Transcription factor VdCmr1 is required for pigment production, protection from UV irradiation, and regulates expression of melanin biosynthetic genes in Verticillium dahliae

Yonglin Wang, Xiaoping Hu, Yulin Fang, Amy Anchieta, Polly H. Goldman, Gustavo Hernandez and Steven J. Klosterman

Abstract

Verticillium dahliae is a soilborne fungus that causes vascular wilt diseases on numerous plant species worldwide. The production of darkly melanized microsclerotia is crucial in the disease cycle of V. dahliae, as these structures allow for long-term survival in soil. Previously, transcriptomic and genomic analysis identified a cluster of genes in V. dahliae that encodes some dihydroxynaphthalene (DHN) melanin biosynthetic pathway homologues found in related fungi. In this study, we explored the roles of cluster-specific transcription factor VdCmr1, as well as two other genes within the cluster encoding a polyketide synthase (VdPKS1) and a laccase (VdLac1), enzymes at initial and endpoint steps in DHN melanin production. The results revealed that VdCmr1 and VdPKS1 are required for melanin production, but neither is required for microsclerotia production. None of the three genes were required for pathogenesis on tobacco and lettuce. Exposure of ΔVdCmr1 and wild-type strains to UV irradiation, or to high temperature (40°C), revealed an approx. 50% reduction of survival in the ΔVdCmr1 strain, relative to the wild-type strain, in response to either condition. Expression profiles revealed that expression of some melanin biosynthetic genes are in part dependent on VdCmr1. Combined data indicate VdCmr1 is a key regulator of melanin biosynthesis, and that via regulation of melanogenesis, VdCmr1 affects survival of V. dahliae in response to abiotic threats. We conclude with a model showing regulation of VdCmr1 by a high osmolarity glycerol response (Hog)-type MAP kinase pathway.

INTRODUCTION

The fungus Verticillium dahliae causes economically important vascular wilt diseases on more than 200 plant species worldwide [1]. The list of plant species affected by V. dahliae is continually expanding as new hosts are identified [2]. V. dahliae is difficult to control, owing in part to the production of melanized resting structures, known as microsclerotia, which can survive for years in the soil [3].

Fungal dihydroxynaphthalene (DHN) melanin is composed of polymerized phenolic or indolic compounds, and its biosynthesis was originally discovered in V. dahliae [4]. DHN-melanin biosynthesis begins with a polyketide synthase (PKS) that catalyses the conversion of acetyl-CoA to 1,3,6,8-tetrahydroxynaphthalene (1,3,6,8-THN). Through a series of downstream reactions catalysed by reductases and dehydratases, 1,8-DHN is produced [4–6].

Melanin has a protective role against UV irradiation in the microsclerotia of V. dahliae, and melanin deposition may further provide protection against temperature extremes, enzymatic lysis, nutrient deprivation and fungicidal activities [4]. The appearance of melanin is tightly coupled with latter stages of microsclerotial development in V. dahliae, and its very appearance implies microsclerotia maturation [7, 8]. Thus, melanin is vitally important to the production of functional microsclerotia. Understanding the genetics and molecular mechanisms that regulate melanin biosynthesis can expand our insights into microsclerotia formation and may lead to novel control measures to counter the threat of Verticillium wilt. Mutants of melanin biosynthesis have been characterized to some extent in V. dahliae [9, 10], including recent studies on molecular genetic analyses of VaygI, a putative enzyme-encoding gene that catalyses an initial step of the melanin biosynthesis [11] and VdPKS1, a...
PKS necessary for melanin production [12]. However, we lack a thorough understanding of the genetic network that regulates melanin biosynthesis in V. dahliae, especially from a putative cluster of melanogenesis-related genes previously identified [7].

The availability of the V. dahliae genome has facilitated genome-scale investigations [13], including those examining the molecular genetic basis to melanin biosynthesis [7, 8, 11, 12]. Analyses of the genomic sequence of V. dahliae have revealed highly homologous gene sets that are known to contribute directly to melanin biosynthesis in other fungi, in addition to orthologues of other signalling components necessary for melanin biosynthesis. Prominent among the latter findings, mitogen-activated protein kinases (MAPKs) control melanin biosynthesis in V. dahliae. Orthologues of the high osmolarity glycerol (HOG) response MAPK pathway, including VdHog1 [14], VdPbs2 [15] and VdMsb [16], are all involved in melanin biosynthesis signalling since each of the gene replacement mutants for each of these strains is melanin deficient, and known melanin biosynthetic gene orthologues were substantially downregulated in VdHog1 and VdPbs2 mutants. Several transcription factors were recently shown to regulate melanin biosynthesis, such as VdMcm1 [17], VdCmr1 [18] and Vta2 [19]. These studies have strengthened understanding of the regulation of melanin biosynthesis in V. dahliae. However, with the exception of the PKS encoding gene, VdPKS1 [12], genes that directly participate in melanin biosynthesis have not been systematically characterized in V. dahliae [13].

Expression of melanin biosynthetic genes in fungi is regulated in part by Cmr1 type transcription factor orthologues, found within secondary metabolism clusters of genes in some plant pathogenic fungi, such as Magnaporthe oryzae, Cochliobolus heterostrophus, Alternaria brassicicola and Botrytis cinerea [20–25]. The role of Cmr1 is important for DHN melanin production, as mutants of Cmr1 and its corresponding homologues typically lack pigmentation, or have an atypical colour [25], indicating that the function of Cmr1 homologues is conserved in fungi. Structurally, Cmr1 possesses two Cys,His, zinc finger domains and one Zn(II), Cys6, binuclear cluster domain, near its N-terminus, and this structure is also highly conserved.

Our previous transcriptomic studies of microsclerotia formation have shown that melanogenesis-associated genes, i.e. tetrahydroxynaphthalene reductase and scytalone dehydratase, were clearly upregulated in developing microsclerotia [7, 8]. Strikingly, genomic analysis of these differentially expressed melanogenesis-associated genes revealed a 48.8 kilobase-long cluster, which is believed to be a gene cluster in part responsible for melanin biosynthesis in V. dahliae [7]. Furthermore, a gene encoding a Cmr1 orthologue, an important regulator of melanin biosynthesis, is located within this cluster, and upregulated during microsclerotia formation as well. However, the role of the Cmr1 homologue and how this homologue may regulate gene expression to activate melanin biosynthesis, microsclerotia formation and pathogenicity have not been elucidated in V. dahliae. Mutation of one of the genes encoding a PKS (VdPKS1, VDAG_00190) was recently examined, revealing that this gene is required for melanin production in V. dahliae, and also for full virulence of the pathogen in cotton [12].

The objectives of the current study were to explore whether melanin biosynthesis and/or pathogenicity is dependent on VdCmr1. Secondary objectives included examination of whether VdCmr1 regulates gene expression of melanin-associated genes, and also whether two additional melanin biosynthetic homologue gene mutants characterized in this study are pathogenic. The results showed that VdCmr1 is required for melanin biosynthesis and microsclerotia formation, and that VdCmr1 regulates expression of genes scattered throughout the genome of V. dahliae that are associated with melanin biosynthesis. We determined definitively that melanogenesis-associated genes in V. dahliae, including VdCmr1, VdPKS1 and a laccase-encoding gene, VdLac1, are not required for pathogenicity on tobacco and lettuce. Based upon the current and previously published data, we propose a model regulatory pathway for melanin biosynthesis to further study melanin biosynthesis in relation to microsclerotia formation and pathogenicity.

METHODS

V. dahliae strains and growth condition

The fungal strain VdLs.17 [26], originally isolated from lettuce, was used as the wild-type and recipient strain in this study to introduce genetic mutations. All strains were regularly cultured on potato dextrose agar (PDA) plates at 25 °C. Cultures were maintained long-term in closed vials on PDA, or as −80 °C stocks in 20 % glycerol. Antibiotic-resistant strains were grown on PDA amended with hygromycin B (25 µg ml⁻¹) or gentamicin (50 µg ml⁻¹). Cultures were grown for 1 month before harvesting.

Targeted gene deletions

For these studies, we used the Broad Institute V. dahliae gene identification numbers, and corresponding functional annotations and sequences [27]. The deletion constructs for the knockout of gene VDAG_00189 (VdLac1) and VDAG_00190 (VdPKS1; [12]) were used in Agrobacterium tumefaciens-mediated transformation (ATMT) of VdLs.17 to obtain independent mutant strains. For constructing VdLac1or VdPKS1 gene deletions, a 5 µl BP clonase reaction included 15–20 ng of co-purified PCR flank products, 60 ng of pA-Hyg-OSCAR [28], 60 ng of pOSCAR and 1 µl BP clonase II enzyme mix (Invitrogen). The BP reaction was carried out at 25 °C for 16 h and terminated using 0.5 µl proteinase K (20 µg µl⁻¹). This generated the final marker vector named as pOSCAR-190 or pOSCAR-189. The reaction mixture was then used to transform E. coli competent cells by standard heat shock methods. Plasmid was co-puriﬁed using the CWBIO EndoFree Plasmid Mdi Kit (Cwbio-tech) and digested with Kpn1 and HindIII to verify deletion
construct structure. ATMT procedures followed the method described [29]. Individual V. dahliae transformants were transferred to PDA plates supplemented with hygromycin B (50 µg ml\(^{-1}\)) and 200 µM cefotaxime. Hygromycin B-resistant transformants were single-spore purified and screened by PCR amplification to identify gene-replacement mutants. Primer pairs were applied to identify gene-replacement mutants, with the hygromycin B resistance gene-specific primers and VdLac1 and VdPKSI gene-specific primers (Table S1, available in the online version of this article).

To delete VDAG_00195 (VdCmr1) in the genome of V. dahliae, a split-marker method was applied similar to that previously described [14]. First, approximately 1.5 kb of upstream (5') and downstream (3') flanking sequences of VdCmr1 were amplified with primer pairs PL62/PL695 and PL696/PL65, respectively. Then, the geneticin-resistance cassette was amplified with the Geneticin/Geneticinrev primers for deletion, which include approximately 20 bp that overlaps with the 5' and 3' flanking sequences, respectively. The two deletion cassettes resulting from fusion PCR with primer pairs PL62/Geneticinrev and Geneticinfor/PL65 (Table S1) were used for protoplast transformation procedures following the method described by Wang et al. [14]. The transformants were selected on TB3 medium with 50 µg ml\(^{-1}\) geneticin.

Screening of all knockouts was initially performed with those primer sets for each gene listed in Table S1. The Southern blot analyses were performed (Figs S1 and S2) to confirm the homologous recombination event of the three genes using a DIG High Prime DNA Labeling and Detection Starter kit according to the manufacturer’s instructions (Roche). Probes were labelled in PCR profiles of 95°C for 2 min, followed by 40 cycles of 95°C for 30 s, 60°C 30 s, 72°C 1 min for, with a final 7 min extension at 72°C. The 50 µl reaction volumes included 5 µl of 10× PCR buffer (with MgCl\(_2\)), 5 µl DIG labelling mix (diluted 0.6 µl 10× PCR DIG Probe synthesis mix in 20.5 µl 10× dNTP mix), 1 µl enzyme mix (Expand Hi Fidelity Taq, Roche), 250 pg plasmid containing the appropriate construct, and 200 nM of each primer. Restriction digestions of the DNA from mutant and wild-type strains were carried in 50 µl reaction volumes with 2 µl of the appropriate enzyme, and 5 µg DNA, unless indicated otherwise. DNA products were ethanol-precipitated and re-suspended in 20 µl of water, and loaded alongside 5 µl DIG-labeled DNA Molecular Weight Marker II (Roche) in a 0.8% agarose gel, run at 60 V for 3.5 h. Gels were transferred to PVDF membrane (BioRad) overnight in 10× SSC, with 10 min depurination, 30 min denaturation and 30 min neutralization steps. Fig. S1(a) shows confirmation of the knockout of VdCmr1. Fig. S2 provides detail on the knockouts of genes VdPKSI and VdLac1.

The VdCmr1 complemented strain was confirmed as shown by expression of a 191 bp cDNA product (Fig. S1b), and this complemented strain was referred to as VdCmr1_C. The VdCmr1 sequence in this study was complemented with both the VDAG_00194 plus the VDAG_00195 sequence because homology searches and previous evidence indicated that these two sequences together encoded the single transcription factor VdCmr1 (Fig. 1, Table 1 and Duressa et al. [7]). Additional sequences available [30] enabled the extension of primers into the 3' flanking region of VdCmr1 to obtain the full-length approx. 5.6 kb fragment used for complementation of strain VdCmr1 (Fig. S1b).

### Exposure to UV irradiation and high and low temperatures

Conidial suspensions of each strain were spread onto potato dextrose agar (PDA; Fisher Scientific) amended with streptomycin (50 µg ml\(^{-1}\)), kanamycin (50 µg ml\(^{-1}\)) and tetracycline (12.5 µg ml\(^{-1}\)) and incubated at 25°C for 2 weeks. The fungus/agar mixture was removed from the plates, suspended in phosphate buffer (0.01 M pH 7.0) and blended in a Waring blender for three 10 s pulses. Conidia and very small hyphal and agar fragments were removed by filtering through Miracloth (22 µm pore size; Fisher Scientific). Material retained on the filter was re-suspended in phosphate buffer and sonicated with a Vibra-Cell probe sonicator (Sonics) for four 2 s pulses, followed by centrifugation for 5 min at 600 g, which pelleted the microsclerotia below a layer of agar which was easily removed by pipetting. The microsclerotial pellets were then dried at room temperature and ground with a mortar and pestle, and filtered again with Miracloth (22 µm pore size). Microscopic examination revealed enrichment in microsclerotia. Liquid suspensions of the microsclerotia-enriched cultures were made in 0.01 M phosphate buffer (pH 7.0) and adjusted to approximately 1×10\(^6\) propagules ml\(^{-1}\) based on dilution plating. There were four replicates per strain, and each replicate was serially diluted in five 10-fold increments, and used in experiments.

For UV light treatments, 100 µl of inocula from each of the dilutions, prepared as described above, were plated onto NP-10 [31]. With lids removed, plates were placed in a biosafety cabinet (Labconco Purifier Logic+) under UV light (253 nm) for 3 h, after which the lids were replaced and the plates were incubated for 2 weeks at 25°C. Colonies were enumerated and proportional germination was determined by comparing values obtained with the UV-irradiated cultures versus those without UV light treatment.

For low temperature treatment, nitrocellulose filters (Whatman 7141154) were soaked in 250 µl of inocula and dilutions, dried at room temperature and incubated at −20°C for 7 days. The filters were placed on NP-10 and incubated for 2 weeks at 25°C, after which the colonies were counted and relative germination determined as above.

For high temperature analysis, dilutions from each inoculum from each strain were plated onto NP-10, and incubated for 24 h at 40°C. The plates were transferred to an incubator at 25°C for 2 weeks, and proportional germination determined as above.
Proportional germination in the three treatments for fungal survival was determined by dividing c.f.u. ml\(^{-1}\) values obtained in each treatment replicate by those obtained following incubation of the same replicate dilutions at 25°C with no treatment. These proportional values were log-transformed and analysed by ANOVA (JMP 12.2), with Tukey’s HSD used for mean comparisons. The two experiments were analysed separately, as there was a statistically significant (\(P<0.05\)) effect of experiment in all three of the parameters measured.

**Nucleic acid manipulation and TaqMan assays**

Conidia were washed from membranes using 2 ml of distilled water and a cell spreader. The membranes containing hyphae were ground to a fine powder using liquid nitrogen in a mortar and pestle. An RNeasy Plant Mini kit (Qiagen, La Jolla, CA) was used to extract nucleic acids from 100 mg of the powder and the extraction steps included the 56°C incubation and DNAse I (Qiagen, La Jolla, CA) on-column digestion. Extractions were further treated with TURBO DNAse (Ambion, Austin, TX) at 37°C for 30 min after extraction. RNA quality was checked using the Nanodrop (Thermo Scientific, Wilmington, DE) and quantified using a Qubit Fluorometer (Invitrogen, Carlsbad, CA). The RNA (250 ng) was reverse transcribed by denaturing at 65°C with 0.5 μg Oligo d(T)\(_{15}\) and 0.77 mM dNTPs for 5 min, chilling on ice for at least 5 min and incubating at 55°C for 45 min with 200 U SuperScript III (Invitrogen, Carlsbad, CA), 1X first strand synthesis buffer, 5 mM DTT and 40 U RNASin (Promega, Madison, WI) in 20 μl reactions followed by 70°C for 15 min to inactivate the reverse transcriptase. Four 20 μl reverse transcription reactions per sample were combined to use as a template. A volume of 2 μl cDNA was used as a template in 20 μl reactions containing: 1X Gene Expression Master Mix (ABI, Carlsbad, CA) and 1X Custom TaqMan Gene Expression Assay (900 nm primer, 200 nM Taqman probe) (ABI, Carlsbad, CA) labelled with FAM and quenched with NFQ. The reaction profile included an initial 95°C 10 min step followed by 40 cycles of 95°C 15 s and 60°C 30 s. Resulting quantification cycle values were analysed using REST 2009 software [32], enabling computation of statistical significance of relative expression analyses. Products were cloned into pCR 4.0-TOPO (Invitrogen) and sequenced to confirm primer specificity. The resulting plasmids were used in a five-step 10-fold dilution standard curve (5 ng to 500 pg) to test the efficiency of the TaqMan Gene Expression Assays. All assays were >90% efficient. There were two biological replicates per treatment, and each sample collected was run in triplicate in single probe reactions.

**Pathogenicity assay**

For pathogenicity assays, conidia were harvested from 15-day-old cultures grown in liquid CM by filtration through
two layers of Miracloth and resuspended at 10^6 conidia/ml in sterile distilled water. For each experiment, 10 two-week-old Nicotiana benthamiana or 10 two-week-old lettuce plants were inoculated with each of the *V. dahliae* genotypes by dipping the roots for 5 min in inoculum, and transferring the plants into potting soil in cups in a greenhouse. There were two replicate treatments, with each treatment containing 20 plants. The height of tobacco seedlings was measured at 45 dpi. Vascular discoloration symptoms of lettuce seedlings inoculated with the above strains were observed by microscopy for conidiophore structure and microsclerotia development showed that the melanogenesis-related genes were upregulated in microsclerotia-producing cultures (Fig. 1b). Examination of this cluster in detail revealed that this cluster comprises two transcription factor encoding genes (*VDAG_00192* and *VDAG_00195; VdCmr1*). *VDAG_00192* encodes a putative transcription factor, while *VdCmr1* encodes a homologue of the transcription factor CMR1 previously reported to be involved in fungal melanin synthesis [20, 21]. Phylogenetic analysis revealed that VdCmr1 exhibited a high degree of amino acid sequence similarity to those CMR1 orthologues from other fungi (Fig. 1c).

**Functional analyses of VdCmr1 and two additional genes of a putative melanin biosynthetic gene cluster in *V. dahliae***

To examine the function of genes in the putative melanin biosynthetic gene cluster in *V. dahliae*, gene deletion mutants were prepared for several key genes through homologous recombination and replacement with a gene conferring hygromycin B resistance (for *VdLac1* and *VdPKSI* or gentamicin resistance (for *VdCmr1*). Screening of the transformants by PCR using gene-specific primers (Table S1) and confirmation of the knockouts by Southern blot revealed that the three genes were successfully replaced (Figs S1 and S2). The *VdLac1* deletion mutant (*VdLac1-5KO*), ectopic strain (*VdLac1-7Ect*), *VdPKSI* deletion mutant (*VdPKSI-7KO*), ectopics strain (*VdPKSI-14Ect*), *VdCmr1* deletion mutant (*VdCmr1-9KO*) and ectopic strain (*VdCmr1-11Ect*) were selected for further comparisons with the wild-type strain VdLS17.

All mutants showed normal growth rate and morphology, as examined by microscopy for conidiophore structure and conidia. However, both *VdPKSI* and *VdCmr1* deletion mutants failed to melanize in culture while the wild-type strain VdLS17 and the *VdLac1* deletion mutant formed melanized microsclerotia (Fig. 2a). Therefore, *VdPKSI* and

---

**RESULTS**

**Identification of VdCmr1**

We have previously created several transcriptomic databases to elucidate molecular processes of microsclerotia biogenesis and melanin synthesis in *V. dahliae* [7, 8, 17]. The timing of melanin production relative to microsclerotial development and in multiple expression libraries was previously characterized by Xiong et al. [8]. Analysis of these libraries revealed that a secondary metabolism gene cluster encodes some melanin biosynthetic gene homologues that are upregulated during microsclerotia formation. The cluster spans a 48.8 kb region in the *V. dahliae* genome and contains melangenesis-related enzyme-encoding genes, such as THN reductases (*VDAG_00183; VDAG_03665*), PKs (*VDAG_00190; VdPKSI*), and a laccase (*VDAG_00189; VdLac1*) (Fig. 1a). Some of genes were likely misassembled, such as *VDAG_00184* that appears to be a truncated PKS (Table 1). In addition, the expression profile of this cluster of genes during microsclerotia development showed that the melanogenesis-related genes were upregulated in microsclerotia-producing cultures (Fig. 1b). Examination of this cluster in detail revealed that

### Table 1. Known and putative melanin biosynthetic genes of *V. dahliae*

<table>
<thead>
<tr>
<th>Gene ID/putative function in <em>V. dahliae</em></th>
<th>Name in <em>V. dahliae</em> reference</th>
<th>Function† (orthologous fungal proteins)</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>VDAG_03665/tetrahydroxynaphthalene reductase</td>
<td>…………</td>
<td>Potentially both tri- and tetra-hydroxynaphthalene reductase [41, 42]</td>
<td>…………</td>
</tr>
<tr>
<td>VDAG_03193</td>
<td>…………</td>
<td>Serylamine dehydratase [43]</td>
<td>…………</td>
</tr>
<tr>
<td>VDAG_00190/conidial yellow pigment biosynthesis PKS</td>
<td>VdPKSI; this study [12]</td>
<td>Polyketide synthase [45]</td>
<td>…………</td>
</tr>
<tr>
<td>VDAG_00194/VDAG_00195/transcription factor Pgi1/CMR1</td>
<td>VdCMR1; this study</td>
<td>Transcription factor [20–22, 25]</td>
<td>…………</td>
</tr>
<tr>
<td>VDAG_00189/laccase</td>
<td>VdLac1; this study</td>
<td>Multicopper oxidase/laccase [46]</td>
<td>…………</td>
</tr>
<tr>
<td>VDAG_00184/amino acid adenylation‡</td>
<td>…………</td>
<td>Non-ribosomal polyketide synthase [47]</td>
<td>…………</td>
</tr>
<tr>
<td>VDAG_00183/versicolorin reductase‡</td>
<td>…………</td>
<td>Tetrahydroxynaphthalene reductase [41]</td>
<td>…………</td>
</tr>
<tr>
<td>VDAG_00190/tetrahydroxynaphthalene reductase§</td>
<td>…………</td>
<td>Tetrahydroxynaphthalene reductase [41]</td>
<td>…………</td>
</tr>
<tr>
<td>VDAG_00034/laccase</td>
<td>…………</td>
<td>Multicopper oxidase/laccase [46]</td>
<td>…………</td>
</tr>
</tbody>
</table>

*The gene ID and functional annotations of these genes in *V. dahliae* are derived from original Broad Institute annotations [27].
†Functions ascribed based upon known fungal orthologues.
‡The gene ORF is only partial as it was misannotated in the genome of VdLS17.
§The putative tetrahydroxynaphthalene reductase encoding gene *VDAG_05181* resides in a previously described lineage specific region of VdLS17 [27], and is presumably the result of a gene duplication specific to VdLS17, and not in the core genomes of all *V. dahliae* strains.
VdCmr1 are essential for appropriate melanization in V. dahliae, but not VdLac1. Microscopic analyses revealed that both VdPKS1 and VdCmr1 deletion mutants produced microsclerotia, but these microsclerotia were devoid of the dark melanization observed in the microsclerotia of the wild-type VdLs.17 strain, or either of the ectopic insertion strains (Fig. 2b).

**VdCmr1 regulates the expression of genes involved in melanin biosynthesis**

Since VdCmr1 is a homologue of the fungal CMR1 transcription factors, we investigated the impact of VdCmr1 on the transcription of melanin-associated genes in V. dahliae by relative expression analyses in TaqMan assays. The expression level of genes associated with DHN melanin biosynthesis located in the cluster revealed that transcripts of the PKS-encoding genes VDAG_00184 and VdPKS1 (VDAG_00190) were significantly (P<0.05) reduced in the VdCmr1 deletion mutants. Transcripts of VdLac1 were upregulated in the mutants, relative to the levels observed in the wild-type VdLs.17 strain (Fig. 3a), suggesting VdCmr1 upregulates VDAG_00184 and VdPKS1, and inhibits expression of VdLac1. The expression level of the transcription factor encoding gene VDAG_00192, within the same gene cluster, was not significantly up or downregulated in both VdCmr1 deletion mutants (Fig. 3a). Relative expression levels of additional homologues of melanin biosynthetic-related genes VDAG_00034 (laccase), VDAG_03665 (scytalone dehydratase), VDAG_04954 (PKS Vayg1), VDAG_05181 (THN reductase), were analysed in two VDAG_00195 deletion mutants (Fig. 3a). Among these genes, VDAG_00034 (laccase) and VDAG_05181 (THN reductase) were not differentially expressed (P<0.05) in the VdCmr1 deletion mutant background (Fig. 3b). The THN-reductase-encoding gene VDAG_03665 was over 100-fold reduced in expression in the VdCmr1 deletion mutants (Fig. 3b). Separate replicate TaqMan assays revealed that VDAG_00183, encoding a THN reductase, was also not differentially expressed in the VdCmr1 deletion mutant strains (data not shown).

We also examined a small subset of genes differentially expressed in microsclerotial development [7], but which are thought to have roles independent of melanin production such as VDAG_00261 (encoding an IDI-3 homologue), and VDAG_03079 (catalase). VDAG_08741 encoding the endo-chitinase VDECH [33] was significantly (P<0.05) upregulated in the VdCmr1 deletion mutants (Fig. 3b), suggestive of inhibition during microsclerotial development, corroborating previous findings [7].

![Fig. 2. Effect of three gene deletions on melanin production and colony morphology in V. dahliae. (a) Colony appearance of V. dahliae wild-type strain (VdLs17), VdLac1 deletion mutant (ΔVdLac1) and ectopic strain EVdLac1 VdPKS1 deletion mutant (ΔVdPKS1) and ectopic strain (EVdPKS1), and VdCmr1 deletion mutant (ΔVdCmr1), ectopic strain (EVdCmr1) and the ΔVdCmr1-complemented strain (VdCmr1_C) on PDA medium after a 2 week incubation at 25°C with top and bottom views. (b) Examination of the microsclerotia produced by the wild-type strain VdLs.17 relative to the microsclerotia produced by the corresponding gene knockout strains for VdCmr1 and VdPKS1. The restoration of pigment production is observed for strain VdCmr1_C. Scale bars=20 µm.](image-url)
Together, these expression data suggest that \textit{VdCmr1} controls gene expression necessary for melanin biosynthesis in \textit{V. dahliae}, and also the expression of two of those genes implicated in microsclerotia development. \textit{VdPKS1}, \textit{VdLac1} and \textit{VdCmr1} are dispensable for pathogenicity

We also assayed two of the deletion mutants prepared in this study in plant pathogenicity assays using lettuce and tobacco. On tobacco, \textit{VdCmr1} and \textit{VdPKS1} mutant strains were as virulent as the wild-type strain \textit{VdLs.17}, as was evident in the comparisons of plant height (Fig. 4a). As compared to the mock-inoculated plants, those plants inoculated with either the \textit{ΔVdPKS1}, \textit{ΔVdCmr1} or wild-type strain \textit{VdLs.17}, showed clear wilt symptoms on tobacco (Fig. 4) and lettuce (Fig. S3). Mutant and \textit{VdLs.17}-inoculated plants also showed indistinguishable levels of stem vascular discolouration in tobacco (Fig. 4b). Thus, genes \textit{VdPKS1} and \textit{VdCmr1}, while critical to melanogenesis, play no role in pathogenesis in tobacco or lettuce, in strain \textit{VdLs.17}.

**Effect of UV irradiation and high and low temperature on the survival of \textit{VdPKS1} and \textit{VdCmr1} mutants**

There were no significant differences in survival (as determined by c.f.u. measurements) among the different strains examined in response to low temperature incubation ($P=0.53$ and $P=0.18$ for experiments 1 and 2, respectively) (Fig. 5).

In response to UV irradiation, a significant ($P<0.0001$) reduction in survival was observed in both the \textit{ΔVdPKS1} and \textit{ΔVdCmr1} strains in comparison to the wild-type strain (Fig. 5).

In response to high temperature, the \textit{ΔVdCmr1} strain showed significantly ($P<0.0001$) lower survival than the wild-type strain in response to high temperature incubation. The \textit{ΔVdPKS1} strain exhibited significantly ($P<0.0001$) higher survival as compared with the wild-type strain following this treatment (Fig. 5).

**Model of the genetic regulation of \textit{VdCmr1}-dependent melanin production**

We explored the regulation of gene expression dependent on \textit{VdCmr1} within the putative melanin biosynthetic cluster of genes in \textit{V. dahliae}, and also some that were expressed at higher levels in microsclerotia production [7], and outside of the cluster. Combined with our previous results of regulation of genes involved in melanin production [14–16], we propose that \textit{VdCmr1} acts as a general regulator of melanin biosynthesis and the cluster of encoded proteins in which it resides is a major contributor to melanin biosynthesis.
Previously, several upstream regulators of VdCmr1 have been identified, including the HOG signalling pathway (Ssk2-Pbs-Hog1 cascade), MADS-box transcription factor VdMcm1 [17] and Vayg1 [11]. Transcriptional analysis of genes involved in melanin biosynthesis revealed that VdCmr1 regulates expression of genes located in this cluster which contributes to melanin production, while also controlling expression of genes at other locations in the genome, some of which may or may not be involved in melanogenesis. Some of these genes were identified previously as differentially expressed during microsclerotia production, and thought to be important for development (Fig. 6). In summary, our results support a genetic network for melanin production in V. dahliae via VdCmr1, in which the Ssk2-Pbs-Hog1 cascade, VdMcm1, Vayg1 and unknown regulators activate VdCmr1 to control transcriptional and post-transcriptional processes of melanin biosynthesis and microsclerotial development in V. dahliae.

DISCUSSION

Melanized microsclerotia formation is critically important in the life cycle and disease spread of V. dahliae [2]. The aim of the current study was to examine the function of the homologue of fungal CMR1, located within a 48.4 kb gene cluster that encodes several other melanogenesis-related genes identified previously in V. dahliae [7, 8]. Based on related DHN melanin biosynthetic pathways in fungi, the PKS enzyme is one of the initial enzymes of the pathway, while the laccase is thought to be a terminal enzyme, acting at the last step of DHN melanin production. The VdCmr1 transcription factor and two other genes (VdLac1 and VdPKSI) were deleted by homologous recombination and...
gene replacement and provided analyses of the phenotypes of these mutants in culture, and in pathogenicity assays. Collectively, our study expands the understanding of the genetics of melanin biosynthesis, its regulation and its relationship to virulence in \textit{V. dahliae}.

DHN melanin is a ubiquitous pigment in the fungal kingdom. A transcription factor involved in DHN melanin biosynthesis, known as CMR or BMR, has been characterized in several fungi, such as \textit{M. oryzae} [22], \textit{C. heterostrophus} [21], \textit{A. brassicicola} [23] and \textit{B. cinerea} [24]. Loss of function of CMR1 homologues, or some of their downstream affected genes in these fungi, typically results in melanin deficiency. We identified \textit{VdCmr1} in this study, as a regulator of melanin biosynthesis in \textit{V. dahliae}. In addition, four melanin biosynthesis-associated gene homologues are located together in a 48.4 kb region in strain VdLs.17, and their organization in the cluster is similar to that observed in \textit{C. heterostrophus} [21]. When \textit{VdLac1} and \textit{VdPKS1} were separately deleted in this cluster in \textit{V. dahliae}, we found that the \textit{VdPKS1} was required for melanin production, but not the laccase. Similarly, Zhang \textit{et al.} [12] also found that \textit{VdPKS1} was required for pigment production in a cotton isolate of \textit{V. dahliae}. With regard to the laccase, a close laccase paralogue encoded by \textit{VDAG}_00034 is outside of the melanin gene cluster, and potentially has an overlapping function that compensated for the \textit{VdLac1} mutation in this study. However, as shown in this study, \textit{VDAG}_00034 was not significantly differentially expressed in the \textit{VdCmr1} mutant strains, suggesting that this gene is not under regulatory control of \textit{VdCmr1}.

The first enzyme in the DHN melanin biosynthesis pathway is PKS. The putative gene cluster containing \textit{VdCmr1} also encodes two PKS genes (\textit{VDAG}_00184 and \textit{VdPKS1}; Table 1). The cluster also contains genes encoding other enzymes involved in melanin biosynthesis, such as THN reductase (\textit{VDAG}_00183) and laccase (\textit{VdLac1}). \textit{VdCmr1} regulates transcription of PKS, laccase, THN reductase-encoding genes. We speculate that \textit{V. dahliae} employs a melanin biosynthetic pathway encoded in part by the 48.8 kb cluster of the secondary metabolism-related genes shown in Fig. 1, and those genes scattered throughout the genome, allowing for their individual regulation by \textit{VdCmr1}. Intriguingly, we also noted that \textit{VdCmr1} regulates the expression of two genes scattered throughout the genome that were previously characterized as up or downregulated in microsclerotia-producing cultures of \textit{V. dahliae}. Since microsclerotial development and melanin production are tightly linked, as previously observed [7, 8], \textit{VdCmr1} may act as a master regulator that controls non-essential aspects of microsclerotial development (Fig. 6), to appropriately coordinate the inclusion of DHN melanin at the later stages of microsclerotial maturation.

The relationship between melanin and virulence in fungi seems at times paradoxical. That is, melanin-deficient mutants are commonly identified as non-pathogenic or as reduced in virulence, not only in \textit{V. dahliae}, but also in other fungi. In this study, pathogenicity assays showed that melanin-deficiency was not associated with reduced virulence as has been reported for the APSES transcription factor \textit{Vst1} mutant of \textit{V. dahliae} [34], or related mutants in other fungi [21]. Many studies have revealed a linkage between \textit{V. dahliae} melanin-deficient strains and reduced virulence or loss of pathogenicity [11, 14, 15, 18] but often many of these types of mutants compromised in melanin production are also defective in microsclerotia production [13]. Based on these accumulated findings, we speculate that DHN melanin alone produced through a \textit{VdCmr1}-dependent pathway is not required for pathogenicity in \textit{V. dahliae}. Interestingly, in support of this conclusion, the \textit{VdCmr1} homologue \textit{Amr1} actually suppresses virulence in \textit{Alternaria brassicicola} [23].

The recent work of Zhang \textit{et al.} [12] showed that deletion of \textit{VdPKS1} resulted in a slight but significant reduction in virulence in the \textit{V. dahliae} cotton isolate V592, although the \textit{VdPKS1} mutant nevertheless caused disease symptoms on cotton. Since the mutant was produced in the cotton isolate V592, it is difficult to directly compare the results of the current study with those obtained by Zhang \textit{et al.} [12]. Some genetic mutants of non-melanogenesis related genes in \textit{V. dahliae} show reduced virulence on one host, but not on another host [27]. It is clear, however, that some pigment mutants of \textit{V. dahliae} can also be compromised in virulence. For example, \textit{Vagl1}, encoding the homologue of fungal enzymes involved in polyketide chain shortening to 1, 3, 6, 8-THN (Table 1), is necessary for melanin and microsclerotia production, and for full virulence in \textit{V. dahliae} [11].

Many studies support a role of fungal DHN melanin in protection from abiotic stresses such as UV irradiation and temperature extremes [35–38]. This current study provides...
further direct evidence of the important role of DHN melanin in the protection of \textit{V. dahliae} from UV irradiation. In this study, both the \DeltaVdPKS1 and \DeltaVdCmr1 strains were compromised in survival rate following UV irradiation, relative to the wild-type strain. Moreover, the \DeltaVdCmr1 strain exhibited a decreased survival rate following exposure to high temperature. However, the \textit{VdPKS1} mutant strain showed increased survival relative to the wild-type strain \textit{VdLs}.17. The increased survival of the \DeltaVdPKS1 strain at the high temperature (60°C) examined is difficult to explain, but may be due to a pleiotropic effect, as suppressor mutations for temperature sensitivity affecting cell wall biogenesis have been identified [39]. Nonetheless, both the \DeltaVdPKS1 and \DeltaVdCmr1 strains, which are compromised in melanin production, showed significant reductions in their survival rates following UV irradiation.

Accumulating evidence indicates MAPK cascades are tightly coupled to the activation of VdCmr1. The HOG signalling pathway positively regulates VdCmr1 [14, 15]. Phenotypes of VdHog1 and VdPbs2 kinase deletion mutants, which are similar to those of the VdCmr1 mutant suggest that VdCmr1 may be a novel downstream regulator of a HOG-like pathway that controls melanin biosynthesis. However, it is unclear how VdHog1 interacts with VdCmr1 at this time. Intriguingly, other genes such as VdMcm1 and Vayg1 also regulate expression of VdCmr1 and are also important for full virulence [11, 17]. Hence, there appears to be a complex interplay between melanin production and virulence in fungi. Taken together our results provide evidence of the association of VdCmr1-dependent melanin production and signalling pathways in \textit{V. dahliae}.

We have demonstrated that while melanin production is VdCmr1-dependent in \textit{V. dahliae}, VdCmr1 is clearly not required for microsclerotia production and pathogenicity on tobacco and lettuce. The VdCmr1 transcription factor also controls the expression of a number of melanin biosynthesis-associated genes. As a critical regulator of melanin production, VdCmr1 may integrate different signalling pathways to balance melanin production and development. The data presented in this study will facilitate future

*Fig. 6.* Schematic diagram depicting VdCmr1-dependent DHN melanogenesis in \textit{V. dahliae}. Key proteins involving the DHN melanogenesis pathway are depicted from the initial acetyl-CoA or malonyl-CoA precursors through production of DHN melanin [4]. The Ssk2-Pbs2-Hog1 signalling cascade is a regulator of melanin biosynthesis in \textit{V. dahliae} [14]. The transcription factor VdMcm1 and the polyketide chain shortening enzyme Vayg1 also modulate DHN melanogenesis. Our work identified several key genes that contribute to DHN melanin biosynthesis and that are regulated by VdCmr1. Some of these genes are found within the cluster enriched in DHN melanin biosynthetic genes within the \textit{V. dahliae} genome. The non-melanin synthesis-related genes, up or downregulated during microsclerotial development [7], are regulated by VdCmr1 as demonstrated in this study; these genes VDAG_03079 (catalase) and VDAG_08741 VDECH (endochitinase, VDAG_08741) also reside outside of the gene cluster enriched in melanin biosynthetic genes. *VDAG_03665* may catalyse both \textit{T4HN} and \textit{T3HN} reductase steps based upon the strong homology of VDAG_03665 to the THR1 protein of \textit{Colletotrichum lagenarium}, which can catalyse both \textit{T4HN} and \textit{T3HN} reductase steps [41].
evaluations of the melanin biosynthetic pathway and development in *V. dahliae*.

**Funding information**

The research was supported in part by the National Natural Science Foundation of China (31570436 and 31371888). Mention of trade names or commercial products in this publication is solely for the purpose of providing specific information and does not imply recommendation or endorsement by the United States Department of Agriculture (USDA). USDA is an equal opportunity provider and employer.

**Conflicts of interest**

The authors declare that there are no conflicts of interest.

**References**

34. Sarmiento-Villamil JL, Garcia-Pedrajas NE, Baeza-Montañez L, Garcia-Pedrajas MD. The APSES transcription factor Vst1 is a key regulator of development in microsclerotium- and resting

Edited by: S. Pöggeler and V. J. Cid

Five reasons to publish your next article with a Microbiology Society journal
1. The Microbiology Society is a not-for-profit organization.
2. We offer fast and rigorous peer review – average time to first decision is 4–6 weeks.
3. Our journals have a global readership with subscriptions held in research institutions around the world.
4. 80% of our authors rate our submission process as ‘excellent’ or ‘very good’.
5. Your article will be published on an interactive journal platform with advanced metrics.

Find out more and submit your article at microbiologyresearch.org.