

1 **Transcription factor VdCf2 regulates growth, pathogenicity**
2 **and the expression of a putative secondary metabolism gene**
3 **cluster in *Verticillium dahliae***

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5 **Running Head:** Functions of VdCf2 in *Verticillium dahliae*

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18 drawing straws.

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SUPPLEMENTAL MATERIAL:

23 **Supplemental figures:**

Verticillium_dahliae L A T E D T S A T A T V L P K P D Q T A S S L F A L Q E P Q R S K S L K R T R E T T P T S F T S L V A G D Q P T I T G S P T K S A R L G L L
Drosophila_melanogaster M I K S T T N P Q E Q R L P R P E D Q S P - - - - - A P P P P P S S A T T S T A A P A T P T H Q V A T - - V I A N M D T L K T A F L P N L

Verticillium_dahliae N R R S P V P P L T G A A A L E D Q R R Q R E E E D A R A D P P G S S E N P S Q R I L S A L A G D A A S V M S R A S D A P Q A P T A S M D V
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Verticillium_dahliae P P P K A P P S V S I P L I N H A A T D T A E A S P Q S A T S A A S I G G T L V T A S P G P M E V D P S A N E Q A T P A H H S H A P D D K N
Drosophila_melanogaster - P K L S H R C F N C D E K F G N A V D L D E H H R L A H Q T P A F L S R C L M C S I Y G I H S A T Q Q P N E Y K C T Q C G S I C T T A M L

Verticillium_dahliae T P G S L S Y P P G S L H A S M M S A P P A R G M S F P M P S P G Q D S P G Q P G G K K H K C P Y C E T E F T R H H N L K S H L L T H S Q E K
Drosophila_melanogaster A A G Q Q - - - G F M E Q Q E A A V T P D D Q L P A M A P R D M R L T P E E Q - - - - - H H Q Q L Q A E H H H Q Q H Q Q Q Q Q Q

Verticillium_dahliae P F I C Q Q C D S R F R R L H D L K R H S K L H T G E K P H I C P K C N R K F A R G D A L A R H S K G A G G C A G R R S S M G S F G A V D
Drosophila_melanogaster Q Q Q Q E L L E Q Q Q R E M Q E Q A Q Q Q V H H H Q Q D Q L A G D Q V A L K V P P L T V K L N K N A N G G A I V S H P Q V I I K E E P L

Verticillium_dahliae G L D D S G M H D D S M T G V S Y G N D E G M T E E E R R H L S T P S I K A S H V P G S L E R P S G G L Y P P P P P Q D R G A S G S N T S P
Drosophila_melanogaster S L S D S G D V V N S V P V Y A I Q A N P G V P A P A S S G V L V G - - - T Q T V P A D L A H K I R H K C P D C R K T F K T P G - - - T L

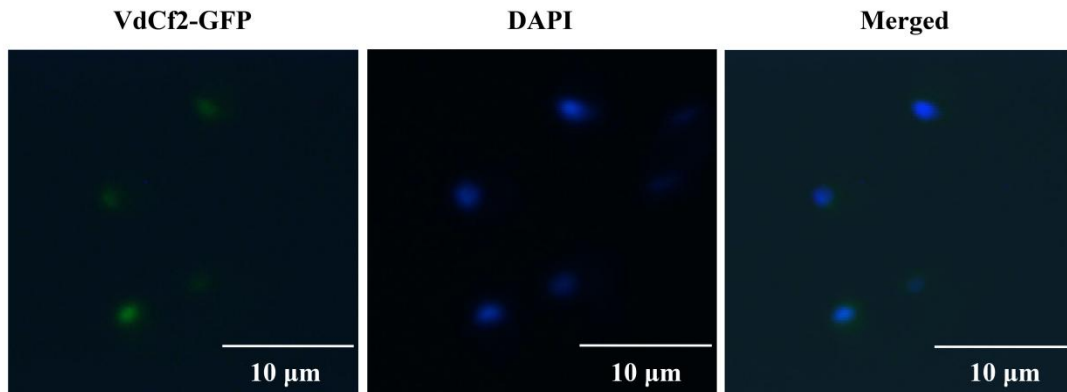
Verticillium_dahliae S M G N S M G G G H T P N T S L S S M P T S G A G S S M Y S Q G G T M T E S P K P L S P G A A H D G T G L S R Q R S P S L T Q Q F Q Q H F
Drosophila_melanogaster A M H R K I H T G E A D A T P K E R P Y T C S Y C G K S F T Q S N T L K Q H T R - I H T G E K P F R C G Y C G R - - A F T V K D Y L N K H L

Verticillium_dahliae G R R P S D R H T P P G T A S N S A P S A N G P P A R A S G S S H G G G A E N G G N M F A T D P G V W T Y I Q T L E T Q V K Q L S E N V A
Drosophila_melanogaster T T H T G E R P F H C G M C E K S F S V K D Y L T R H I R - - T H T G - - - - - E K P Y T C P Y C D K R F I T Q R S A L T V H T T

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25 **Figure S1.** Amino acid sequence alignment of VdCf2 in *V. dahliae* and Cf2 in *D.*

26 *melanogaster*.

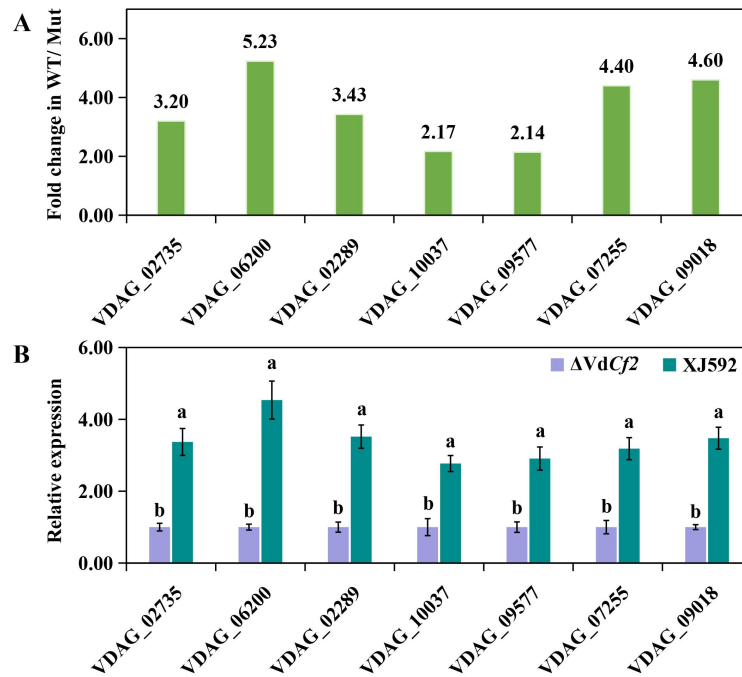


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28 **Figure S2.** The colocalization of VdCf2-GFP fusion protein with DAPI-stained

29 nucleus in *V. dahliae*.

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32 **Figure S3.** The RNA-seq data and RT-qPCR result had same expression tendency. **A.**

33 Fold change of seven up-regulated differentially expression genes in the mycelia of

34 XJ592 strain compared to that of $\Delta VdCf2$ strain according to RNA-seq analysis. WT

35 represents XJ592 strain and Mut represents $\Delta VdCf2$ strain. **B.** Expression pattern of

36 seven up-regulated differentially expression genes was quantified by RT-qPCR

37 experiment. The RNA sample was generated from remaining mycelia of

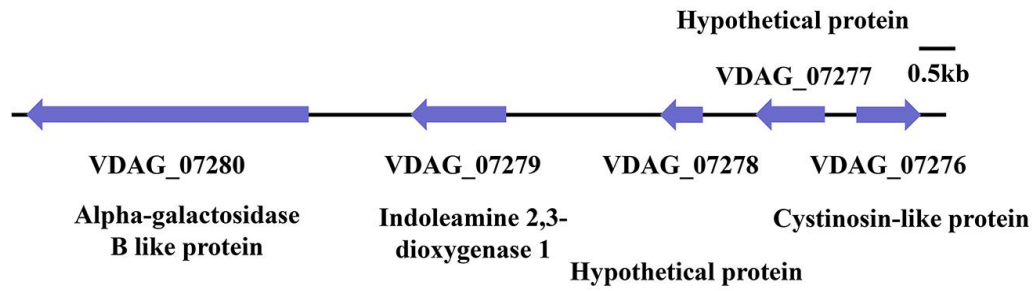
38 transcriptome sequencing. The β -tubulin gene (*VDAG_10074*) was used as internal

39 reference. Error bars indicate standard errors calculated from three replicates and

40 different letters represent statistical significance ($P = 0.05$) determined by Student t

41 test.

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44 **Figure S4.** Sequence pattern diagram. Schematic representation of gene position and
 45 direction in *Vd276-280* gene cluster. Arrows directions represent gene directions. The
 46 amino acid sequence of each gene in *Vd276-280* gene cluster was blast to its
 47 homologues in other *Verticillium* species to accomplish gene function annotation,
 48 respectively.

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