Fig. S3. FvCyp1, FvScp1, FvSel1 Protein blast results

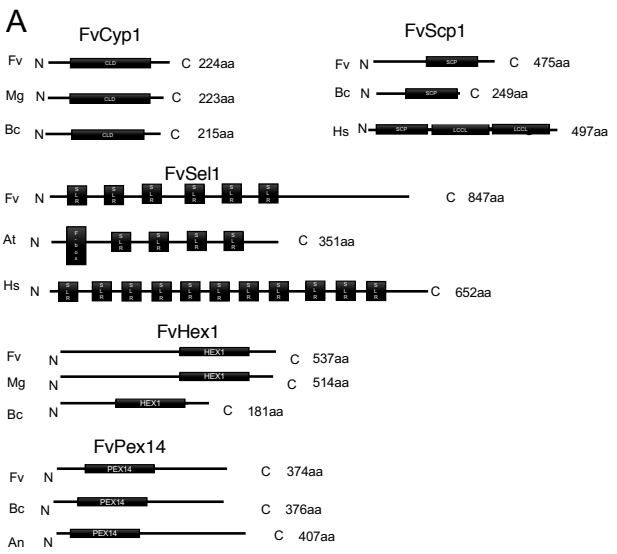

Fig. S3. Comparison of conserved domains in *F. verticillioides* (Fv), *Magnaporthe grisea* (Mg), *Botrytis cinerea* (Bc), *Homo sapiens* (Hs), *Arabidodpsis thaliana* (At) and *Aspergillus nidulans* (An). (A) Schematic representation of protein orthologues shows the location and alignment of conserved domains. Physical map of FvCyp1, FvScp1, FvSel1, FvHex1 and FvPex14 and their homologs showing putative domains (black box): cyclophilin-like domain (CLD) (PF04126), sperm-coating protein (SCP)-like extracellular protein domain (PF00188), Sel1-like repeat (SLR) (PF08238), Hex1(cd04469) and a Pex14_N (pfam04695). (B) Amino acid alignment of four fungal FvStp1 homologs by using CLUSTAL O (1.2.2) multiple sequence alignment.

B

FvCyp1

```
FV      MRPSLFKPLLPRHNCFSAARTSSSLPQLSNTI---------KSVRFFSASSAVMGNKVFF
Mg      MRTTLLRPLVPRQNIFSSSIPRTSFVKPNFVATPKSPINNTTRVRFYS--STMSKPNVFF
Bc      ---MLFV---PRT---ASALKSTSLPLLRNTFINNS--FTSISSRQFHASKSNMAIKTYF
            *:    **    :::  :*:     .              * :   .:    :.:*

FV      DIEWEGPVFQ-NGKPTSTVQSQRGRINFNLYDKEVPKTAENFRALCTGEKGF-GYKGSSF
Mg      DISFNGV---------------TKRVEFKLYDDVVPKTADNFRRLCVGEPGVGGYKDSGF
Bc      DVTWEGPVLDASGKPTSTVQEQAGRITFNLYDDVVPKTAENFRALCTGEKGF-GYAGSSF
        *: ::*                  *: *:***. *****:*** **.** *. **  *.*

FV      HRIIPDFMLQGGDFTRGNGTGGKSIYGEKFADENFKLTHDRPGLLSMANAGPNTNGSQFF
Mg      HRIIPDFMLQGGDFTRGNGTGGKSVYGEKFADENFQIKHTRPGLLSMANAGPNTNGSQFF
Bc      HRIIPQFMLQGGDFTRGNGTGGKSIYGEKFADENFERKHTRPGLLSMANAGPNTNGSQFF
        *****:******************:*********: .* **********************

FV      ITTVVTSWLNGRHVVFGEVADEESMNVVKALEATGSGSGAVKYQKRATIVDSGEL
Mg      ITTVKTSWLDGKHVVFGEVVSGFE-DVIKPIEALGSSSGTPK--TKVTIVNAGTV
Bc      VTTVVTSWLDGKHVVFGEVADDESLMIVKALEATGSGSGKVQYNKKPTIVKSGEL
        .*** ****.*.*******. . ::*.** **.** : :: ***.*:
```

FvScp1

```
Fv      ------------SGGDDLSLDGAYNTVMLAYHNI-----HRLNHSASALEWDDELAGYAE
Bc      LHVTTTVYPSTTLAPVPTATPTDYVSTALYHHNI-----HRANHSVPLLKWDTKLVASAQ
Hs      ----------ESHSRVRRAIPREDKEEILMLHNKLRGQVQPQASNMEYMTWDDELEKSAA
                  .    :          *  **      :     .   : ** :*   *

Fv      NTANGCVFEHDMNQGNGGYGQNLAS-WGATSDIDGLKNKAAAGGITNQWYNNEMANW--A
Bc      VLAATCKWGHSMNINGGGYGQNIAA-YGSTNAKALGANKEMAVAATDMWYNGEQPTYLPS
Hs      AWASQCIWEHGPTSLLVSIGQNLGAHWGRYRS---------PGFHVQSWYDEVK-DYTYP
          *  * : *  .    . ***:.: :*                .: **:     :

Fv      FYGQENP--PADMNIDLYGHFTQVVWKDSTKVGCATVKCPAG-TVLSF--PSWYTVCNYN
Bc      YYGKNN---PDLTTFEQWGHFSQMVWLGTNSVGCATQLCQPMDIWPSM--PAWYTVCNYS
Hs      YPSECNPWCPERCSGPMCTHYTQIVWATTNKIGCAVNTCRKMTVWGEVWENAVYFVCNYS
        : .: *   *   .     *::*:**  :..:***.  *       ..   : * ****.

Fv      PQGNFG----------------------------------------------------------
Bc      PPGNMGGQYGVNVFPPLRHPSVNV-----------------------VNA----------
Hs      PKGNWIGEAPYKNGRPCSECPPSYGGSCRNNLCYREETYTPKPETDEMNEVETAPIPEEN
        * **
```

FvSel1

```
Fv      LYMRSKWLEF-------------------------------------------------GK
At      -MKQRTWPC---------------------------------RSEGSRFSSLSF--LKP
Hs      INKRENLLEKKKNQRKIRIKGIQNKDILKRNKNHLQKQAEKNFTDEGDQLFKMGIKVLQQ
          : .

Fv      FGNRVDKREAYIGYKRAAEL--GHGR---------------------------------
At      H--DKDKRSRISSINKATAKSTTSSRSSSSSSSSRPPSNEFGDFSMLP-----------
Hs      SKSQKQKEEAYLLFAKAADM--GNLK----AMEKMADALLFGNFGVQNITAAIQLYESLA
             :*..      :*:       :

Fv      --------------SEYRMGMLYEQSNDMSKAK---------------EHYYRGLSLK--
At      ----------------YDILMKI--AA-----PF-----------------SHPNLQAA
Hs      KEGSCKAQNALGFLSSYGIGMEYDQAKALIYYTFGSAGGNMMSQMILGYRYLSGINVLQN
                       * : *    :                              .:

Fv      -------------------------DSASLYRMGMMSLLGQHGETKDYSTGLERIQAAADS
At      SLVCKSWRD--------AL-KPLRESMLLIRWGKKYKHGRGGVRANLDKALDSFLKGAMR
Hs      CEVALSYYKKVADYIADTFEKSEGVPVEKVSLGQLHLIGRKGLDQDYYKALHYFLKAAKA
                                      *     *: *   :  ..*. :  .*

Fv      SDEDAPQGAYVYGMLIGRDLPDITIPEGLLPNNPLTTKMYIEKSAYLGFAKAQLKMGQAY
At      ------------------------------------------------GSTLAMVDAGLVY
Hs      ------------------------------------------------GSANAMAFIGKMY
                                                        * : *    *  *

Fv      ELCQFGCDFNPSFSLHYYGLAAKQGLPEAALGVSRWFLFGYEGVFKKNESLAYKYAQEAA
At      WERG-----EKEKAVNLYRRASELGDAVGQCNLGIAYLQV----QPSNPKEAMKWLKQSA
Hs      LEGNAAVPQNNATAFKYFSMAASKGNAIGLHGLGLLYFHGKGVP--LNYAEALKYFQKAA
                  :   :.. :  *:. *   .   :.  ::         *   * *: :::*

Fv      AAKLPTGEFALGYYNEIGIHVEKSLSEARKWYQLAADHGNQDALGRLDSLDEN-------
At      ENGYVRAQYQLALCLHHGRVVQTNLLEATKWYLKAAEGGYVRAMYNISLCYSVGEGLPQN
Hs      EKGWPDAQFQLGFMYYSGSGIWKDYKLAFKYFYLASQSGQPLAIYYLAKMYATGTGVVRS
              .:: *.     *  : ..   * *::  *:: *   *:  :
```

FvHex1

```
Fv      ----------------------APSVVVQSMLGPVFKQYRVLDMQEGSIVAMTETGDVKQ
Mg      RYLGVDLFTKELREESSSISTPSPSVVVQTMCGPVFKQYRVLDMQAGHIVAMTETGDVKQ
Bc      RYLGVDLFTRQLNEESSFIANPSPSVVVQTMLGPVFKQYRVLDLQDHSVVAMTETGDVKQ
                           :******:* ***********:*   :***********

Fv      GLPVIDQSNLYSRLSSAFESGRGSVRVLVLNDGARELAVDMKVIHGSRL
Mg      NLPVSEQSNLYERLQRAFESGRGSVRALVVSDNGRELVCDMAVLHGSRL
Bc      AIPVLDQSNLWTRLKEAFEGGRGSIRIMVVADGGREIAVDMKTVHGSRL
         :** :****: **. ***.*****:* :*: * .**:. ** .:*****
```

FvPex14

```
Fv      ------------------------------------------------------DAVRHAPHE
Bc      MSDSDSEPKSPGVPAWQRRGEEEQSSEPQDAAIEPPSRAAVLEQARKFLEEDEVRNASTD
An      MSD---PTSKPSIPKWQQQDSGSSPSTSDEKNADYGDRSTLLEQASSFLQDDSIRDAPTD
                                                          * :*.*  :

Fv      KKVEFLKSKGIDEAEIHALLGQDESTTETEAPIPGTTSS-------YAPTP---T-----
Bc      KKIAFLESKGLDGDDIQELLGVSRNNEATNTSITEVKSP-------DPKTQ---PQSLT-
An      RKIAFLESKGLTDTEIDGLLGVSRNAEASSGSGSGGDNSVEERKSTSAPSTETFNPAVSK
        :*: **:***:   :*. *** ...   :.        .           :

Fv      --ETLPP---TPASHPPVDRPPVVTYPEFLAKAPRPPPLVTKERLFNALYAVTGLSTLIY
Bc      --RHSPPSTQPSYAQIPREQAPIITYPEFLVQPSAATPLITKHRLLTTLYLFGSLSFLLY
An      PTPPTPSSNSRPVNLTPRDVPPIITYPEFLLHQSKPPPLVTLRSVLYTLYTAAGLGATLY
           *          * :  *::****** :     **:* . :: :**   .*.  :*

Fv      GTSRYVIRPMVDSQAE-------------------------------------------
Bc      GTNTFLIRPMLNTLTESRLSLSSATLNNLQKLIHKLENSVSEIPPTYHHHKSL-QSEYLD
An      GAGEYLVKPMLAALTDARHDLAQTTEENLKKLNEKLELNVSQLPPSLITKSTASVGDATE
        *:  ::::**: : ::
```