

## Comparative Analysis of a Putative HLH Transcription Factor Responsible for Conidiation in *Aspergillus* Species

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Asexual reproduction or conidiation in aspergilli is a primary mean to produce their progenies that is environmentally and genetically controlled tightly. Previously, intensive researches in the model fungus *Aspergillus nidulans* disclosed some genes playing important roles in asexual and sexual development. Among them, one gene encoding a putative helix-loop-helix (HLH) transcription factor, named *ndrA*, has been isolated and characterized as a downstream regulator of developmental master regulator NsdD. By using comparative genome search of *A. nidulans* NdrA protein, its orthologues have been identified in *A. fumigatus* and *A. flavus*, respectively (*AfudrnA* and *AfldrnA*). Deletion of the *ndrA* genes in both *Aspergillus* species made them unable to produce the conidia yet abundant production of sclerotia in *A. flavus*. Complementation of *ndrA* deletion strains by intact *ndrA* ORFs has restored the conidiation as in the control strains. In *A. fumigatus*, *ndrA* deletion also resulted in loss of conidiation phenotype. Northern analyses showed that the *ndrA* genes in both *Aspergillus*

species are highly expressed at the early stage of the conidiation. Interestingly, the *ndrA* genes were found to be necessary for the proper expression of *brlA* genes. Antifungal sensitivity test revealed that the *ndrA* genes might be responsible for the sensitivity or resistance to some antifungal agents. However, *ndrA* deletion did not greatly influence the growth in both strains. And the *A. flavus ndrA* gene did not affect the aflatoxin production. Taken together, *ndrA* genes in *Aspergillus* species could be an important positive regulator of conidiation under the regulation of the *nsdD* gene yet upstream of the *brlA* gene.