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Identification of Cryptic Products of the Gliotoxin Gene Cluster Using NMR-Based Comparative Metabolomics and a Model for Gliotoxin Biosynthesis

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Supporting Information

ABSTRACT: Gliotoxin, a major product of the *gli* non-ribosomal peptide synthetase gene cluster, is strongly associated with virulence of the opportunistic human pathogen *Aspergillus fumigatus*. Despite identification of the *gli* cluster, the pathway of gliotoxin biosynthesis has remained elusive, in part because few potential intermediates have been identified. In addition, previous studies suggest that knowledge of *gli*-dependent metabolites is incomplete. Here we use differential analysis by 2D NMR spectroscopy (DANS) of metabolite extracts derived from *gli* knock-out and wild-type (WT) strains to obtain a detailed inventory of *gli*-dependent metabolites. DANS-based comparison of the WT metabolome with that of Δ*gliZ*, a knock-out strain devoid of the gene encoding the transcriptional regulator of the *gli* cluster, revealed nine novel *gliZ*-dependent metabolites including unexpected structural motifs. Their identification provides insight into gliotoxin biosynthesis and may benefit studies of the role of the *gli* cluster in *A. fumigatus* virulence. Our study demonstrates the utility of DANS for correlating gene expression and metabolite biosynthesis in microorganisms.

Filamentous fungi produce remarkably diverse metabolomes including many small molecules of polyketide synthase (PKS) or non-ribosomal peptide synthetase (NRPS) origin that play important roles in pathogenesis.[1] The opportunistic pathogen *Aspergillus fumigatus*, a causative agent of invasive aspergillosis, produces copious amounts of gliotoxin (**1**), a representative member of a small family of epipolythiodioxopiperazines (ETPs) that is strongly associated with *A. fumigatus* virulence.[2] Gliotoxin and related ETPs are products of the *gli* NRPS gene cluster.[3] Knock-out mutations of *gliP* (Δ*gliP*), a three-module NRPS (see Figure S7 in the Supporting Information for domain architecture),[3,4] *gliI* (Δ*gliI*), encoding a putative pyridoxal 5′-phosphate (PLP) binding domain,[5] or *gliZ* (Δ*gliZ*), a Zn_2Cys_6 binuclear transcription factor, abolishes gliotoxin biosynthesis.[6] Δ*gliP* has been shown to be significantly less virulent than the wild-type (WT) strain in immunosuppressed mice,[6c] confirming that gliotoxin and perhaps other *gli*-dependent metabolites play a role in overcoming host resistance.

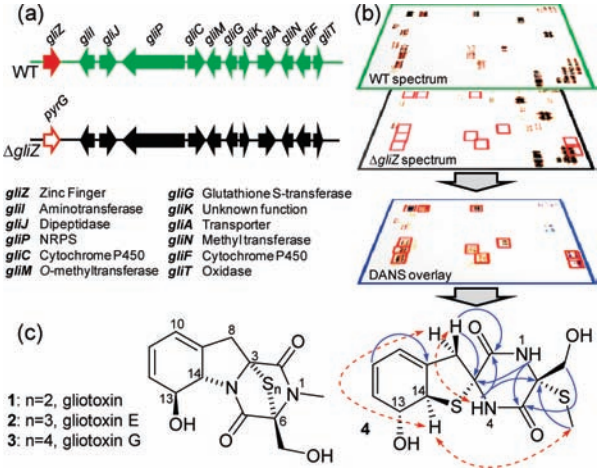

Figure 1. Identification of *gliZ*-dependent metabolites via DANS. (a) Gliotoxin gene cluster in *A. fumigatus* WT and mutant strain Δ*gliZ*, in which *gliZ* is replaced by the selection marker *pyrG*, encoding orotidine-5′-phosphate decarboxylase. (b) DANS overlay technique (schematic). Signals in the DANS overlay serve as markers for compounds whose biosyntheses depend on *gliZ* expression. (c) Examples for *gliZ*-dependent metabolites identified in this study and structure elucidation of **4** (HMBC, blue arrows; ROESY, red arrows).

Previous studies suggest that knowledge of *gli*-dependent metabolites is incomplete.[6d] In addition, the sequence of steps in the biosynthesis of the gliotoxins has remained unclear, in part because few potential biosynthetic intermediates or shunt metabolites have been identified. We hypothesized that NMR-based comparative metabolomics of *gli*-knock-out and WT or *gli*-over-expressing strains could provide a comprehensive overview of *gli*-dependent metabolites, including shunt metabolites and other cryptic products.[7] Recent studies, including the identification of bacillaene as the product of the mixed PKS/NRPS gene cluster *pksX* in *Bacillus subtilis*[8] and the identification of mating pheromones in *Caenorhabditis elegans*,[9] have demonstrated the utility of differential analysis by 2D NMR spectroscopy (DANS) for

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connecting metabolites with their biosynthetic pathways. In these examples, DANS combined with HPLC-MS analyses provided a comprehensive overview of the metabolic changes caused by knocking out small-molecule biosynthetic genes, which in each case led to the identification of several previously undetected metabolites derived from the knocked-out pathway.

For metabolic comparison, we used WT *A. fumigatus* and the mutant strain Δ*gliZ*.[6d] Knock-outs of *gliZ* have been shown to stop the expression of the majority of genes in the *gli* cluster with the exception of *gliT*.[6d,10] Therefore, DANS-based comparison of the Δ*gliZ* and WT metabolomes should enable identification of any metabolites whose biosyntheses directly or indirectly depend on *gli* expression (Figure 1).

In preparation for NMR spectroscopic analyses, we fractionated both the Δ*gliZ* and WT metabolomes into three metabolite pools of reduced complexity and limited polarity range, which ensured that both very polar (pool 1) and very nonpolar (pool 3) metabolites would be detected (see methods in Supporting Information) For the resulting three WT pools and three Δ*gliZ* pools, we acquired high-resolution dqfCOSY spectra. Compared to other 2D NMR spectroscopic techniques such as TOCSY[11] or HSQC,[12] dqfCOSY offers distinct advantages for the detection of novel or unanticipated compounds, because crosspeak fine structure in dqfCOSY spectra provides greater structural information, including full signal multiplicity and coupling constants.[13] Furthermore, dqfCOSY crosspeak fine structures can be easily modeled,[13] which helps resolve peak overlap and facilitates recognition of minor components.[9] dqfCOSY spectra also offer better sensitivity than HSQC, often enabling characterization of trace components representing <0.1% of a sample.[14]

For DANS, dqfCOSY spectra obtained for the three WT metabolite pools were compared with the corresponding Δ*gliZ* pools using an overlay algorithm designed to highlight WT signals that were completely absent from the Δ*gliZ* spectra. This approach excluded compounds from the analysis whose biosynthesis was not entirely *gliZ*-dependent. DANS revealed more than 20 distinct *gliZ*-dependent spin systems in WT pool 2 (Figures 2 and S1) and a smaller number of *gliZ*-dependent signals in WT pool 1. No *gliZ*-dependent signals were observed in WT pool 3.

In the spectra of WT pool 1, DANS revealed two major *gliZ*-dependent spin systems which correspond to structural motifs also present in the gliotoxins, including an α-substituted serine and a 5,6-disubstituted cyclohexa-2,4-dien-1-ol bearing a methylene group in position 5. However, chemical shift values and coupling constants indicated that this metabolite does not represent a known compound (Table S1). HR-MS revealed a molecular formula of $C_{13}H_{16}N_2O_4S_2$ which, in conjunction with ROESY and HMBC data obtained for a purified sample, established the structure of **4** as shown, featuring a sulfur bridge between C-3 and C-14 as part of an unusual 6,9-diaza-1-sulfaspiro[4.5]decane system (Figure 1). Compound **4** is a novel metabolite with a structural motif rarely observed in nature, featuring a sulfur- and nitrogen-bound spiro atom. Notably, the configurations at C-13 and C-14 in **4** are opposite to those found in gliotoxin **1**, assuming that the configurations at C-3 and C-6 in **4** are the same as in **1**, which seems likely given that both **1** and **4** are 3,6-*cis*-disulfurized.

Analysis of *gliZ*-dependent signals in the WT pool 2 spectra revealed spin systems whose NMR data closely matched those of the known ETPs **1**−**3** (Figure 1) and the bis-methylsulfanyl derivative **8**,[15] in addition to a large number of unknown compounds (see Figure 2 for structures and Figure S1 for DANS overlay spectrum). For further structural assignments, we

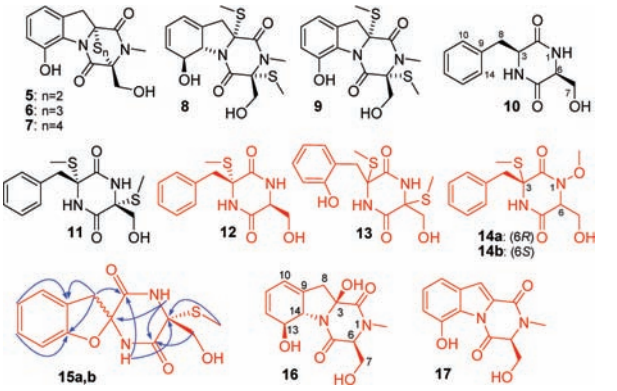

Figure 2. Identification of *gliZ*-dependent metabolites in pool 2. Structures shown in red represent novel metabolites. The relative configuration of **13**, which occurs as one single diastereomer, could not be determined but likely corresponds to that of **11**.

fractionated WT pool 2 via HPLC and characterized fractions containing one or more of the *gliZ*-dependent compounds detected by DANS, using HSQC, HMBC, and ROESY spectra as well as HPLC-MS. These analyses confirmed the presence of the gliotoxins **1**−**3** and **8**, as well as their dehydro derivatives **5**−**7** and **9**.[15c,16] We further identified cyclo(L-Phe-L-Ser) (**10**),[17] not previously reported from *A. fumigatus* extracts nor other gliotoxin-producing fungi, as well as bis-*N*-norgliovictin (**11**), a known *A. fumigatus* metabolite[18] not previously associated with the *gli* cluster.

All other *gliZ*-dependent metabolites detected in WT pool 2 represented novel compounds (Figure 2). These include the four diketopiperazines **12**, **13**, **14a**, and **14b**. Compounds **14a**/**b** represent diastereomeric *N*-methoxy derivatives of **12**, as was shown via $^{1}H,^{15}N$ HMBC. These diketopiperazines are accompanied by two indolopyrazines, **16** and **17**, representing non-sulfurized derivatives of gliotoxin. In addition, DANS revealed a second type of spirocyclic scaffold, the 6,9-diaza-1-oxaspiro-[4.5]decanes **15a** and **15b**. The two diastereomers **15a**/**b** appear to be derived from **13** via intramolecular substitution at C-3, as isolated samples of **13** slowly convert into mixtures of **15a** and **15b** (Figure S6). HR-MS confirmed the molecular formulas of all new compounds (see Tables S1−S11 for spectroscopic data), and the *gliZ*-dependence of their biosynthesis was corroborated via DANS and HPLC-MS in two independent replicates (Figures S2 and S3).

To test whether *gliZ* overexpression would reveal additional *gliZ*-dependent metabolites, we compared the *A. fumigatus* WT metabolome with that of a *gliZ*-overexpressing (OE) strain via DANS.[6d] Although we observed differences in the relative amounts of some of the metabolites **1**−**17** in the OE strain, we did not detect any new *gliZ*-dependent metabolites. Next, we investigated the effect of deletion of two additional *gli* genes, *gliP* and *gliI*. DANS- and HPLC-MS-based comparison of Δ*gliP* and Δ*gliI* mutant metabolomes with WT showed that none of the *gliZ*-dependent compounds **1**−**17** are produced by these two mutant strains. These results further support that biosynthesis of **1**−**17** requires the *gli* cluster.

Of the 19 *gliZ*-dependent compounds we identified, nine represent novel compounds, several of which feature structural motifs not previously associated with *gli* products. These structural features are of interest considering the putative pathway of gliotoxin biosynthesis in *A. fumigatus* (Figure 3).[3] Only the first and last steps in gliotoxin biosynthesis, the condensation between L-Phe and L-Ser by GliP and the oxidation of dithiol gliotoxin by GliT, have been elucidated,[4,10a] and many aspects of

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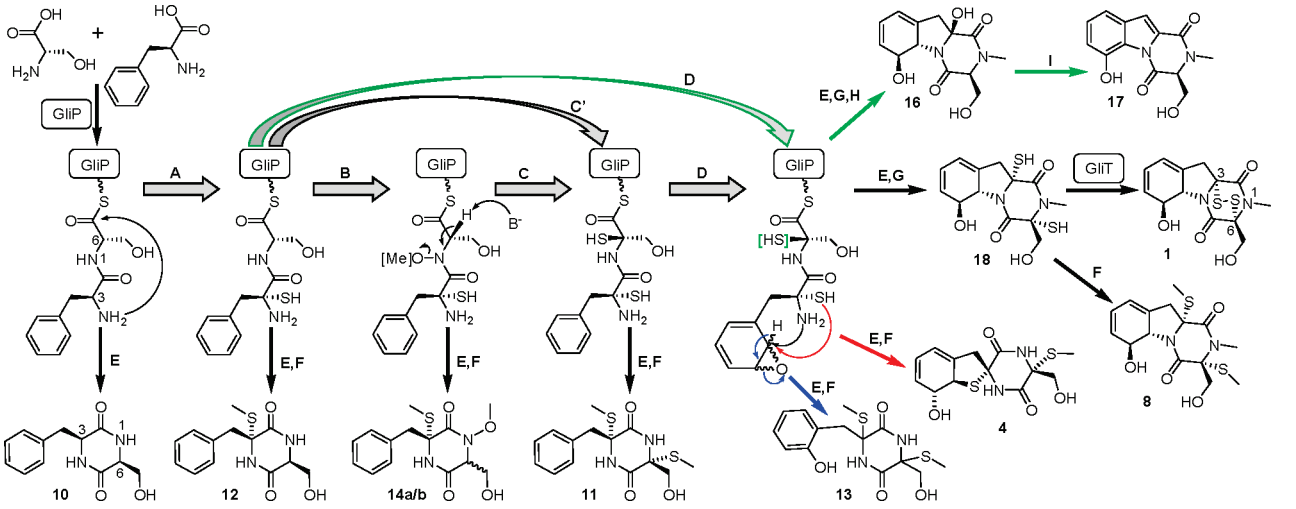

Figure 3. Proposed biogenesis of *gliZ*-dependent metabolites. Oxidation and sulfurization at C-3 (A) is followed by *N*-1-oxidation (B) and C-6 sulfurization (C or C′). Epoxidation (D) is followed by pyrollidine, thiophane, or phenol formation (black, red, and blue arrows, respectively). Aminolysis (E) of the resulting GliP-tethered intermediates and methylation of thiols (F) produce compounds **4**, **10**−**14a/b**. *N*-1-Methylation (G) and aminolysis (E) result in formation of dithiol, which is *S*-methylated (F) to form **8** or oxidized by GliT[10a] to produce gliotoxin, **1**. Hydrolysis (H) of species oxidized (and possibly sulfurized) only at C-3 (green arrows) produces **16**, which aromatizes (I) to form **17**.

the intervening steps remain unclear. *In vitro* experiments conducted with recombinant GliP demonstrated that GliP couples the amino acids Phe and Ser, producing a Phe-Ser-GliP intermediate.[4] Further observations indicated that GliP is capable of producing cyclo(L-Phe-L-Ser), but kinetic data suggested that the rate of cyclic dipeptide formation may be too low to be enzymatically relevant.[4] Our studies show that **10** is a major component of the *A. fumigatus* WT metabolome, with a gliotoxin-to-cyclo(L-Phe-L-Ser) molar ratio of roughly 2:1, and that this abundant production of **10** is *gliZ*-dependent. The abundance of **10** suggests that the *in vivo* rate of formation is much greater than that *in vitro*, perhaps due to presence of additional factors, for example other *gli* components, *in vivo*. It has been proposed that **10** is an intermediate in gliotoxin biosynthesis;[5] however, the structural features of the *gliZ*-dependent metabolites we identified are consistent with pathways involving tethered intermediates (Figure 3). Furthermore, the addition of synthetic **10** to Δ*gliP* cultures did not rescue the production of any of the *gliZ*-dependent metabolites as assessed by DANS and HPLC-MS (Supporting Information), suggesting that **10** may not be a biosynthetic intermediate.

All of the *gliZ*-dependent compounds **1**−**17** except **10** are oxidized at the α-carbon of Phe, and in the case of compound **12** only at that position, suggesting that oxidation and sulfurization at C-3 occurs at an early stage in the biosynthesis following formation of the Phe-Ser dipeptide. Oxidation at C-3 could involve *gliC* or *gliF*, encoding putative cytochrome P450 monooxygenases. Alternatively, *gliI*, encoding a putative PLP cofactor domain characteristic of amino transferases,[5] may function in transforming the free amino group of the Phe moiety into the corresponding imine, as previous studies suggested that installation of sulfur at the α-position of diketopiperazines may proceed via imine intermediates.[19] Such a mechanism would be consistent with the hypothesis that gliotoxin biosynthesis proceeds via successive elaboration of a tethered dipeptide. Our finding that Δ*gliI* does not produce any of the *gliZ*-dependent compounds **1**−**17** does not allow distinguishing between these possibilities. However, the absence of all *gliP*-dependent metabolites from Δ*gliI* is consistent with the observation that *gliP* transcription is abolished in this mutant (Figure S5). Sulfurization at C-3, yielding a C-3 thiol intermediate, likely involves GliG, recently demonstrated to possess glutathione *S*-transferase activity *in vitro*.[20] Compound **12** would then form via methylation of the thiol, either before or after aminolysis of the thioester. All sulfurized diketopiperazines identified in this study (except for the four ETPs) are *S*-methylated and thus likely derived from methylation of corresponding thiols, which is also suggested by the finding that, in *Gliocladium deliquescens*, gliotoxin is converted into bisdethiobis(methylthio)gliotoxin, **8**.[15c]

The identification of compounds **11** and **14a/b** suggests that sulfurization at C-3 is followed by oxidation of the peptide backbone at C-6 and N-1, with *O*-methylation of the resulting hydroxamic acid derivatives by the putative *O*-methyltransferase GliM. Aside from spirocyclic **15a/b**, compounds **14a/b** are the only *gliZ*-dependent metabolites that occur as a pair of epimers, likely as a result of deprotonation/enolization at C-6. Oxidation at C-6, perhaps involving *gliC* or *gliF*, could occur independently from hydroxylation of N-1; however, sulfurization at C-6 could also be accomplished via dehydration of a hydroxamic acid intermediate followed by sulfurization of the resulting imine, as had been proposed previously on the basis of synthetic studies[21] and a shunt metabolite detected in a Δ*gliG* strain.[20] This mechanism is also suggested by the lack of *N*-hydroxylated or methoxylated compounds other than the C-6 non-sulfurized **14a/b**. Release and methylation of the bis-3,6-disulfurized dipeptide would then produce compound **11**.

As a next step, the disulfurized dipeptide appears to undergo epoxidation of the phenyl ring by one of two putative cytochrome P450 monooxygenases, GliC or GliF. The relative configurations observed for compound **4** strongly suggest that this oxidation step is not entirely stereoselective and produces both the (13*S*,14*R*)- and (13*R*,14*S*)-diastereomers (Figure 4). Nucleophilic opening of the (13*S*,14*R*)-diastereomer by the C-3 amino group could lead to formation of the pyrrolidine ring of gliotoxin, whereas nucleophilic attack by the C-3 thiol results in formation of the thiophane ring in **4**. Alternatively, the phenyl ring is oxidized to form the *ortho*-substituted phenol found in

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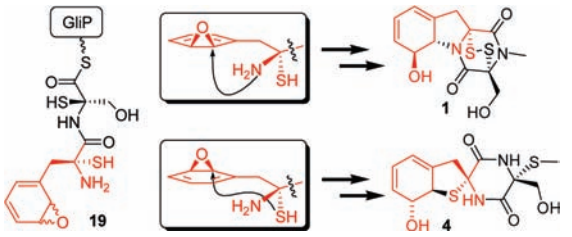

Figure 4. Different configurations of putative epoxide intermediate **19** result in formation of either gliotoxin (**1**) or spirocyclic **4**.

compound **13**, perhaps via the shown epoxide intermediate. The biosyntheses of **13**, spirocyclic compound **4**, and the gliotoxins **1**−**3** and **8** are completed via diketopiperazine formation and *S*-methylation (in the case of **4** and **13**) or *N*-methylation, possibly involving *gliN*, and epidithio bridge formation via GliT in the case of the EPTs.[10a] Lastly, compounds **16** and **17**, which both lack oxidation at C-6, appear to be derived from epoxidation of an intermediate oxidized only at C-3, followed by pyrrolidine and diketopiperazine formation. As the relative configuration at C-3 in **16** is opposite to that of C-3 in all identified C-3-sulfurized compounds, the C-3-OH group in **16** could be derived from substitution of a thiol or methylsulfanyl group. Elimination of water from **16** would form a dihydroindole that could easily aromatize to form **17**.

Additional studies will be needed to test and further expand this model, to clarify the mechanism of sulfur incorporation,[20] and to determine whether tethered intermediates or diketopiperazines are the substrates of the *gli*-encoded oxidases and methyltransferases. Furthermore, variation of growth conditions could induce biosynthesis of additional *gliZ*-dependent metabolites.

In conclusion, our comparison of the WT and Δ*gliZ* metabolomes via DANS revealed nine new compounds featuring several unexpected structural motifs, despite the fact that *A. fumigatus*'s metabolome, and specifically gliotoxin and its associated biosynthetic genes' role in virulence, had already been studied extensively. In particular, DANS facilitated detection of minor or unstable metabolites (e.g., **4** and **13**) missed by conventional analysis. Further investigations of the role of the *gli*-cluster in *A. fumigatus* virulence may benefit from the expanded knowledge of *gli*-associated structures and help clarify the biological roles of the newly identified compounds. Finally, our results suggest that the use of NMR-based comparative metabolomics for the examination of orphan PKS/NRPS gene clusters in microorganisms can significantly accelerate discovery of new structures and biosynthetic annotation.

■ ASSOCIATED CONTENT

Supporting Information. Experimental procedures, construction of mutants, NMR spectra for pool 2, HPLC chromatograms, spectroscopic data, and complete ref 1a. This material is available free of charge via the Internet at http://pubs.acs.org.

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