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Corrigendum

Corrigendum to “Molecular dialogues between *Trichoderma* and roots: Role of the fungal secretome” [Fungal Biol Rev 32 (2018) 62–85]

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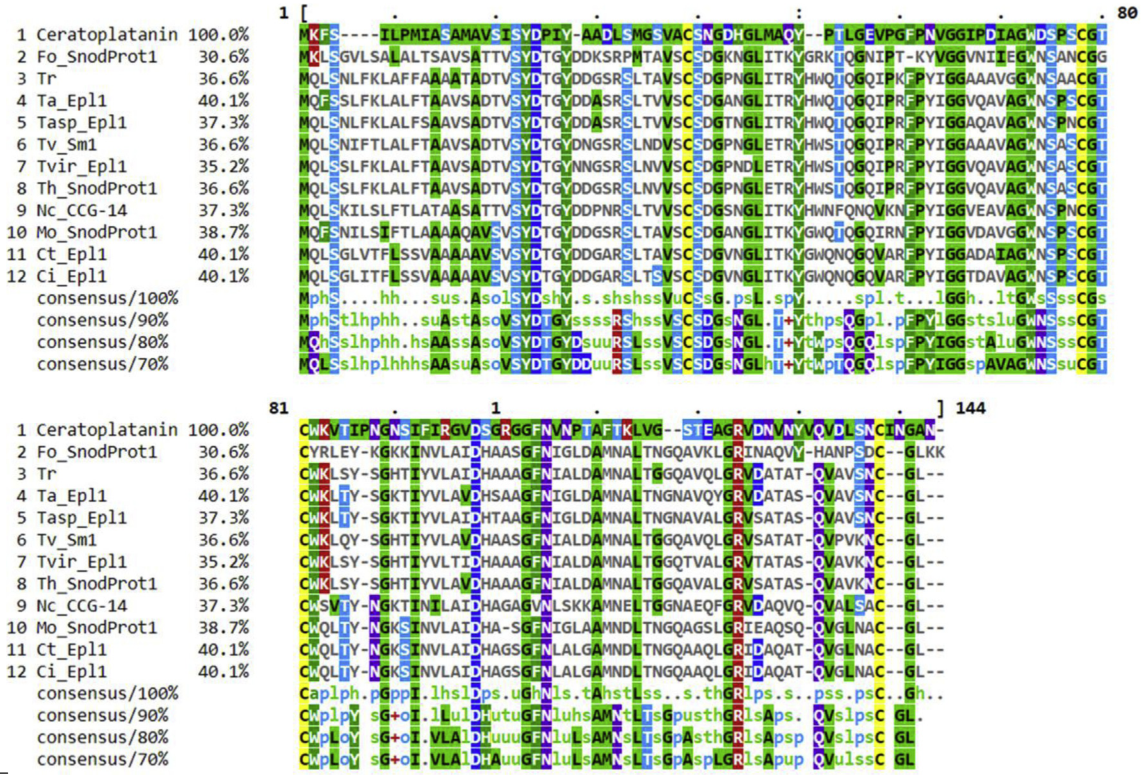
When this paper was first published the artwork for Figures 5 and 6 were switched in error. They are correctly printed below:



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                              1 [         .         .         .         .         :         .         .         . 80
 1 Ceratoplatanin 100.0%       MKFS----ILPMIASAMAVSISYDPIY-AADLSMGSVACSNGDHGLMAQY--PTLGEVPGFPNVGGIPDIAGWDSPSCGT
 2 Fo_SnodProt1    30.6%       MKLSGVLSALALTSAVSATTVSYDTGYDDKSRPMTAVSCSDGKNGLITKYGRKTQGNIPT-KYVGGVNIIEGWNSANCGG
 3 Tr              36.6%       MQLSNLFKLAFFAAAATADTVSYDTGYDDGSRSLTAVSCSDGPNGLITRYHWQTQGQIPKFPYIGGAAAVGGWNSAACGT
 4 Ta_Epl1         40.1%       MQFSSLFKLALFTAAVSADTVSYDTGYDDASRSLTVVSCSDGANGLITRYHWQTQGQIPRFPYIGGVQAVAGWNSPSCGT
 5 Tasp_Epl1       37.3%       MQLSNLFKLALFSAAVSADTVSYDTGYDDASRSLTVVSCSDGTNGLITRYHWQTQGQIPRFPYIGGAQAVAGWNSPNCGT
 6 Tv_Sm1          36.6%       MQLSNIFTLALFTAAVSADTVSYDTGYDNGSRSLNDVSCSDGPNGLETRYHWSTQGQIPRFPYIGGAAAVAGWNSASCGT
 7 Tvir_Epl1       35.2%       MQLSSLFKLALFTAAVSADTVSYDTGYNNGSRSLNVVSCSDGPNDLETRYHWSTQGQIPRFPYIGGVQAVAGWNSASCGT
 8 Th_SnodProt1    36.6%       MQLSSLFKLALFTAAVSADTVSYDTGYDDGSRSLNVVSCSDGPNGLETRYHWSTQGQIPRFPYIGGVQAVAGWNSASCGT
 9 Nc_CCG-14       37.3%       MQLSKILSLFTLATAASATTVSYDTGYDDPNRSLTVVSCSDGSNGLITKYHWNFQNQVKNFPYIGGVEAVAGWNSPNCGT
10 Mo_SnodProt1    38.7%       MQFSNILSIFTLAAAAQAVSVSYDTGYDDGSRSLTAVSCSDGANGLITKYGWQTQGQIRNFPYIGGVDAVGGWNSPSCGT
11 Ct_Epl1         40.1%       MQLSGLVTFLSSVAAAAAVSVSYDTGYDDGARSLTAVSCSDGVNGLITKYGWQNQGQVARFPYIGGADAIAGWNSPSCGT
12 Ci_Epl1         40.1%       MQLSGLITFLSSVAAAAAVSVSYDTGYDDGARSLTSVSCSDGVNGLITKYGWQNQGQVARFPYIGGTDAVAGWNSPSCGT
   consensus/100%              MphS....hh...sus.AsolSYDshY.s.shshssVuCSsG.psL.spY.....spl.t...lGGh..ltGWsSssCGs
   consensus/90%               MphStlhphh..suAstAsoVSYDTGYssssRShssVSCSDGsNGL.T+YthpsQGpl.pFPYlGGstsluGWNSssCGT
   consensus/80%               MQhSslhphh.hsAAssAsoVSYDTGYDsuuRSLssVSCSDGsNGL.T+YtWpsQGQlspFPYIGGstAluGWNSssCGT
   consensus/70%               MQLSslhplhhhsAAsuAsoVSYDTGYDDuuRSLssVSCSDGsNGLhT+YtWpTQGQlspFPYIGGspAVAGWNSsuCGT

                             81         .         1         .         .         .         .    ] 144
 1 Ceratoplatanin 100.0%       CWKVTIPNGNSIFIRGVDSGRGGFNVNPTAFTKLVG--STEAGRVDNVNYVQVDLSNCINGAN-
 2 Fo_SnodProt1    30.6%       CYRLEY-KGKKINVLAIDHAASGFNIGLDAMNALTNGQAVKLGRINAQVY-HANPSDC--GLKK
 3 Tr              36.6%       CWKLSY-SGHTIYVLAIDHAAAGFNIALDAMNALTGGQAVQLGRVDATAT-QVAVSNC--GL--
 4 Ta_Epl1         40.1%       CWKLTY-SGKTIYVLAVDHSAAGFNIGLDAMNALTNGNAVQYGRVDATAS-QVAVSNC--GL--
 5 Tasp_Epl1       37.3%       CWKLTY-SGKTIYVLAIDHTAAGFNIGLDAMNALTNGNAVALGRVSATAS-QVAVSNC--GL--
 6 Tv_Sm1          36.6%       CWKLQY-SGHTIYVLAVDHAASGFNIALDAMNALTGGQAVQLGRVSATAT-QVPVKNC--GL--
 7 Tvir_Epl1       35.2%       CWKLSY-SGHTIYVLTIDHAAAGFNIALDAMNALTGGQTVALGRVTATAS-QVAVKNC--GL--
 8 Th_SnodProt1    36.6%       CWKLSY-SGHTIYVLAVDHAAAGFNIALDAMNALTGGQAVALGRVSATAS-QVAVKNC--GL--
 9 Nc_CCG-14       37.3%       CWSVTY-NGKTINILAIDHAGAGVNLSKKAMNELTGGNAEQFGRVDAQVQ-QVALSAC--GL--
10 Mo_SnodProt1    38.7%       CWQLTY-NGKSINVLAIDHA-SGFNIGLAAMNDLTNGQAGSLGRIEAQSQ-QVGLNAC--GL--
11 Ct_Epl1         40.1%       CWQLTY-NGKSINVLAIDHAGSGFNLALGAMNDLTNGQAAQLGRIDAQAT-QVGLNAC--GL--
12 Ci_Epl1         40.1%       CWQLTY-NGKSINVLAIDHAGSGFNLALGAMNDLTNGQAAQLGRIDAQAT-QVGLNAC--GL--
   consensus/100%              Caplph.pGppI.lhslDps.uGhNls.tAhstLss..s.thGRlps.s..pss.psC..Gh..
   consensus/90%               CWplpY sG+oI.lLulDHutuGFNluhsAMNtLTsGpusthGRlsAps. QVslpsC  GL.
   consensus/80%               CWpLoY sG+oI.VLAlDHuuuGFNluLsAMNsLTsGpAsthGRlsApsp QVslpsC  GL
   consensus/70%               CWpLoY sG+oI.VLAlDHAuuGFNluLsAMNsLTsGpAspLGRlsApup QVulssC  GL
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Fig. 5 – Sequence alignments of ceratoplatanin and Sm1/Epl1 orthologs. The sequences used to generate the alignment

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1749-4613/

are: six *Trichoderma* sequences (Tr, *T. reesei* XP_006970000.1; Ta_Epl1, *T. atroviride* XP_013937770; Tasp_Epl1, *T. asperellum* CAL80753.1; Tv_Sm1, *T. virens* XP_013959806.1; Tvir_Epl1 *T. viride* CAL80756; Th_Snod-Prot1, *T. harzianum* KKP05841.1), ceratoplatanin itself (*Ceratocystis platani* AGQ22226.1), and predicted Sm1/Epl1 orthologs from other Sordariomycetes (Fo_SnodProt1, *Fusarium oxysporum* XP_018240137; Nc_CCG-14, *Neurospora crassa* XP_958708.1; Mo_SnodProt1, *Magnaporthe oryzae* XP_003710181.1; Ct_Epl1, *Colletotrichum tofieldiae* KZL71046.1; Ci_Epl1, *Colletotrichum incanum* KZL84107.1). The alignment was generated by MUSCLE at www.phylogeny. fr and plotted by EMBO MView online tool at http://www.ebi.ac.uk/Tools/msa/mview/; colour coding is by identity and amino acid chemical properties.

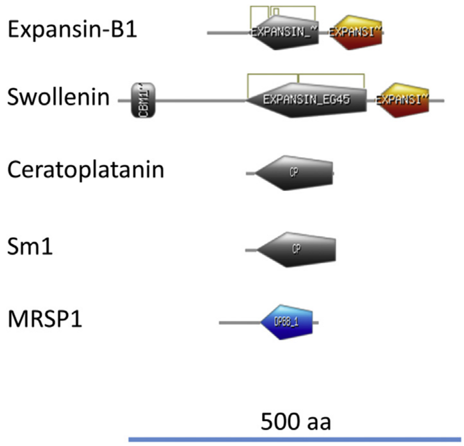

Fig. 6 – Similarity of some *Trichoderma* secreted proteins to expansins. Domain analyses of: a typical plant expansin (*Zea mays* NP_001288510.1 expansin-B1 precursor), *T. reesei* swollenin (CAB92328.1), ceratoplatanin (*Ceratocystis fimbriata*, AGQ22233.1), *T. virens* Sm1 (XP_013959806.1), and *T. virens* MRSP1 (XP_013952052.1). The maps are shown in descending order with respect to their expansin-like properties, from a plant expansin down to MRSP1, whose only hint of similarity to expansins is the double j/b-barrel (DPBB_1) fold (expansin Domain 1, grey). Prediction of domain structures: for expansin B1 and swollenin, Prosite (http://prosite.expasy.org/); for ceratoplatanin and Sm1, Pfam (CP domain is apparently not in the Prosite database); for MRSP1, coordinates generated by JGI's automated pipeline were taken from the protein page (Prosite and Pfam scans did not detect the DPBB_1 fold; which was originally detected by a combination of other methods (see Horwitz *et al.* (2013)). Combined graphics were generated by the Prosite domain drawing tool (via ExPasy).