA in *A. fumigatus* eliminates the production of gliotoxin and other secondary metabolites, decreasing the virulence of this human pathogen. UW-Madison researchers now have identified another global regulator of secondary metabolism, called VeA. VeA is a conserved protein that interacts with LaeA in an as yet unknown mechanism. Overexpression of veA upregulates secondary metabolism in *A. flavus* to a greater degree than overexpression of laeA. This gene could be used to increase the production of important natural products, including novel products with medicinal value.

The Wisconsin Alumni Research Foundation (WARF) is seeking commercial partners interested in developing methods of using VeA, a newly identified global regulator of secondary metabolism, to increase or decrease production of secondary metabolites in fungi.

Bayram O., Krappmann S., Ni M., Bok J.W., Helmstaedt K., Valerius O., Braus-Stromeyer S., Kwon N.J., Keller N.P., Yu J.H. & Braus G.H. 2008. *VelB/VeA/LaeA Coordinated Light Information, Fungal Development and Secondary Metabolism*. *Science* 320, 1504-1506.

Bayram O., Krappmann S., Ni M., Bok J.W., Helmstaedt K., Valerius O., Braus-Stromeyer S., Kwon N.J., Keller N.P., Yu J.H. & Braus G.H. 2008. *VelB/VeA/LaeA Coordinated Light Information, Fungal Development and Secondary Metabolism*. *Science* 320, 1504-1506.

Amaike S. & Keller N.P. 2009. Distinct Roles for VeA and LaeA in Development and Pathogenesis of *Aspergillus flavus* . *Eukary. Cell* 8, 1051-1060.

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Application area

Increasing production of useful secondary metabolites, such as penicillin or lovastatin

Decreasing production of toxic secondary metabolites, such as aflatoxin

Advantages

Provides a simple method of increasing or decreasing secondary metabolite production

Upregulates secondary metabolism to a greater degree than LaeA

May enable new treatments for fungal infections

May be used to identify new secondary metabolite biosynthesis gene clusters

Institution

[Wisconsin Alumni Research Foundation](#)

Inventors

[Nancy Keller](#)

[Saori Campen](#)

联系我们



叶先生

电 话 : 021-65679356

手 机 : 13414935137

邮 箱 : yeingsheng@zf-ym.com