

Mutations and differential transcription of mating-type and pheromone receptor genes in *Hirsutella sinensis* and the natural *Cordyceps sinensis* insect–fungi complex

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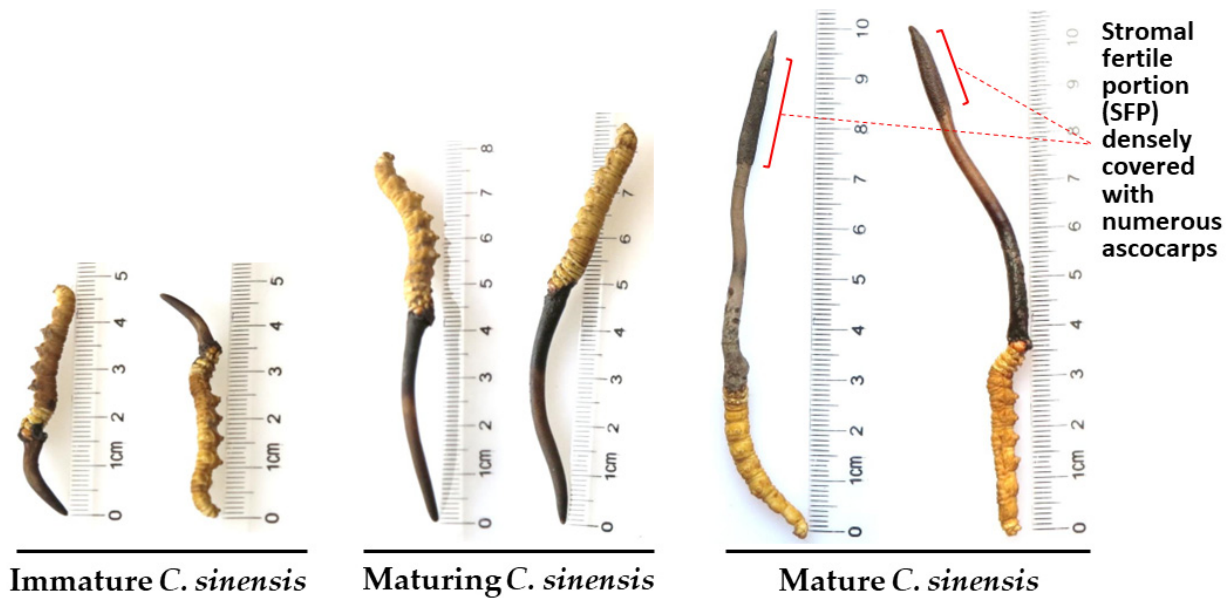


Figure S1. Images of immature, maturing, and mature natural *C. sinensis* insect-fungal complexes (modified from [50]). The right two pictures show mature *C. sinensis* specimens with the expanded stromal fertile portion (SFP) close to the tip of the *C. sinensis* stroma, which is densely covered with numerous ascocarps.

JQ325153 1 CCGTGCACCATGGCCAAATCCCATCAACATGATTCCCAATCCTCAGTGGAAATGCGACTGACTACGAAGCGATCTGG 76
 FJ654187 1 TCAG----- 80
 JQ325237 1 ----- 76
 KM197536 1 ----- 76
 GCQL01020543 1157 TCAG----- 1071
 OSIN7649 1 ----- 66
 (translation=) M A N P I N M I P N P Q W N A T D Y E A I W
 (variate aa=) I
 JQ325153 77 AAAGGCCTCGAGGCACAGGTCAATCCTTTCTCGCAGATTCTCTGCCTGGAGGGGGATT-----TCCGCCAGCTCGACGATGC 156
 FJ654187 81 ----- 160
 JQ325237 77 -----T-----C-----T-----GC----- 156
 KM197536 77 -----T----- 156
 GCQL01020543 1077 ----- 998
 OSIN7649 67 ----- 146
 (translation=) K G L E A Q V N P F S Q I L C L E G D F F R Q L D D A
 (variate aa=) G
 JQ325153 157 TCGGAAGCTGTTTCATTGCTCGGAAGCTCATGTAAAGTTTGAAGTTTACCACCTTCCCTAATCGAATCTAC 236
 FJ654187 161 -----TAA-----TGA-----TAA----- 240
 JQ325237 157 -----C-----TAA-----TGA-----TAA----- 236
 KM197536 157 -----A-----C-----TAA-----TGA-----TAA----- 236
 GCQL01020543 997 ----- 968
 OSIN7649 147 ----- 176
 (translation=) A K L F I A R K L M
 JQ325153 237 AGGGAACACGTTCAGGAGTCAGTCCGTGTATGTCAATGACGGCAATGGACCCGATCGCGTCTACCTTGGAGCTCCCGACA 316
 FJ654187 241 ----- 320
 JQ325237 237 ----- 316
 KM197536 237 ----- 316
 GCQL01020543 967 ----- 890
 OSIN7649 177 ----- 254
 (translation=) E H V Q E S V L Y V N D G N G P D R V Y L G A P R H
 JQ325153 317 TTTTGTCTGTTGGTGGTGGCATGATTCTCCAGATTCTGGCTACGCGCCGTACTGGATCCGACGTTCCGTGTGCGAAAGTCG 396
 FJ654187 321 -----C----- 400
 JQ325237 317 ----- 396
 KM197536 317 ----- 396
 GCQL01020543 889 ----- 810
 OSIN7649 253 ----- 334
 (translation=) F V V G G G M I L Q I S G Y A P Y W I R R S V S K V
 (variate aa=) A
 JQ325153 397 TTACTGCAACAGTGCTCGCGCCTCCCTCGCCCAAGGATATCAAGATCCCTCGTCTCCCAACGCGTACATCTTGTACCGT 476
 FJ654187 401 ----- 480
 JQ325237 397 -----G-----T----- 476
 KM197536 397 -----C-----G----- 476
 GCQL01020543 809 ----- 730
 OSIN7649 335 ----- 414
 (translation=) V T A T V L A P P S P K D I K I P R P P N A Y I L Y R
 JQ325153 477 AAGGAGCGCCACCATCATGTCAAGGATGCAAATCCTGGCATCAGCAACACGAGATTGTAAGTTTTCATAGCCGCTCCTC 556
 FJ654187 481 -----T-----T----- 560
 JQ325237 477 ----- 556
 KM197536 477 ----- 556
 GCQL01020543 739 ----- 672
 OSIN7649 315 ----- 472
 (translation=) K E R H H H V K D A N P G I T N N E I
 (variate aa=) Y
 JQ325153 557 CTTTCTGCCATCGTGTCTTAATGTCTCTCTCAGCCCAAATCTTGGGCAAGCTTGAACATGGAGTCGAACGACGTCAGA 636
 FJ654187 561 ----- 640
 JQ325237 557 ----- 636
 KM197536 557 -----A-----A----- 636
 GCQL01020543 671 ----- 625
 OSIN7649 473 ----- 519
 (translation=) S Q I L G k A W N M E S N D V R
 (variate aa=) I
 JQ325153 637 CAGAAGTACAAGGACATGTCTCAGCAAGTCAAGCAAGCTCTCCTGGAGAAGCACCCAGACTACCAAGTATAAACCGCGTCG 716
 FJ654187 641 -----C----- 720
 JQ325237 637 -----C----- 716
 KM197536 637 -----G-----C----- 716
 GCQL01020543 624 -----C----- 545
 OSIN7649 520 -----C----- 599
 (translation=) Q K Y K D M S Q Q V K Q A L L E K H P D Y Q Y K P R R
 (variate aa=) R
 JQ325153 717 TCCTTGCGAGCGCGCGCGCGTCTGTCGCCAGTCCGAACCAAACCCGAAGCAATCTACGTCGAGAAATGCCGCTACTA 796
 FJ654187 721 -----A-----A-----A-----C----- 800
 JQ325237 717 -----A-----A-----C----- 796
 KM197536 717 ----- 796
 GCQL01020543 544 ----- 465
 OSIN7649 600 ----- 679
 (translation=) P C E R R R R R R A S P N Q N P K Q S T S R N A A T
 JQ325153 797 GGGACGCCGCGATCTCGAGTGAAGATACTTCTACTGCCACCGGAGATACCAACACTGCGAATGGTTTCTGAGCGTCTG 873
 FJ654187 801 -----TAA-----TGA-----TGA----- 877
 JQ325237 797 -----A-----G-----A-----A----- 873
 KM197536 781 -----CC-----GG-----A-----TAA----- 873
 GCQL01020543 464 -----CC-----GG-----TGA-----TGA-----AAC 391
 OSIN7649 664 ----- 750
 (translation=) R D A A I S S E D T S T A T G D T N T A N G F
 (variate aa=) N T G
 GCQL01020543 390 TTCTGCACTCTAGCACTGAGAATCACGTTCCCTCACGACAGCGACTGAAACTGAAAGTGAAGACGGTCCAAGGCACAAG 311
 GCQL01020543 310 CATAACGACAAGAAAATAAAAAAAAAAATAAGCAATCCTTCTTTTACAACACACGTTCTAGATGCGAATACATACCCCGA 231
 GCQL01020543 230 GCTCCAAAATTGAGACTCGAAATAGTGCATCGACCCCACTTCCGTACGATTACGAATCCGTTTACGAACACCATCAAA 151
 GCQL01020543 150 TATACCCCGCTGAAAACACCAAGTTTATCAAAGCAGTTACGAAGCTGCAAGAAGAAGAACACCAGATGGGCTTCCCCCGGC 71
 GCQL01020543 70 CCGAGCTGGCGCTTCAGGGGAGCGGCCAGGGTCACGCAGATAGTACATAGTTGCCGAAAAGGAG

Figure S2. Alignment of the MAT1-2-1 gene sequences with the transcriptome sequences obtained from *H. sinensis* Strain L0106 and natural *C. sinensis*. JQ325153, FJ654187, JQ325237 and KM197536 are the MAT1-2-1 gene sequences found in *H. sinensis* Strains GS09_121, CS2, XZ12_16, and XZ12_16, respectively [10,59]. GCQL01020543 is the transcriptome sequence obtained from the *H. sinensis* strain L0106 [52]. OSIN7649 is the metatranscriptome sequence obtained from natural *C. sinensis* collected from Deqin County, Yunnan Province, China [54]. The triplets shown in alternating brown and green indicate the open reading frame. The sequences in pink represent introns, and the underlined triplets “TAA” and “TGA” shown in blue are stop codons. The protein sequence was translated from the transcript sequences. The nucleotide and amino acid residues in red represent point mutations and variants, respectively. Hyphens indicate identical bases, and spaces denote unmatched sequence gaps.

KC437356 6530 ATGACGACAAGAAATGAGGTTATGCAGCGCTTGTCTTCTGTCCGAGCTGACGTTCTTCTGAACCTCCTCACGGACGATGC 6609
GAGW01008880
OSIN7648 1 ----- 80
(translation=) M T T R N E V M Q R L S S V R A D V L L N F L T D D A

KC437356 6610 AATTTTCCAGCTTGCCTCCCGATATCACGAATCGACGACAGAGCGCGACGTTCTTACACCCGTGAGCACCAGCAGCAT 6689
GAGW01008880 1129 ----- 160
OSIN7648 81 ----- 160
(translation=) I F Q L A S R Y H E S T T E A D V L T P V S T A A A

KC437356 6690 CTCGCGCCACTAGGCAGACCAAGAGCATCTTGTGATCGAGCGAAGCGACCTCTCAATGCCTTCATGGCATTCCGAAGT 6769
GAGW01008880 161 ----- 238
OSIN7648 161 ----- 238
(translation=) S R A T R Q T K E A S C D R A K R P L N A F M A F R

KC437356 6770 ATGTTTCATCTCTTTACGACGTTGAAGTGGCTGACACGGACATTCTAGGTTACTACTTGAAGCTGTTTCCCGACGTGC 6849
GAGW01008880 239 ----- 288
OSIN7648 239 ----- 288
(translation=) S Y Y L K L F P D V

KC437356 6850 AGCAGAAGACCGCTTCTGGGTTTCTCACCACCTTGTGGCACAAAGACCCGTTGAGAAACAAGTGGGCGCTGATTGCGAAG 6929
GAGW01008880 1129 ----- 1088
OSIN7648 289 ----- 348
(translation=) Q Q K T A S G F L T T L W H K D P F R N K W A L I A K

KC437356 6930 GTGTACTCCTTCGTGCGAGATCAGATTGGCAAGGACAAGTTTCTCTATCATATTTTCATGAGCCTTGCTTGTCTTACCAT 7009
GAGW01008880 1087 ----- 988
OSIN7648 359 ----- 428
(translation=) V Y S F V R D Q I G K D K V S L S Y F M S L A C P T M

KC437356 7010 GACCATCATCGAGCCCGCTGCGTACCTGAACGCGCTTGGGTGGTGTGTCCAAGATGACGACGCTGGATCGCAGAAGCTAT 7089
GAGW01008880 987 ----- 908
OSIN7648 429 ----- 508
(translation=) T I I E P A A Y L N A L G W C V Q D D D A G S Q K L

KC437356 7090 TCCAAGACGAATCTTCTGCAAACCTGGACCAGTCCAGCTTGCTCTCGGCGGAATACCCAGCACCAGAAATCGAACTCTTG 7169
GAGW01008880 907 ----- 828
OSIN7648 509 ----- 588
(translation=) F Q D E S S A N L D Q S S L L S A E Y P S T E I E L L

KC437356 7170 TCCGCCCTCGTCAACATTGGGTACTTTCCCGATCACGGCGCCGACCTTGTGGAGAGAATGGGATCCAGCCACAGTGGCAT 7249
GAGW01008880 827 ----- 748
OSIN7648 589 ----- 668
(translation=) S A L V N I G Y F P D H G A D L V E R M G S S H S G I

KC437356 7250 CATGGCTCCGCGTGCCGCAATTGCACTCCTCCAGTGTCTTACAGAAAGGAAAAGATCGATTTTCAACACAATCAGAA 7329
GAGW01008880 747 ----- 668
OSIN7648 669 ----- 748
(translation=) M A P R A A N C T P P V S Y T K E K I D F I N T I R

KC437356 7330 GCGATCCAGTTTCAAGCGACAAAGGAGATCCTCGGTGATTGCTACGATGAAACCACAATCAAGCTTCTGGGTGTCAAGTCA 7409
GAGW01008880 667 ----- 588
OSIN7648 729 ----- 828
(translation=) S D P V Q A T K E I L G D C Y D E T T I K L L G V K S

KC437356 7410 CACAATGTGGAGAGTGTGACTCCATCAGCACTTGTCCATGCAACGCGAATATCAGGCTCCGCGATTTTTTTATGACTA 7489
GAGW01008880 587 ----- 508
OSIN7648 789 ----- 863
(translation=) H N V E S V D S I T H L S M Q R E Y Q A P R F F Y D Y
(variant aa=) F

KC437356 7490 CTCCGTCAGTTACGACGGATGGACTTCGGCGGTTGCAATGAGCCCGTGATGAACCTTGAACAATCTCCCCGAGAACGAAA 7569
GAGW01008880 507 ----- 428
OSIN7648 864 ----- 934
(translation=) S V S Y A G M D F G G S N E P V M N L N N L P E N E

KC437356 7570 CTTTCGACATCGACAGTCTTTTGTATCTCGATAAGATCCTTGGTCAATCGCAGTCAGAGGCGAAAGAAGTGAGTGAAGC 7649
GAGW01008880 427 ----- 359
OSIN7648 935 ----- 1003
(translation=) T F D I D S P F D L D K I L G Q S Q S E G E R

KC437356 7650 ATCCCATTACAGATGTTTTTAGCTAACGGCGCCTAGCTTCTCATCTTCTCCGAGTCTCCACACAACCTCTGGACGA 7729
GAGW01008880 358 ----- 316
OSIN7648 1004 ----- 1046
(translation=) T S H L P P S P P H N P L D D

KC437356 7730 CTTTACTTTGCGTTC TAGAGGAAACGGGAGGCTCGACAGGAGCGGTATCAATTCGGGAGCTACAAAAGGGGAGGCAC 7809
GAGW01008880 315 ----- 236
OSIN7648 1047 ----- 1065
(translation=) F Y F A F

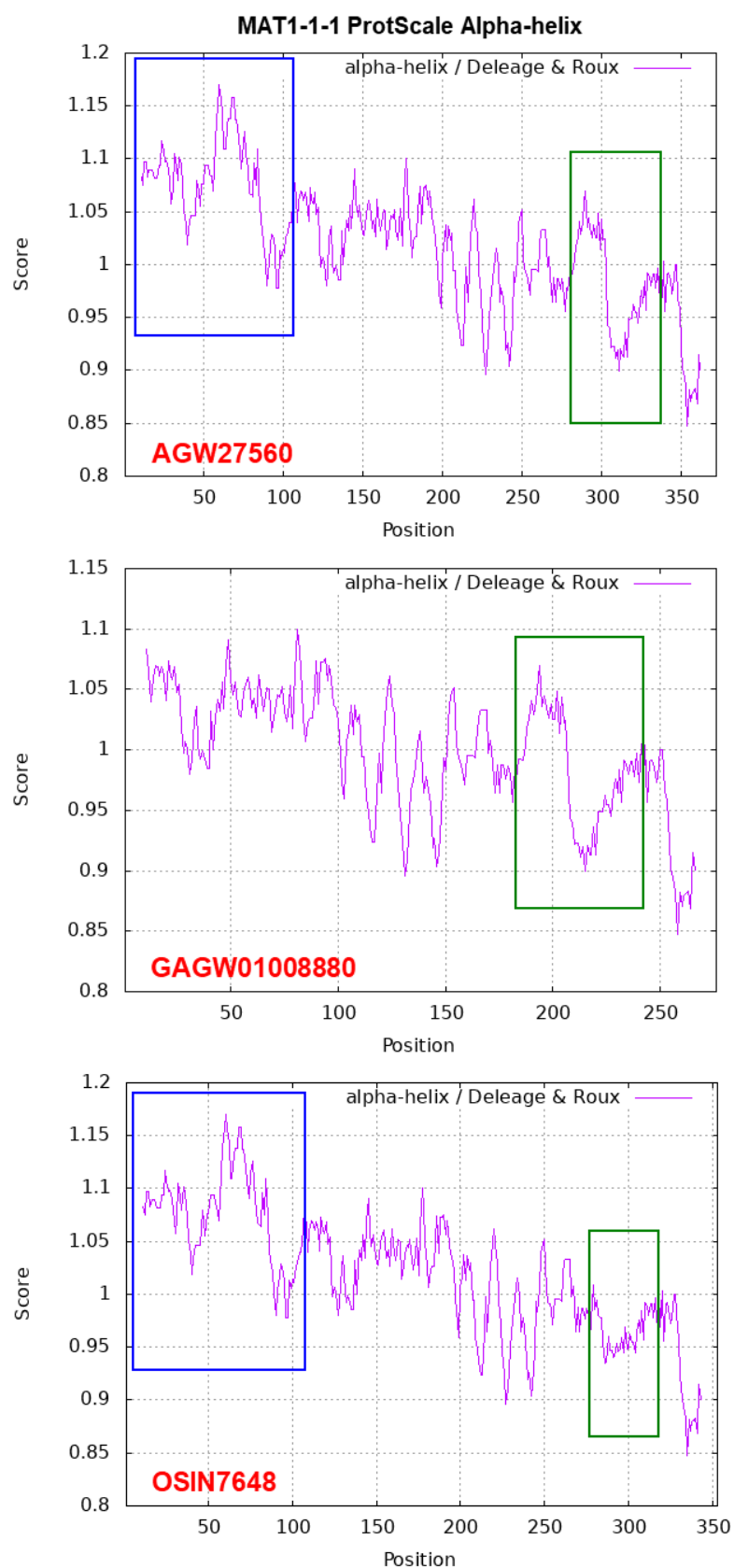
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GAGW01008880 235 ----- 156

KC437356 7850 GTAGGGGACGAGGGACGATGCACGATTTCTCGTCCAGGAAGTGAATTTTGCAGTGAATCCATCTTGCTCAGCGGGAGAT 7969
GAGW01008880 155 ----- 76

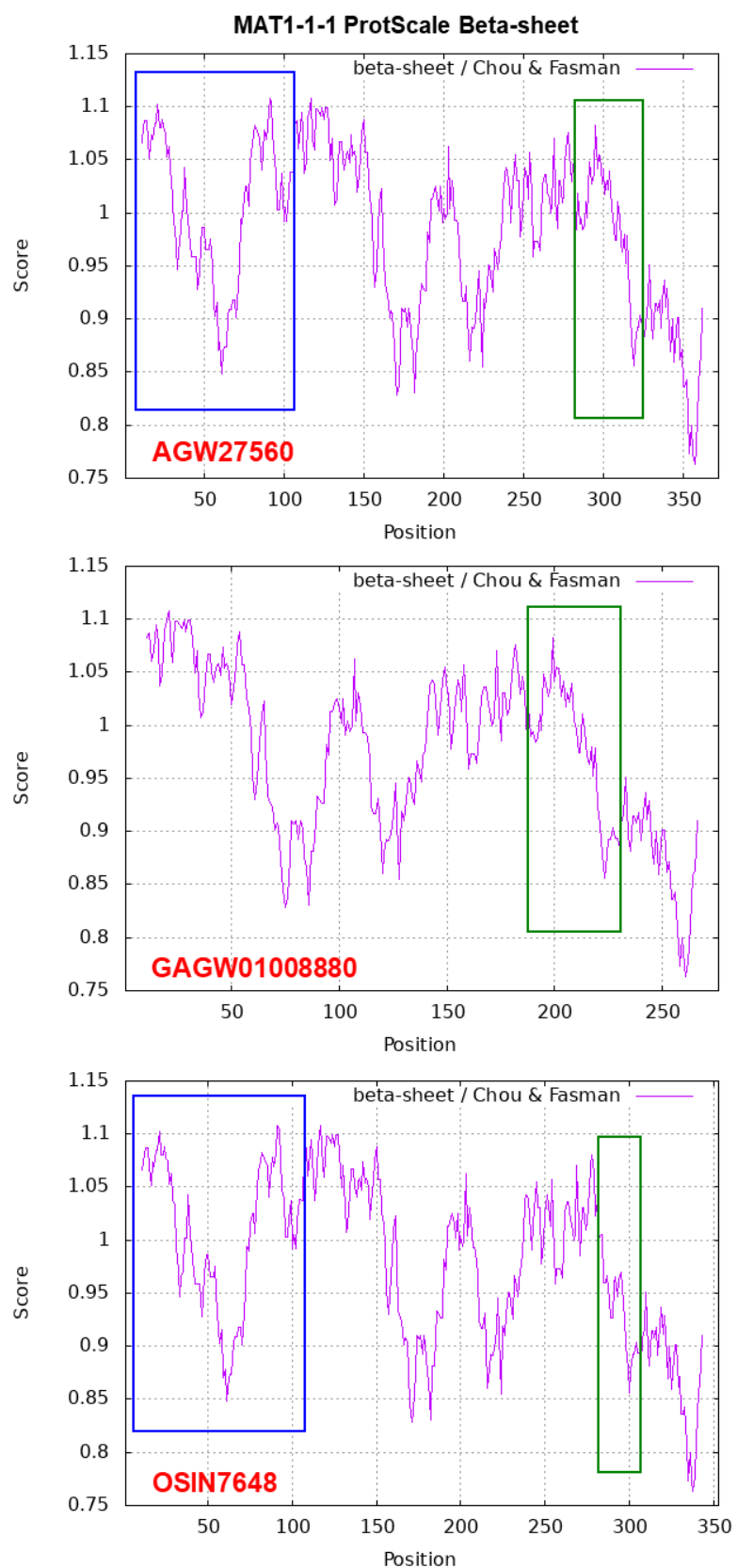
KC437356 7970 GGATCAAAGACAGAGAAAGGGGGCGTGCCGGGTAGACATGACAGGACCTAGGGCACAATCACTACTTCCGGTG 8044
GAGW01008880 75 ----- 1
(translation=) -C-----A-----

Figure S3. Alignment of the MAT1-1-1 genome sequences FC437356 and KR004003 of *H. sinensis* Strains CS68-2-1229 and GS09_225 and the transcriptome sequences of natural *C. sinensis*. FC437356 is the MAT1-1-1 gene of the *H. sinensis* strain CS68-2-1229 [37]. The sequence segments in pink represent introns I and II. The metatranscriptome assemblies OSIN7648 and GAGW01008880 are the MAT1-1-1 transcripts of natural *C. sinensis* specimens collected from Deqin County of Yunnan Province and Kangding County of Sichuan Province, China, respectively [53–54]. The triplets shown in alternating brown and green indicate the open reading frame. The underlined “TAG” triplets in blue represent stop codons. The protein sequence was translated from the transcript sequences. Amino acid residues in red represent variants. Hyphens indicate identical bases, and spaces denote unmatched sequence gaps.

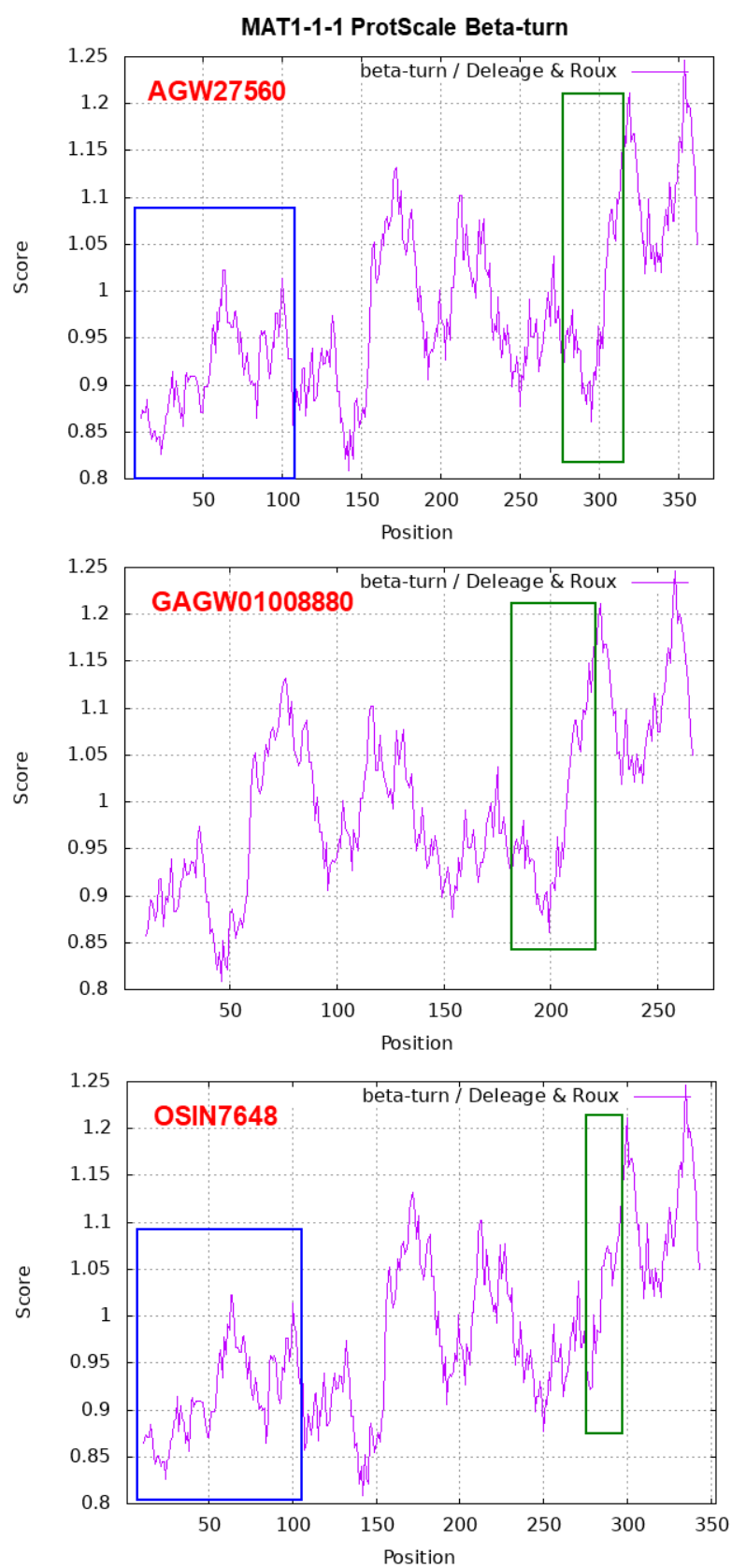
The original plots for Panel 2A (ProtScale α -helix) of Figure 2



The original plots for Panel 2B (ProtScale β -sheet) of Figure 2



The original plots for Panel 2C (ProtScale β -turn) of Figure 2



The original plots for Panel 2D (ProtScale coil) of Figure 2

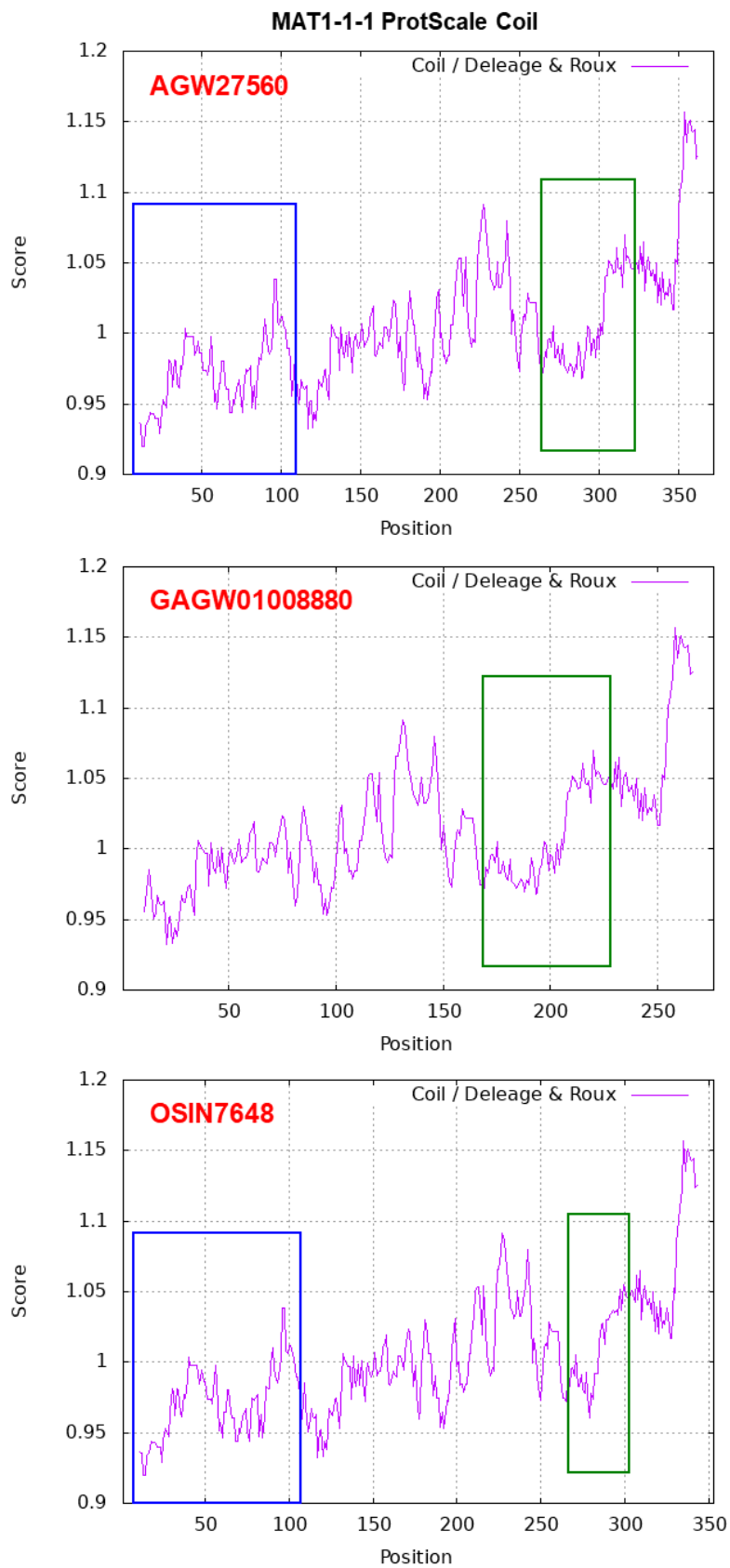
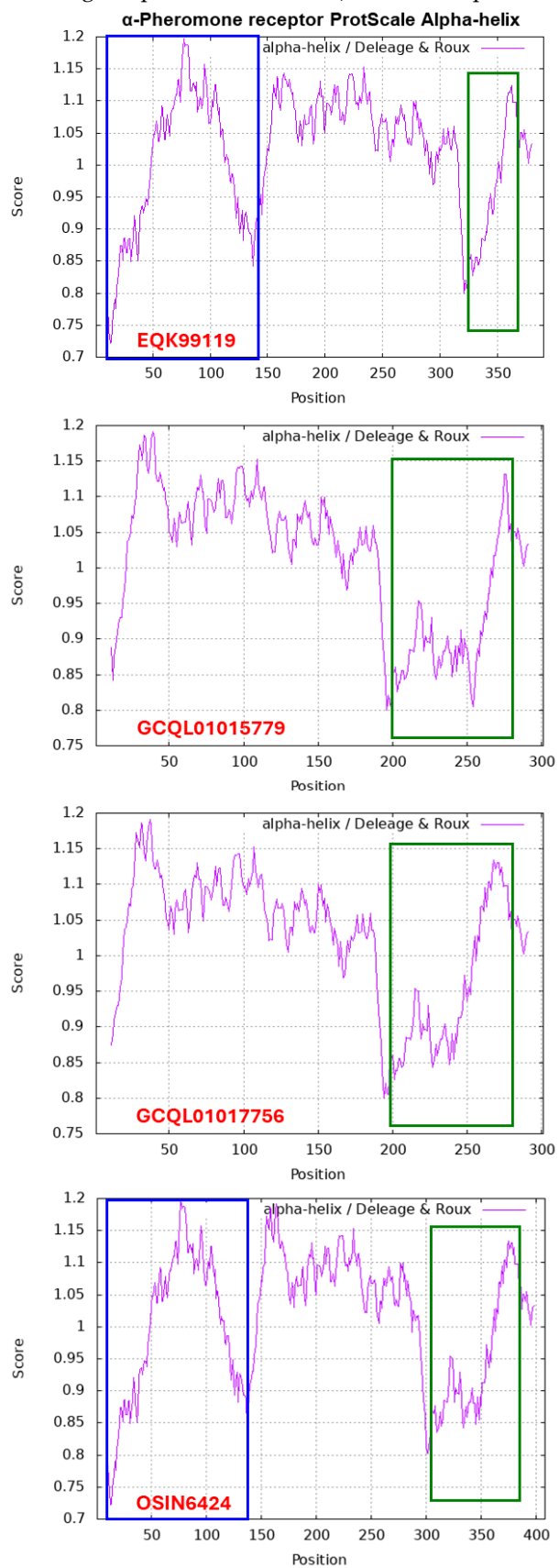
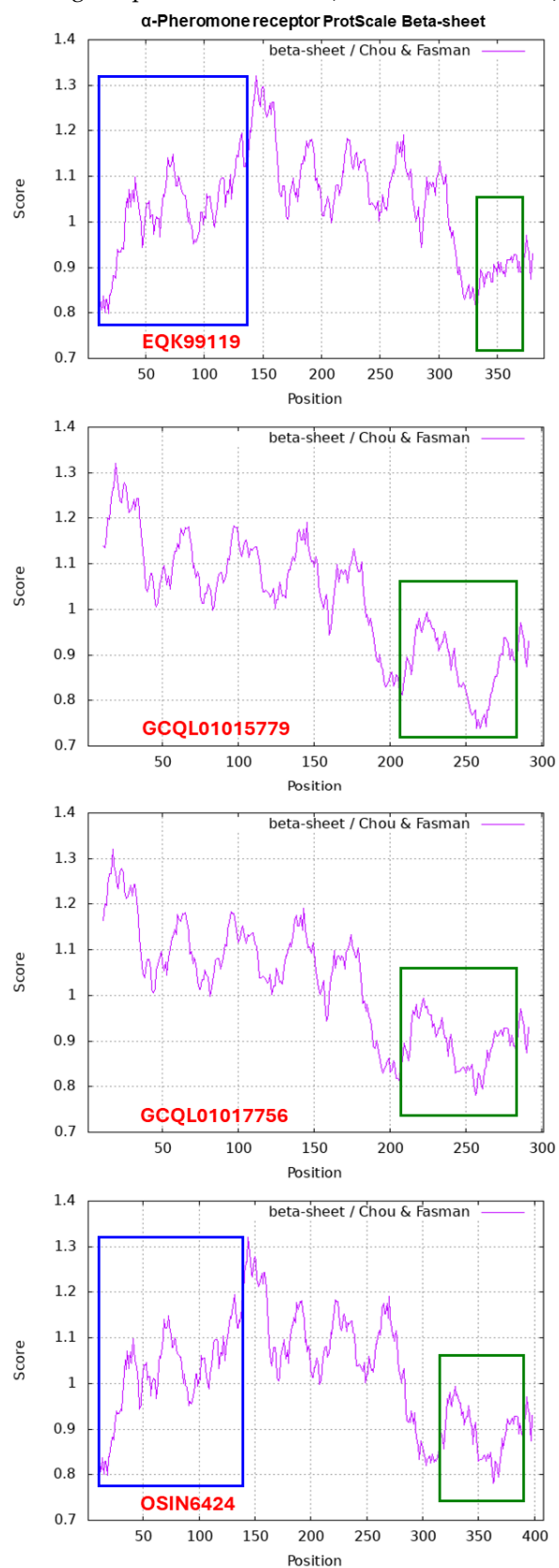


Figure S4. Original ExPASy ProtScale plots for the MAT1-1-1 protein α -helix (Figure 2 Panel 2A in the main text containing 3 plots: upper, middle, and lower plots), β -sheet (Figure 2 Panel 2B in the main text containing 3 plots), β -turn (Figure 2 Panel 2C in the main text containing 3 plots) and coil (Figure 2 Panel 2D in the main text containing 3 plots). The MAT1-1-1 protein sequence AGW27560 (372 aa; upper plots in all panels) of the *H. sinensis* strain CS68-2-1229 was compared with the metatranscriptome MAT1-1-1 sequences GAGW01008880 (276 aa; middle plots in all panels) and OSIN7648 (353 aa; lower plots in all panels) of natural *C. sinensis* (the original plots are included in Figure S4 in the supplementary file) [37,53–54]. The open boxes in green indicate the variable segment regions of the MAT1-1-1 proteins.

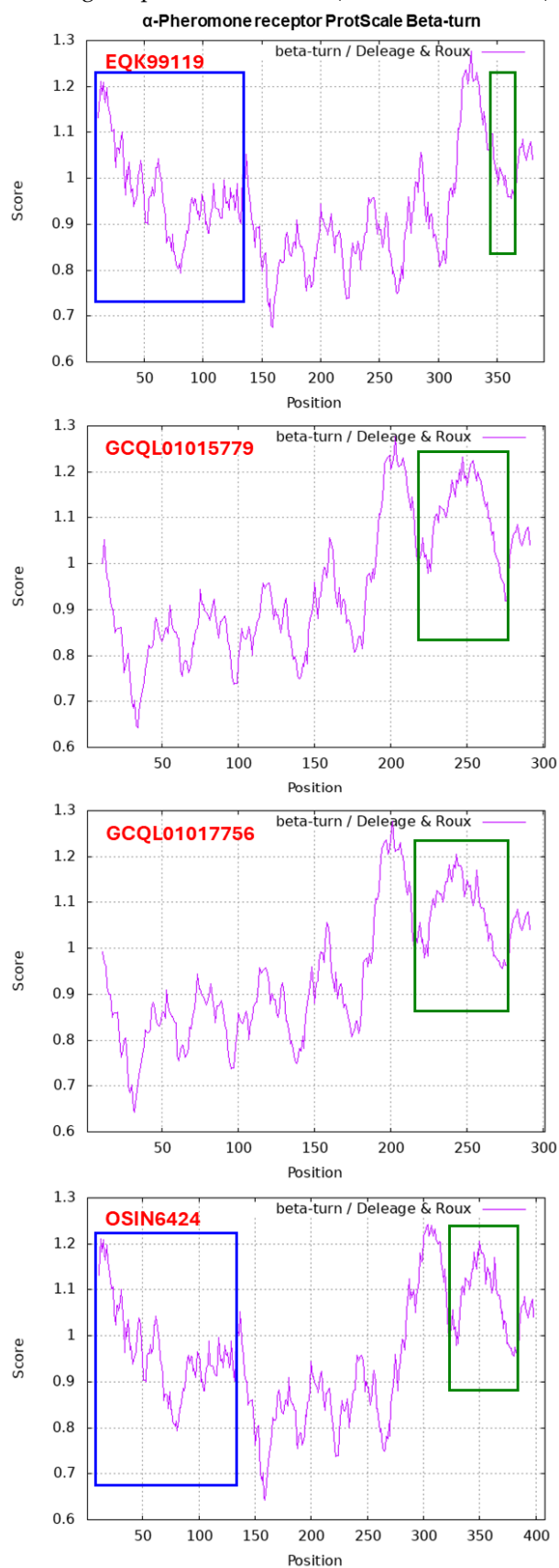
The original plots for Panel 8A (ProtScale Alpha-helix) of Figure 8



The original plots for Panel 8B (ProtScale Beta-sheet) of Figure 8



The original plots for Panel 8C (ProtScale Beta-turn) of Figure 8



The original plots for Panel 8D (ProtScale Coil) of Figure 8

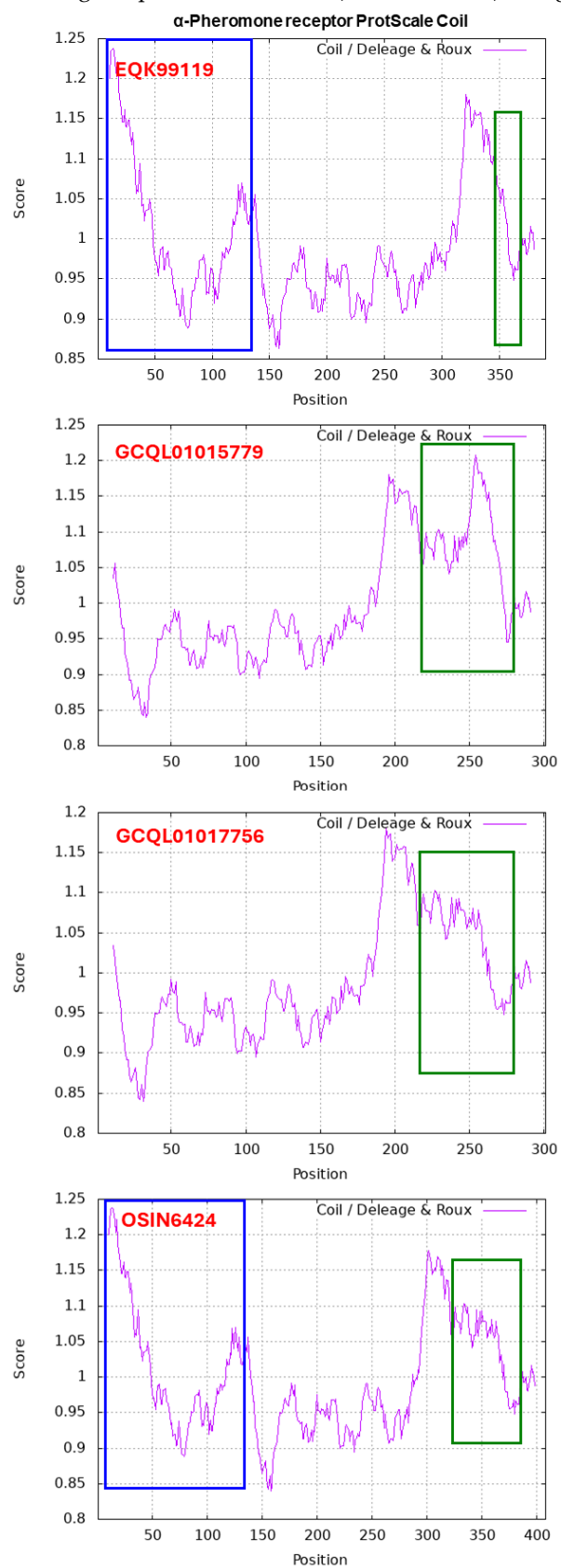


Figure S5. Original ExPASy ProtScale plots for the α -pheromone receptor protein α -helix (Figure 8 Panel 8A in the main text containing 4 plots: upper, middle, and lower plots), β -sheet (Figure 8 Panel 8B in the main text containing 4 plots), β -turn (Figure 8 Panel 8C in the main text containing 4 plots) and coil (Figure 8 Panel 8D in the main text containing 4 plots) of α -pheromone receptor proteins. The α -pheromone receptor protein sequence EQK99119 (390 aa; upper plots in all panels) of the *H. sinensis* strain Co18 was compared with the transcriptome and metatranscriptome α -pheromone receptor sequences and GCQL01017756 (301 aa; upper middle plots in all panels) and GCQL01015779 (301 aa; lower middle plots in all panels) of the *H. sinensis* strain L0106 and OSIN6424 (408 aa; lower plots in all panels) of natural *C. sinensis* [36,52,54]. The open boxes in green indicate the variable segment regions of the α -pheromone receptor proteins.

Table S1. Differential occurrence of the MAT1-1-1 and MAT1-2-1 genes in 237 *H. sinensis* strains.

22 strains containing only the MAT1-1-1 gene	66 strains containing only the MAT1- 2-1 gene	149 strains containing both the MAT1-1-1 and MAT1-2-1 genes
CS09-143	CC1406-203 XZ-CD-41	1229 NP10_1 SC09_47 XZ09_32
CS09-229	CS2 XZ-CD-59	Co18 NP10_2 SC09_57 XZ09_46
GS03	GS09_337 XZ-CD-64	CS6-251 QH01 SC09_65 XZ09_48
IOZ07	QH02 XZ-ML-191	CS18-266 QH03 SC09_77 XZ09_59
QH07_188	QH05 XZ-LZ05-6	CS25-273 QH04 SC09_87 XZ09_71
QH07_197	QH09_11 XZ-LZ06_1	CS26-277 QH06 SC09_97 XZ09_80
XZ05_3	QH09_187 XZ-LZ06_7	CS34-291 QH07 SC09_107 XZ09_95
XZ05_6	QH-LJ-214 XZ-LZ06_21	CS36-1294 QH08 SC09_117 XZ09_100
XZ07_H2	QH-LJ-236 XZ-LZ06_61	CS37-295 QH09_20L SC09_128 XZ09_106
XZ07_108	QH-QL-206 XZ-LZ06_108	CS68-2-1228 QH09_33L SC09_147 XZ09_113
XZ07_154	QH-QL-207 XZ-LZ07_30	CS68-2-1229 QH09_37 SC09_157 XZ09_118
XZ07_166	QH-YS-188 XZ-LZ07_64	CS68-5-1216 QH09_46 SC09_167 XZ10_7
XZ07_176	QH-YS-189 XZ-LZ07_H1	CS70-1208 QH09_56 SC09_180 XZ10_15
XZ07_180	QH-YS-196 XZ-LZ07_H2	CS70-1211 QH09_66 SC09_190 XZ10_17
XZ08_4	QH-YS-197A XZ-NQ_74	CS70-1212 QH09_78 SC09_200 XZ10_23
XZ08_10	QH-YS-197B XZ-NQ_80	CS71-1218 QH09_93 SC10_4 XZ12_1
XZ08_26	QH-YS-199 XZ-NQ_84	CS71-1219 QH09_122 SC10_18 XZ12_16
XZ08_59	SC-2 XZ-NQ_86	CS71-1220 QH09_131 SC10_21 XZ12_33
XZ08_A1	SC-3 XZ-NQ_92	CS76-1284 QH09_151 TB01 XZ12_43
XZ08_B1	SC-4 XZ-NQ_139	CS91-1291 QH09_164 TB02 YN01
YN07_6	SC-5 XZ-NQ_154	CS560-961 QH09_173 TB03 YN02
YN07_8	SC-7 XZ-NQ_155	CS561-964 QH09_201 TB04 YN03
	SCK05-4-3 XZ-NQ_156	GS01 QH09_210 TB05 YN09_3
	XZ07_11 XZ-NQ_166	GS02 QH10_1 TB06 YN09_6
	XZ07_46 XZ-NQ_176	GS04 QH10_4 TB07 YN09_22
	XZ08_33 XZ-NQ_180	GS05 QH10_7 TB08 YN09_51
	XZ08_38 XZ-SN_44	GS09_111 SC01 XZ05_2 YN09_61
	XZ-CD-A1 YN-1	GS09_121 SC02 XZ05_7 YN09_64
	XZ-CD-B1 YN-4	GS09_131 SC03 XZ05_8 YN09_72
	XZ-CD-4 YN-5	GS09_143 SC04 XZ05_12 YN09_81
	XZ-CD-10 YN-6	GS09_201 SC05 XZ06_124 YN09_85
	XZ-CD-26 YN-8	GS09_225 SC06 XZ06_152 YN09_89
	XZ-CD-30 ZJB12195	GS09_229 SC07 XZ06_260 YN09_96
		GS09_281 SC08 XZ07_133 YN09_101
		GS09_311 SC09_1 XZ08_24 YN09_140
		GS10_1 SC09_21 XZ08_56
		GS10_10 SC09_36 XZ09_4
		ID10_1 SC09_37 XZ09_15

Table S2. Amino acid scales for ProtScale analysis (<https://web.expasy.org/protscale/>) to predict secondary structures (α -helices, β -turns, and coils [57] and β -sheets [56]) of proteins.

Chemical-physical property				α -Helix	β -Sheet	β -Turn	Coil
Aspartic acid	Asp	D	Acidic	0.924	0.540	1.197	1.197
Glutamic acid	Glu	E	Acidic	1.504	0.370	1.149	0.761
Alanine	Ala	A	Aliphatic	1.489	0.830	0.788	0.824
Isoleucine	Ile	I	Aliphatic	1.003	1.600	0.240	0.886
Leucine	Leu	L	Aliphatic	1.236	1.300	0.670	0.810
Valine	Val	V	Aliphatic	0.990	1.700	0.387	0.772
Phenylalanine	Phe	F	Aromatic	1.195	1.380	0.624	0.797
Tryptophan	Trp	W	Aromatic	1.090	1.370	0.546	0.941
Tyrosine	Tyr	Y	Aromatic	0.787	1.470	0.795	1.109
Arginine	Arg	R	Basic	1.224	0.930	0.912	0.893
Histidine	His	H	Basic	1.003	0.870	0.970	1.068
Lysine	Lys	K	Basic	1.172	0.740	1.302	0.897
Asparagine	Asn	N	with polar neutral side chains	0.772	0.890	1.572	1.167
Cysteine	Cys	C	with polar neutral side chains	0.966	1.190	0.965	0.953
Glutamine	Gln	Q	with polar neutral side chains	1.164	1.100	0.997	0.947
Methionine	Met	M	with polar neutral side chains	1.363	1.050	0.436	0.810
Serine	Ser	S	with polar neutral side chains	0.739	0.750	1.316	1.130
Threonine	Thr	T	with polar neutral side chains	0.785	1.190	0.739	1.148
Glycine	Gly	G	Unique amino acids	0.510	0.750	1.860	1.251
Proline	Pro	P	Unique amino acids	0.492	0.550	1.415	1.540

Note: An amino acid scale was defined at <https://web.expasy.org/protscale/> as follows:

An **amino acid scale** is defined by a numerical value assigned to each type of amino acid. The most frequently used scales are the hydrophobicity or hydrophilicity scales and the secondary structure conformational parameter scales, but many other scales exist, which are based on the different chemical and physical properties of the amino acids. This program provides 57 predefined scales entered from the literature.

Table S3. Percent similarity between the sequences of the ITS1, 5.8S, and/or ITS2 segments of the parental fungi (Genotype #1 *H. sinensis* AB067721 and the AB067719-type Group E fungus) and the segment sequences of the offspring variant Genotypes #13 (KT339190, in the semiejected ascospores) and #14 (KT339178, in the fully ejected ascospores) of *O. sinensis* (adapted from [5–6,15]).

	Percent similarity			
	ITS1-5.8S-ITS2	ITS1	5.8S	ITS2
<u>vs. Genotype #13 of <i>O. sinensis</i> (KT339190)</u>				
Genotype #1 AB067721 (<i>H. sinensis</i>)	86.3%	100%	94.8%	64.2%
Group E AB067719 fungus	88.2%	71.5%	100%	99%
<u>vs. Genotype #14 of <i>O. sinensis</i> (KT339178)</u>				
Genotype #1 AB067721 (<i>H. sinensis</i>)	87.7%	67.9%	94.9%	100%
Group E AB067719 fungus	89.2%	100%	100%	71.5%

[REFERENCES]

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