

Table S1. Yeast species and isolates from corn leaf samples in each province.

Taxa	Strain DMKU-			
	Suphan Buri	Chainat	Nakhon Sawan	Phetchabun
Phylum Ascomycota				
Subphylum Saccharomycotina				
<i>Candida intermedia</i>	CP563	CP635,	CP669, CP705, CP791	-
<i>Candida quercitrusa</i>	-	-	-	CP719
<i>Candida saopaulonensis</i>	-	CP793, CP802	-	CP708, CP715
<i>Candida uthaithanina</i>	-	CP825	-	-
<i>Meyerozyma caribbica</i>	CP566, CP628	CP629, CP649, CP813	CP666, CP670, CP679, CP696, CP783	CP710, CP724, CP749, CP767,
<i>Kodamaea ohmeri</i>	CP586	-	-	-
<i>Metschnikowia lophuriensis</i>	-	CP816	CP680	CP722
<i>Pichia bruneiensis</i>	-	CP805, CP826	-	CP733, CP737, CP753, CP761
<i>Pichia kudriavzevii</i>	CP565		CP672	
<i>Wickerhamomyces anomalus</i>	CP571, CP577	CP657	-	-
Phylum Basidiomycota				
Subphylum Agaricomycotina				
<i>Dioszegia zsolttii</i>	CP555	CP647	CP780	-
<i>Hannaella oryzae</i>	-	-	CP701, CP775	-
<i>Hannaella pagnoccae</i>	-	CP636, CP810	-	CP723
<i>Hannaella phetchabunensis</i>	-	CP812	-	-
<i>Hannaella phyllophila</i>	-	CP648	CP667	CP763
<i>Hannaella siamensis</i>	CP590	CP631, CP822	-	CP721, CP743
<i>Hannaella sinensis</i>	CP553, CP568, CP595, CP606, CP610	CP630, CP637, CP643, CP652, CP655, CP792, CP803, CP819	CP665, CP668, CP677, CP690, CP703, CP787,	CP712, CP716, CP728, CP742, CP765
<i>Vishiacozya aff. heimaeyensis</i>	CP576	CP796	-	-
<i>Kwoniella bestiolae</i>	CP619	-	-	-
<i>Kwoniella heveanensis</i>	-	CP820	-	-
<i>Papiliotrema flavescens</i>	CP611	CP634, CP642, CP654, CP806, CP808	CP700, CP786	CP714, CP720, CP734, CP740, CP760, CP768
<i>Papiliotrema laurentii</i>	CP560, CP567, CP585	CP797	CP660	-

Table S1. Cont

Taxa	Strain DMKU-			
	Suphan Buri	Chainat	Nakhon Sawan	Phetchabun
<i>Papiliotrema rajasthanensis</i>	CP552, CP580, CP592, CP603, CP621	CP800, CP823	CP691, CP776, CP790	CP754
<i>Papiliotrema ruineniae</i>	-	CP818	CP781	-
<i>Plapiliotrema plantarum</i>	-	CP801	-	-
<i>Saitozyma flava</i>	CP620	-	-	CP758
Subphylum Pucciniomycotina				
<i>Cystobasidium calyptogenae</i>	CP557	-	-	-
<i>Symmetrospora vermiculata</i>	CP558	CP821	CP771	-
<i>Rhodotorula mucilaginosa</i>	CP573, CP596	-	-	-
<i>Rhodotorula paludigena</i>	CP572, CP591, CP604, CP614, CP625	CP640, CP645, CP650, CP794	CP659, CP693, CP702, CP777, CP785	CP730, CP746, CP752, CP757
<i>Rhodotorula toruloides</i>	-	-	CP699	-
<i>Rhodotorula aff. toruloides</i>	CP570	CP639	-	-
<i>Rhodosporeidiobolus nylandii</i>	CP589	-	-	-
<i>Rhodosporeidiobolus ruineniae</i>	-	-	CP694, CP706	CP713
<i>Rhodosporeidiobolus fluviialis</i>	-	CP658	-	-
<i>Rhodosporeidiobolus odoratus</i>	CP622	-	-	-
<i>Sporobolomyces blumeae</i>	CP551, CP575, CP601, CP605, CP613	-	CP683, CP779	-
<i>Sporobolomyces nakasei</i>	-	-	-	CP727, CP735, CP741, CP751, CP756, CP762
<i>Sporobolomyces carnicolor</i>	-	CP799	-	CP707
Subphylum Ustilaginomycotina				
<i>Anthracoystis elionuri</i>	CP623	CP646, CP809, CP824	CP675, CP784	-
<i>Dirkmeia churashimaensis</i>	CP554, CP562, CP574, CP583, CP593, CP608, CP612, CP617	CP638, CP644, CP653, CP815	CP661, CP692, CP774, CP778	CP709
<i>Moesziomyces antarcticus</i>	CP556, CP564, CP624	-	CP671, CP681, CP684, CP697, CP770	CP726, CP745

Table S1. *Cont*

Taxa	Strain DMKU-			
	Suphan Buri	Chainat	Nakhon Sawan	Phetchabun
<i>Ustilago trichophora</i>	CP626	CP641	-	-
<i>Ustilago siamensis</i>	CP597	-	-	-
<i>Ustilago sparsa</i>	CP569, CP579, CP584, CP602, CP607, CP615	CP798, CP814	CP663, CP698, CP704	CP725, CP732

Table S2. Sequence similarity analysis of the D1/D2 region of corn phylloplane yeasts and their closely related species.

M13 profile	Strain with the same profile	Representative strain	GenBank accession no.	Closest specie (GenBank accession no.)	Nucleotide substitutions/gap/total nt	% identity	Identification
	DMKU-	DMKU-					
1	CP563, CP635, CP669, CP705, CP791	CP563	LC430847	<i>Candida intermedia</i> (U44809)	2/1/475	99.37	<i>Candida intermedia</i>
		CP669	LC430848	<i>Candida intermedia</i> (U44809)	2/1/481	99.38	<i>Candida intermedia</i>
2	CP719	CP719	LC430849	<i>Candida quercitrusa</i> (U45831)	3/2/529	99.06	<i>Candida quercitrusa</i>
3	CP708, CP715, CP793	CP715	LC430850	<i>Candida saopaulonensis</i> (AY695398)	1/0/454	99.78	<i>Candida saopaulonensis</i>
		CP793	LC430851	<i>Candida saopaulonensis</i> (AY695398)	1/1/502	99.60	<i>Candida saopaulonensis</i>
4	CP802	CP802	LC430852	<i>Candida saopaulonensis</i> (AY695398)	1/0/456	99.78	<i>Candida saopaulonensis</i>
5	CP825	CP825	LC430853	<i>Candida uthaithanina</i> (AB588752)	1/0/543	99.82	<i>Candida uthaithanina</i>
6	CP628, CP666	CP628	LC430865	<i>Meyerozyma caribbica</i> (AY187283)	1/0/533	99.81	<i>Meyerozyma caribbica</i>
7	CP813, CP749, CP724	CP724	LC430864	<i>Meyerozyma caribbica</i> (AY187283)	1/0/533	99.81	<i>Meyerozyma caribbica</i>
8	CP679, CP710, CP767	CP679	LC430862	<i>Meyerozyma caribbica</i> (AY187283)	1/0/533	99.81	<i>Meyerozyma caribbica</i>
9	CP566	CP566	LC430858	<i>Meyerozyma caribbica</i> (AY187283)	0/0/558	100	<i>Meyerozyma caribbica</i>
10	CP629	CP629	LC430859	<i>Meyerozyma caribbica</i> (AY187283)	1/1/544	99.63	<i>Meyerozyma caribbica</i>
11	CP649, CP783	CP649	LC430860	<i>Meyerozyma caribbica</i> (AY187283)	2/0/510	99.61	<i>Meyerozyma caribbica</i>
12	CP670	CP670	LC430861	<i>Meyerozyma caribbica</i> (AY187283)	2/2/534	99.25	<i>Meyerozyma caribbica</i>
13	CP696	CP696	LC430863	<i>Meyerozyma caribbica</i> (AY187283)	2/0/521	99.62	<i>Meyerozyma caribbica</i>
14	CP586	CP586	LC430854	<i>Kodamaea ohmeri</i> (GU597323)	1/0/430	99.77	<i>Kodamaea ohmeri</i>
15	CP680, CP816	CP680	LC430855	<i>Metschnikowia lophuriensis</i> (AB697756)	0/0/406	100	<i>Metschnikowia lophuriensis</i>
		CP816	LC430857	<i>Metschnikowia lophuriensis</i> (AB697756)	0/0/417	100	<i>Metschnikowia lophuriensis</i>

Table S2. Cont

M13 profile	Strain with the same profile	Representative strain	GenBank accession no.	Closest specie (GenBank accession no.)	Nucleotide substitutions/gap/total nt	% identity	Identification
	DMKU-	DMKU-					
16	CP722	CP722	LC430856	<i>Metschnikowia lopburiensis</i> (AB697756)	0/0/408	100	<i>Metschnikowia lopburiensis</i>
17	CP761, CP733, CP805	CP761	LC430868	<i>Pichia bruneiensis</i> (KY108804)	2/4/519	95.95	<i>Pichia bruneiensis</i>
18	CP737	CP737	LC430866	<i>Pichia bruneiensis</i> (KY108804)	1/3/504	96.03	<i>Pichia bruneiensis</i>
19	CP753	CP753	LC430867	<i>Pichia bruneiensis</i> (KY108804)	2/4/519	95.95	<i>Pichia bruneiensis</i>
20	CP826	CP826	LC430869	<i>Pichia bruneiensis</i> (KY108804)	3/1/498	95.98	<i>Pichia bruneiensis</i>
21	CP565	CP565	LC430870	<i>Pichia kudriavzevii</i> (EF550222)	0/0/522	100	<i>Pichia kudriavzevii</i>
22	CP672	CP672	LC430871	<i>Pichia kudriavzevii</i> (EF550222)	0/0/524	100	<i>Pichia kudriavzevii</i>
23	CP571, CP577	CP571 CP577	LC430873 LC430874	<i>Wickerhamomyces anomalus</i> (U74592) <i>Wickerhamomyces anomalus</i> (U74592)	0/0/524 0/0/544	100 100	<i>Wickerhamomyces anomalus</i> <i>Wickerhamomyces anomalus</i>
24	CP657	CP657	LC430872	<i>Wickerhamomyces anomalus</i> (U74592)	2/0/534	99.63	<i>Wickerhamomyces anomalus</i>
25	CP555, CP647	CP555 CP647	LC428178 LC428179	<i>Dioszegia zsolttii</i> (AF544245) <i>Dioszegia zsolttii</i> (AF544245)	1/0582 1/0533	99.83 99.81	<i>Dioszegia zsolttii</i> <i>Dioszegia zsolttii</i>
26	CP780	CP780	LC428180	<i>Dioszegia zsolttii</i> (AF544245)	1/0549	99.82	<i>Dioszegia zsolttii</i>
27	CP701	CP701	LC428181	<i>Hannaella oryzae</i> (AF075511)	0/0/530	100	<i>Hannaella oryzae</i>
28	CP775	CP775	LC428182	<i>Hannaella oryzae</i> (AF075511)	0/0/531	100	<i>Hannaella oryzae</i>
29	CP636	CP636	LC428183	<i>Hannaella pagnoccae</i> (FJ828959)	2/0557	99.64	<i>Hannaella pagnoccae</i>
30	CP723, CP810	CP810	LC428184	<i>Hannaella pagnoccae</i> (FJ828959)	0/0/550	100	<i>Hannaella pagnoccae</i>
31	CP812	CP812	LC428185	<i>Hannaella phetchabunensis</i> (AB922849)	0/0/543	100	<i>Hannaella phetchabunensis</i>
32	CP648, CP667	CP648	LC428186	<i>Hannaella phyllophila</i> (AB934929)	0/0/553	100	<i>Hannaella phyllophila</i>

Table S2. Cont.

M13 profile	Strain with the same profile	Representative strain	GenBank accession no.	Closest specie (GenBank accession no.)	Nucleotide substitutions/gap/total nt	% identity	Identification
	DMKU-	DMKU-					
33	CP763	CP763	LC428187	<i>Hannaella phyllophila</i> (AB934929)	0/0/549	100	<i>Hannaella phyllophila</i>
34	CP631	CP631	LC428188	<i>Hannaella siamensis</i> (AB922844)	0/0/504	100	<i>Hannaella siamensis</i>
35	CP590, CP743, CP822	CP590 CP743	LC428189 LC428190	<i>Hannaella siamensis</i> (AB922844) <i>Hannaella siamensis</i> (AB922844)	0/0/561 0/0/516	100 100	<i>Hannaella siamensis</i> <i>Hannaella siamensis</i>
36	CP721	CP721	LC428191	<i>Hannaella siamensis</i> (AB922844)	0/0/544	100	<i>Hannaella siamensis</i>
37	CP742	CP742	LC428201	<i>Hannaella sinensis</i> (AF189884)	0/0/538	100	<i>Hannaella sinensis</i>
38	CP568, CP606, CP610, CP630, CP637, CP643, CP652, CP655, CP665, CP668, CP703, CP712, CP716, CP728, CP765, CP803	CP568 CP652 CP728	LC428192 LC428193 LC428200	<i>Hannaella sinensis</i> (AF189884) <i>Hannaella sinensis</i> (AF189884) <i>Hannaella sinensis</i> (AF189884)	0/0/578 0/0/526 0/0/516	100 100 100	<i>Hannaella sinensis</i> <i>Hannaella sinensis</i> <i>Hannaella sinensis</i>
39	CP787	CP787	LC428195	<i>Hannaella sinensis</i> (AF189884)	0/0/532	100	<i>Hannaella sinensis</i>
40	CP792	CP792	LC428196	<i>Hannaella sinensis</i> (AF189884)	0/0/532	100	<i>Hannaella sinensis</i>
41	CP819	CP819	LC428197	<i>Hannaella sinensis</i> (AF189884)	0/0/554	100	<i>Hannaella sinensis</i>
42	CP553, CP690	CP553 CP690	LC428198 LC428194	<i>Hannaella sinensis</i> (AF189884) <i>Hannaella sinensis</i> (AF189884)	0/0/578 1/0/518	100 99.81	<i>Hannaella sinensis</i> <i>Hannaella sinensis</i>
43	CP595	CP595	LC428199	<i>Hannaella sinensis</i> (AF189884)	0/0/549	100	<i>Hannaella sinensis</i>
44	CP677	CP677	LC428202	<i>Hannaella sinensis</i> (AF189884)	0/1/534	99.81	<i>Hannaella sinensis</i>
45	CP576, CP796	CP576 CP796	LC370333 LC370334	<i>Vishniacozyma heimaeyensis</i> (DQ000317) <i>Vishniacozyma heimaeyensis</i> (DQ000317)	10/1/562 10/1/562	98.04 98.04	<i>Vishniacozyma</i> aff. <i>heimaeyensis</i> <i>Vishniacozyma</i> aff. <i>heimaeyensis</i>

Table S2. Cont.

M13 profile	Strain with the same profile	Representative strain	GenBank accession no.	Closet specie (GenBank accession no.)	Nucleotide substitutions/gap/total nt	% identity	Identification
	DMKU-	DMKU-					
46	CP619	CP619	LC428203	<i>Kwoniella bestiolae</i> (FJ534903)	0/0/559	100	<i>Kwoniella bestiolae</i>
47	CP820	CP820	LC428204	<i>Kwoniella heveanensis</i> (AF075467)	1/0/557	99.82	<i>Kwoniella heveanensis</i>
48	CP611, CP634, CP760	CP611 CP760	LC428255 LC428259	<i>Papiliotrema flavescens</i> (AB035042) <i>Papiliotrema flavescens</i> (AB035042)	1/0/511 0/0/526	99.81 100	<i>Papiliotrema flavescens</i> <i>Papiliotrema flavescens</i>
49	CP642, CP700, CP720, CP734, CP740, CP786, CP808	CP786	LC428261	<i>Papiliotrema flavescens</i> (AB035042)	0/0/530	100	<i>Papiliotrema flavescens</i>
50	CP654, CP768	CP654 CP768	LC428256 LC428260	<i>Papiliotrema flavescens</i> (AB035042) <i>Papiliotrema flavescens</i> (AB035042)	0/0/509 0/1/533	100 99.81	<i>Papiliotrema flavescens</i> <i>Papiliotrema flavescens</i>
51	CP714	CP714	LC428257	<i>Papiliotrema flavescens</i> (AB035042)	0/0/511	100	<i>Papiliotrema flavescens</i>
52	CP585, CP660	CP585 CP660	LC428262 LC428266	<i>Papiliotrema laurentii</i> (AF075469) <i>Papiliotrema laurentii</i> (AF075469)	1/0/551 556/557	99.82 99.82	<i>Papiliotrema laurentii</i> <i>Papiliotrema laurentii</i>
53	CP560, CP567	CP560 CP567	LC428263 LC428264	<i>Papiliotrema laurentii</i> (AF075469) <i>Papiliotrema laurentii</i> (AF075469)	1/0/551 513/514	99.82 99.81	<i>Papiliotrema laurentii</i> <i>Papiliotrema laurentii</i>
54	CP797	CP797	LC428265	<i>Papiliotrema laurentii</i> (AF075469)	1/0/557	99.82	<i>Papiliotrema laurentii</i>
55	CP691, CP823, CP592	CP691 CP592	LC428268 LC428273	<i>Papiliotrema rajasthanensis</i> (AM262324) <i>Papiliotrema rajasthanensis</i> (AM262324)	0/0/556 1/0/577	100 99.83	<i>Papiliotrema rajasthanensis</i> <i>Papiliotrema rajasthanensis</i>
56	CP776	CP776	LC428269	<i>Papiliotrema rajasthanensis</i> (AM262324)	0/1/556	99.82	<i>Papiliotrema rajasthanensis</i>
57	CP603, CP754, CP790, CP800	CP603 CP790	LC428274 LC428270	<i>Papiliotrema rajasthanensis</i> (AM262324) <i>Papiliotrema rajasthanensis</i> (AM262324)	0/0/560 0/0/564	100 100	<i>Papiliotrema rajasthanensis</i> <i>Papiliotrema rajasthanensis</i>
58	CP552, CP580	CP552 CP580	LC428271 LC428272	<i>Papiliotrema rajasthanensis</i> (AM262324) <i>Papiliotrema rajasthanensis</i> (AM262324)	1/0/577 0/0/577	99.83 100	<i>Papiliotrema rajasthanensis</i> <i>Papiliotrema rajasthanensis</i>

Table S2. Cont.

M13 profile	Strain with the same profile	Representative strain	GenBank accession no.	Closet specie (GenBank accession no.)	Nucleotide substitutions/gap/total nt	% identity	Identification
	DMKU-	DMKU-					
59	CP621	CP621	LC428267	<i>Papiliotrema rajasthanensis</i> (AM262324)	0/0/519	100	<i>Papiliotrema rajasthanensis</i>
60	CP781, CP818	CP781 CP818	LC428275 LC428276	<i>Papiliotrema ruineniae</i> (LK023764) <i>Papiliotrema ruineniae</i> (LK023764)	0/1/533 0/0/539	99.81 100	<i>Papiliotrema ruineniae</i> <i>Papiliotrema ruineniae</i>
61	CP806	CP806	LC428277	<i>Papiliotrema ruineniae</i> (LK023764)	0/0/510	100	<i>Papiliotrema ruineniae</i>
62	CP801	CP801	LC370335	<i>Papiliotrema plantarum</i> (LC370335)	0/0/567	100	<i>Papiliotrema plantarum</i>
63	CP620	CP620	LC428278	<i>Saitozyma flava</i> (AF075497)	1/0/537	99.81	<i>Saitozyma flava</i>
64	CP758	CP758	LC428279	<i>Saitozyma flava</i> (AF075497)	1/0/545	99.82	<i>Saitozyma flava</i>
65	CP557	CP557	LC430175	<i>Cystobasidium calyptogenae</i> (AB025996)	0/0/563	100	<i>Cystobasidium calyptogenae</i>
66	CP558	CP558	LC430216	<i>Symmetrospora vermiculata</i> (AB279731)	0/0/563	100	<i>Symmetrospora vermiculata</i>
67	CP771	CP771	LC430217	<i>Symmetrospora vermiculata</i> (AB279731)	0/0/484	100	<i>Symmetrospora vermiculata</i>
68	CP821	CP821	LC430218	<i>Symmetrospora vermiculata</i> (AB279731)	0/0/542	100	<i>Symmetrospora vermiculata</i>
69	CP573	CP573	LC430182	<i>Rhodotorula mucilaginosa</i> (NG_055716)	1/0/555	99.82	<i>Rhodotorula mucilaginosa</i>
70	CP596	CP596	LC430181	<i>Rhodotorula mucilaginosa</i> (NG_055716)	0/1/539	99.81	<i>Rhodotorula mucilaginosa</i>
71	CP572	CP572	LC430183	<i>Rhodotorula paludigena</i> (AF070424)	0/0/556	100	<i>Rhodotorula paludigena</i>
72	CP604, CP640, CP730, CP752, CP746, CP757	CP604 CP640 CP730 CP752	LC430185 LC430188 LC430192 LC430193	<i>Rhodotorula paludigena</i> (AF070424) <i>Rhodotorula paludigena</i> (AF070424) <i>Rhodotorula paludigena</i> (AF070424) <i>Rhodotorula paludigena</i> (AF070424)	0/0/476 0/0/515 0/0/512 0/0/475	100 100 100 100	<i>Rhodotorula paludigena</i> <i>Rhodotorula paludigena</i> <i>Rhodotorula paludigena</i> <i>Rhodotorula paludigena</i>
73	CP591	CP591	LC430184	<i>Rhodotorula paludigena</i> (AF070424)	0/0/558	100	<i>Rhodotorula paludigena</i>
74	CP614, CP650, CP785	CP614 CP650	LC430186 LC430190	<i>Rhodotorula paludigena</i> (AF070424) <i>Rhodotorula paludigena</i> (AF070424)	0/0/521 0/0/525	100 100	<i>Rhodotorula paludigena</i> <i>Rhodotorula paludigena</i>

Table S2. Cont.

M13 profile	Strain with the same profile	Representative strain	GenBank accession no.	Closest specie (GenBank accession no.)	Nucleotide substitutions/gap/total nt	% identity	Identification
	DMKU-	DMKU-					
74		CP785	LC430195	<i>Rhodotorula paludigena</i> (AF070424)	0/0/525	100	<i>Rhodotorula paludigena</i>
75	CP625	CP625	LC430187	<i>Rhodotorula paludigena</i> (AF070424)	0/0/541	100	<i>Rhodotorula paludigena</i>
76	CP659	CP659	LC430191	<i>Rhodotorula paludigena</i> (AF070424)	0/0/525	100	<i>Rhodotorula paludigena</i>
77	CP645, CP693, CP702, CP777, CP794	CP645 CP702 CP794	LC430189 LC430194 LC430196	<i>Rhodotorula paludigena</i> (AF070424) <i>Rhodotorula paludigena</i> (AF070424) <i>Rhodotorula paludigena</i> (AF070424)	0/0/487 0/0/525 0/0/521	100 100 100	<i>Rhodotorula paludigena</i> <i>Rhodotorula paludigena</i> <i>Rhodotorula paludigena</i>
78	CP570, CP639, CP690, CP699	CP570 CP639 CP690 CP699	LC431632 LC431633 LC428194 LC430199	<i>Rhodotorula toruloides</i> (AF070426) <i>Rhodotorula toruloides</i> (AF070426) <i>Rhodotorula toruloides</i> (AF070426) <i>Rhodotorula toruloides</i> (AF070426)	5/0/581 5/0/547 1/0/518 1/0/488	99.14 99.08 99.81 99.81	<i>Rhodotorula</i> aff. <i>toruloides</i> <i>Rhodotorula</i> aff. <i>toruloides</i> <i>Rhodotorula toruloides</i> <i>Rhodotorula toruloides</i>
79	CP589	CP589	LC430177	<i>Rhodospiridiobolus nylandii</i> (AF387123)	0/1/522	99.81	<i>Rhodospiridiobolus nylandii</i>
80	CP694, CP706, CP713	CP694 CP706 CP713	LC430178 LC430179 LC430180	<i>Rhodospiridiobolus ruineniae</i> (AF070434) <i>Rhodospiridiobolus ruineniae</i> (AF070434) <i>Rhodospiridiobolus ruineniae</i> (AF070434)	0/0/524 1/0/520 0/0/456	100 99.81 100	<i>Rhodospiridiobolus ruineniae</i> <i>Rhodospiridiobolus ruineniae</i> <i>Rhodospiridiobolus ruineniae</i>
81	CP658	CP658	LC430176	<i>Rhodospiridiobolus fluvialis</i> (AF070422)	1/0/539	99.81	<i>Rhodospiridiobolus fluvialis</i>
82	CP622	CP622	LC430215	<i>Rhodospiridiobolus odoratus</i> (AF387125)	1/0/509	99.80	<i>Rhodospiridiobolus odoratus</i>
83	CP551, CP601, CP683	CP551 CP601 CP683	LC430200 LC430202 LC430203	<i>Sporobolomyces blumeae</i> (AY213010) <i>Sporobolomyces blumeae</i> (AY213010) <i>Sporobolomyces blumeae</i> (AY213010)	0/0/530 0/0/496 0/1/487	100 100 99.79	<i>Sporobolomyces blumeae</i> <i>Sporobolomyces blumeae</i> <i>Sporobolomyces blumeae</i>
84	CP613, CP779	CP613 CP779	LC430205 LC430206	<i>Sporobolomyces blumeae</i> (AY213010) <i>Sporobolomyces blumeae</i> (AY213010)	0/1/471 0/1/520	99.79 99.81	<i>Sporobolomyces blumeae</i> <i>Sporobolomyces blumeae</i>
85	CP575, CP605	CP575 CP605	LC430201 LC430204	<i>Sporobolomyces blumeae</i> (AY213010) <i>Sporobolomyces blumeae</i> (AY213010)	0/0/530 0/1/492	100 99.81	<i>Sporobolomyces blumeae</i> <i>Sporobolomyces blumeae</i>

Table S2. Cont.

M13 profile	Strain with the same profile	Representative strain	GenBank accession no.	Closest specie (GenBank accession no.)	Nucleotide substitutions/gap/total nt	% identity	Identification
	DMKU-	DMKU-					
86	CP741, CP751, CP762	CP741	LC430211	<i>Sporobolomyces nakasei</i> (KY109757)	1/0/511	99.81	<i>Sporobolomyces nakasei</i>
		CP751	LC430212	<i>Sporobolomyces nakasei</i> (KY109757)	1/0/510	99.81	<i>Sporobolomyces nakasei</i>
		CP762	LC430214	<i>Sporobolomyces nakasei</i> (KY109757)	0/0/511	100	<i>Sporobolomyces nakasei</i>
87	CP727, CP735, CP756	CP727	LC430209	<i>Sporobolomyces nakasei</i> (KY109757)	1/0/715	99.81	<i>Sporobolomyces nakasei</i>
		CP735	LC430210	<i>Sporobolomyces nakasei</i> (KY109757)	1/0/715	99.81	<i>Sporobolomyces nakasei</i>
		CP756	LC430213	<i>Sporobolomyces nakasei</i> (KY109757)	0/0/511	100	<i>Sporobolomyces nakasei</i>
88	CP799	CP799	LC430208	<i>Sporobolomyces carnicolor</i> (AY070008)	0/0/458	100	<i>Sporobolomyces carnicolor</i>
89	CP623, CP675, CP784, CP809	CP675	LC430821	<i>Anthracocystis elionuri</i> (AY740157)	1/0/544	99.82	<i>Anthracocystis elionuri</i>
		CP784	LC430822	<i>Anthracocystis elionuri</i> (AY740157)	0/0/558	100	<i>Anthracocystis elionuri</i>
		CP809	LC430823	<i>Anthracocystis elionuri</i> (AY740157)	0/0/555	100	<i>Anthracocystis elionuri</i>
90	CP646, CP824	CP646	LC430820	<i>Anthracocystis elionuri</i> (AY740157)	0/0/555	100	<i>Anthracocystis elionuri</i>
91	CP554, CP583, CP593, CP617, CP638, CP778	CP554	LC430825	<i>Dirkmeia churashimaensis</i> (AB548955)	0/0/531	100	<i>Dirkmeia churashimaensis</i>
		CP583	LC430829	<i>Dirkmeia churashimaensis</i> (AB548955)	0/0/420	100	
		CP593	LC430830	<i>Dirkmeia churashimaensis</i> (AB548955)	0/0/549	100	
		CP709	LC430833	<i>Dirkmeia churashimaensis</i> (AB548955)	0/0/566	100	
92	CP562, CP608, CP774	CP562	LC430826	<i>Dirkmeia churashimaensis</i> (AB548955)	0/0/531	100	<i>Dirkmeia churashimaensis</i>
		CP608	LC430831	<i>Dirkmeia churashimaensis</i> (AB548955)	0/0/551	100	
93	CP574, CP644, CP653, CP692	CP574	LC430827	<i>Dirkmeia churashimaensis</i> (AB548955)	0/0/531	100	<i>Dirkmeia churashimaensis</i>
94	CP612, CP661, CP815	CP612	LC430832	<i>Dirkmeia churashimaensis</i> (AB548955)	0/0/540	100	<i>Dirkmeia churashimaensis</i>
		CP815	LC430828	<i>Dirkmeia churashimaensis</i> (AB548955)	0/0/556	100	<i>Dirkmeia churashimaensis</i>
95	CP556, CP681, CP684	CP681	LC430834	<i>Moesziomyces antarcticus</i> (JN940521)	0/0/545	100	<i>Moesziomyces antarcticus</i>
		CP684	LC430835	<i>Moesziomyces antarcticus</i> (JN940521)	0/0/544	100	<i>Moesziomyces antarcticus</i>

Table S2. Cont.

M13 profile	Strain with the same profile	Representative strain	GenBank accession no.	Closest specie (GenBank accession no.)	Nucleotide substitutions/gap/total nt	% identity	Identification
	DMKU-	DMKU-					
96	CP564, CP624, CP671, CP697, CP745, CP726, CP770	CP697	LC430836	<i>Moesziomyces antarcticus</i> (JN940521)	0/0/545	100	<i>Moesziomyces antarcticus</i>
97	CP626, CP641	CP626 CP641	LC430837 LC430838	<i>Ustilago trichophora</i> (AY740125) <i>Ustilago trichophora</i> (AY740125)	0/0/567 0/0/505	100 100	<i>Ustilago trichophora</i> <i>Ustilago trichophora</i>
98	CP597	CP597	LC430839	<i>Ustilago siamensis</i> (AB117963)	0/1/536	99.81	<i>Ustilago siamensis</i>
99	CP569, CP579, CP607, CP615, CP663, CP798	CP569 CP579 CP663 CP798	LC430840 LC430845 LC430846 LC430844	<i>Ustilago sparsa</i> (JN367335) <i>Ustilago sparsa</i> (JN367335) <i>Ustilago sparsa</i> (JN367335) <i>Ustilago sparsa</i> (JN367335)	0/0/529 0/0/490 2/0/556 1/0/559	100 100 99.64 99.82	<i>Ustilago sparsa</i> <i>Ustilago sparsa</i> <i>Ustilago sparsa</i> <i>Ustilago sparsa</i>
100	CP584, CP704, CP814 CP732	CP584 CP732	LC430841 LC430843	<i>Ustilago sparsa</i> (JN367335)	0/0/494 0/0/550	100 100	<i>Ustilago sparsa</i> <i>Ustilago sparsa</i>
101	CP602, CP698, CP725	CP698	LC430842	<i>Ustilago sparsa</i> (JN367335)	0/0/529	100	<i>Ustilago sparsa</i>

Table S3. Sequence similarity analysis of the ITS region of corn phylloplane isolates showing ≥ 2 nucleotide substitutions in the D1/D2 region

Isolate	GenBank accession no. of D1/D2, ITS region	Closest species	Nucleotide substitutions/ gap/total nt		Identification
			D1/D2 region	ITS region	
DMKU-CP570	LC431632, LC431624	<i>Rhodotorula toruloides</i> CBS 349 (AF070426, AF444489)	5/0/581	5/4/584	Potential new species closest to <i>Rhodotorula toruloides</i>
DMKU-CP639	LC431633, LC431626	<i>Rhodotorula toruloides</i> CBS 349 (AF070426, AF444489)	5/0/547	5/4/584	Potential new species closest to <i>Rhodotorula toruloides</i>
DMKU-CP576	LC370333, LC431625	<i>Vishniacozyma heimaeyensis</i> CBS 8933 ^T (DQ000317, KF036591)	10/1/562	19/11/492	Potential new species closest to <i>Vishniacozyma heimaeyensis</i>
DMKU-CP796	LC370334, LC431630	<i>Vishniacozyma heimaeyensis</i> CBS 8933 ^T (DQ000317, KF036591)	10/1/562	19/11/492	Potential new species closest to <i>Vishniacozyma heimaeyensis</i>

Table S4. Similarity coefficient between yeast communities in pairwise comparisons based on the Jaccard similarity index.

	S1	S2	S3	S4	S5	S6	S7	S8	S9	S10	S11	S12	S13	S14	S15
S1	1.00														
S2	0.32	1.00													
S3	0.29	0.40	1.00												
S4	0.29	0.24	0.36	1.00											
S5	0.22	0.23	0.33	0.25	1.00										
S6	0.24	0.20	0.28	0.22	0.32	1.00									
S7	0.12	0.13	0.22	0.00	0.13	0.11	1.00								
S8	0.18	0.32	0.38	0.15	0.20	0.23	0.15	1.00							
S9	0.47	0.29	0.33	0.39	0.44	0.21	0.06	0.20	1.00						
S10	0.35	0.24	0.46	0.33	0.32	0.27	0.14	0.28	0.39	1.00					
S11	0.37	0.19	0.29	0.44	0.26	0.29	0.00	0.10	0.33	0.35	1.00				
S12	0.18	0.19	0.50	0.13	0.20	0.31	0.29	0.33	0.20	0.42	0.14	1.00			
S13	0.15	0.10	0.25	0.11	0.24	0.14	0.20	0.27	0.17	0.33	0.12	0.18	1.00		
S14	0.18	0.19	0.29	0.21	0.50	0.29	0.15	0.29	0.33	0.35	0.16	0.23	0.19	1.00	
S15	0.18	0.19	0.29	0.28	0.33	0.29	0.15	0.29	0.26	0.35	0.22	0.33	0.19	0.57	1.00