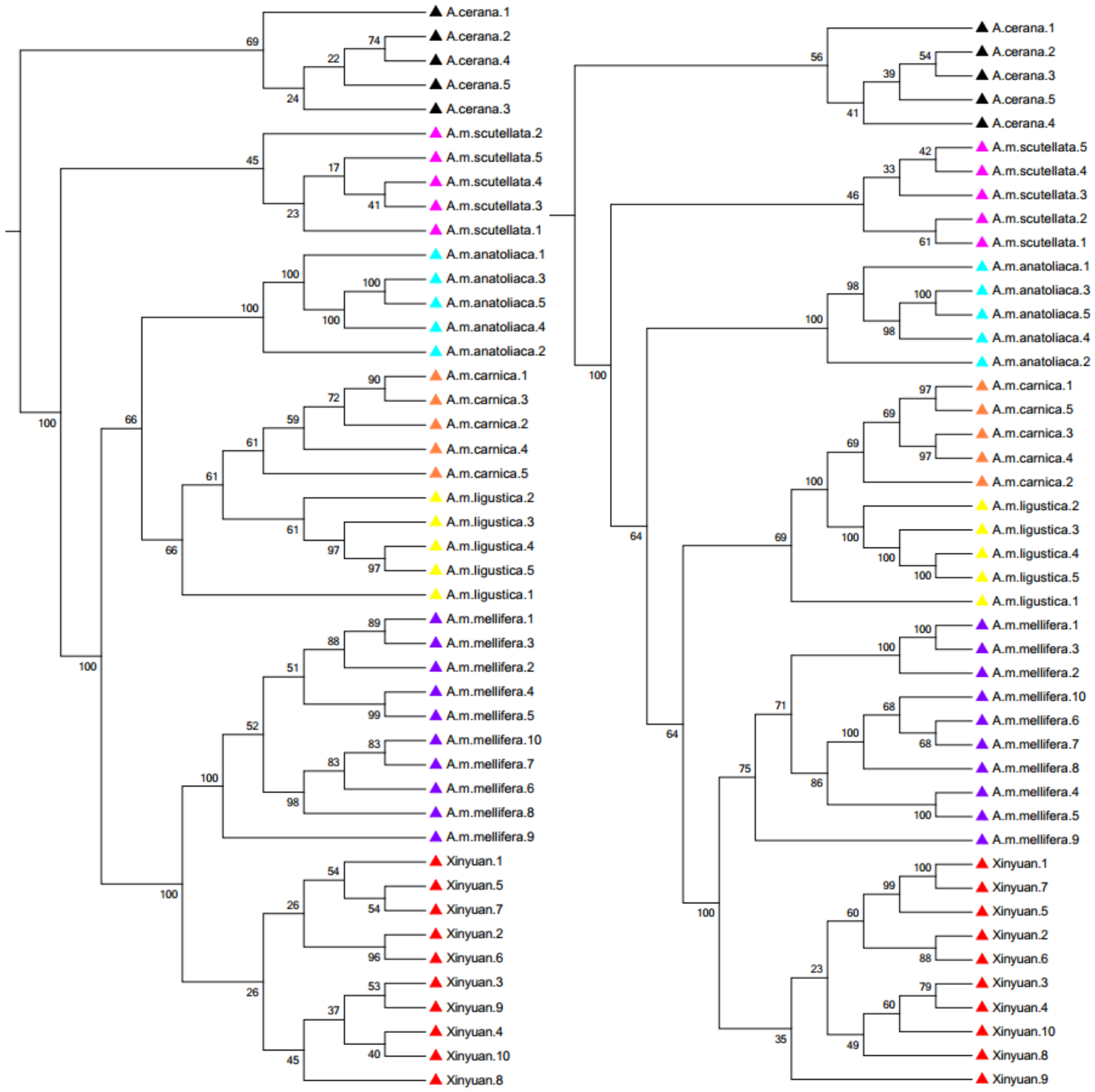
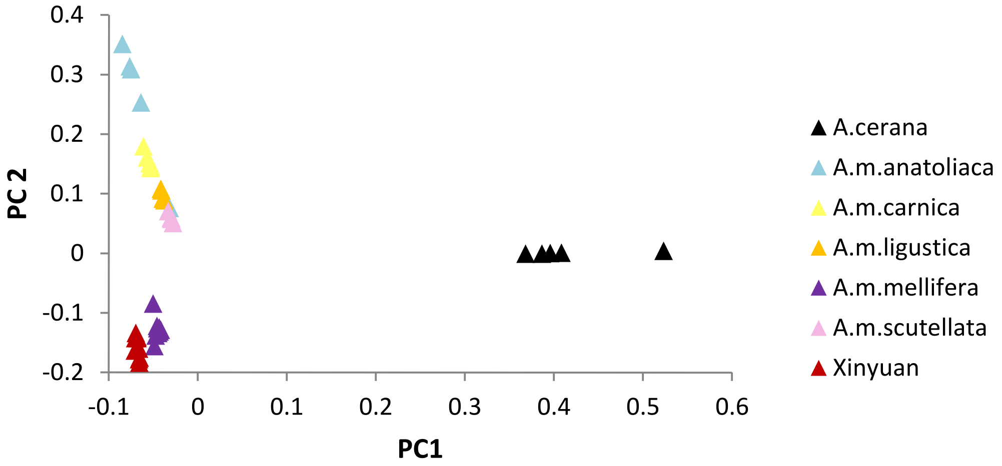
Supplementary Materials

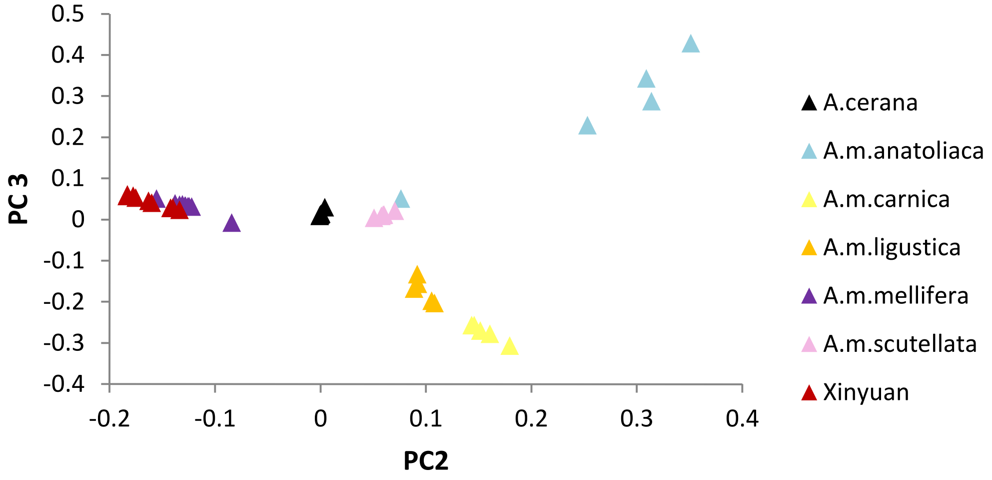


(A) (B)

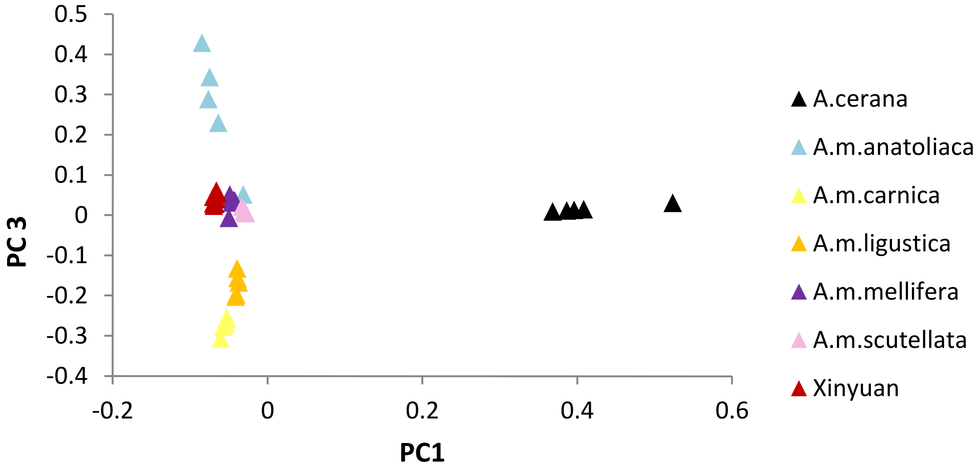
Supplementary Fig. 1. The neighbor joining trees derived from 100 bootstrap replicates based on the distance of all individuals calculated using SNPs from gene (A) and non-gene regions (B). The trees show similar topologies.


0.4
0.3
0.2
0.1
0
-0.1
-0.2
PC 2
-0.1
0
0.1
0.2
0.3
0.4
0.5
0.6
PC1
A.cerana
A.m.anatoliaca
A.m.carnica
A.m.ligustica
A.m.mellifera
A.m.scutellata
Xinyuan

(A)

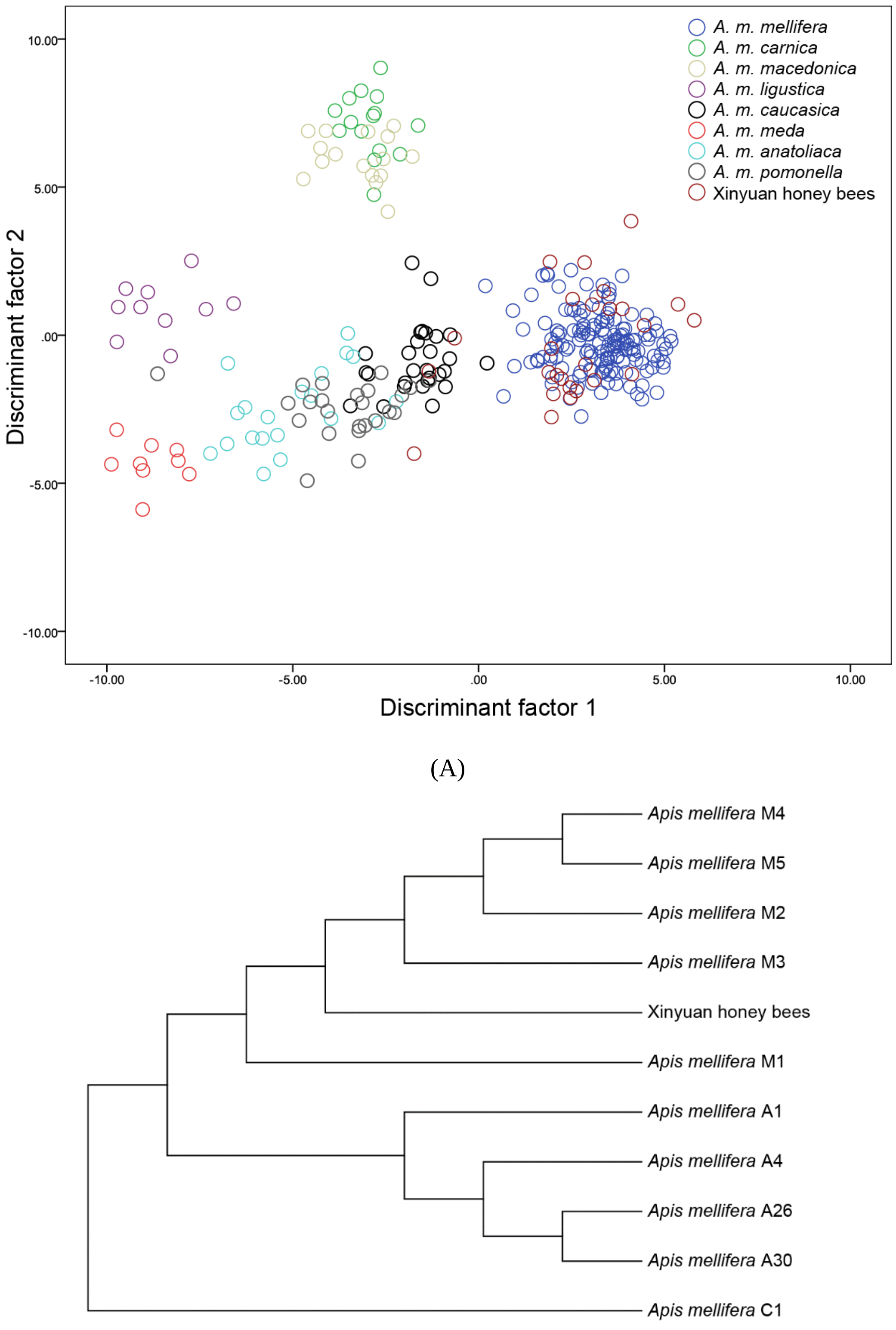

0.5
0.4
0.3
0.2
0.1
0
-0.1
-0.2
-0.3
-0.4
PC 3
-0.2
-0.1
0
0.1
0.2
0.3
0.4
PC2
A.cerana
A.m.anatoliaca
A.m.carnica
A.m.ligustica
A.m.mellifera
A.m.scutellata
Xinyuan

(B)


0.5
0.4
0.3
0.2
0.1
0
-0.1
-0.2
-0.3
-0.4
PC 3
-0.2
0
0.2
0.4
0.6
PC1
A.cerana
A.m.anatoliaca
A.m.carnica
A.m.ligustica
A.m.mellifera
A.m.scutellata
Xinyuan

(C)

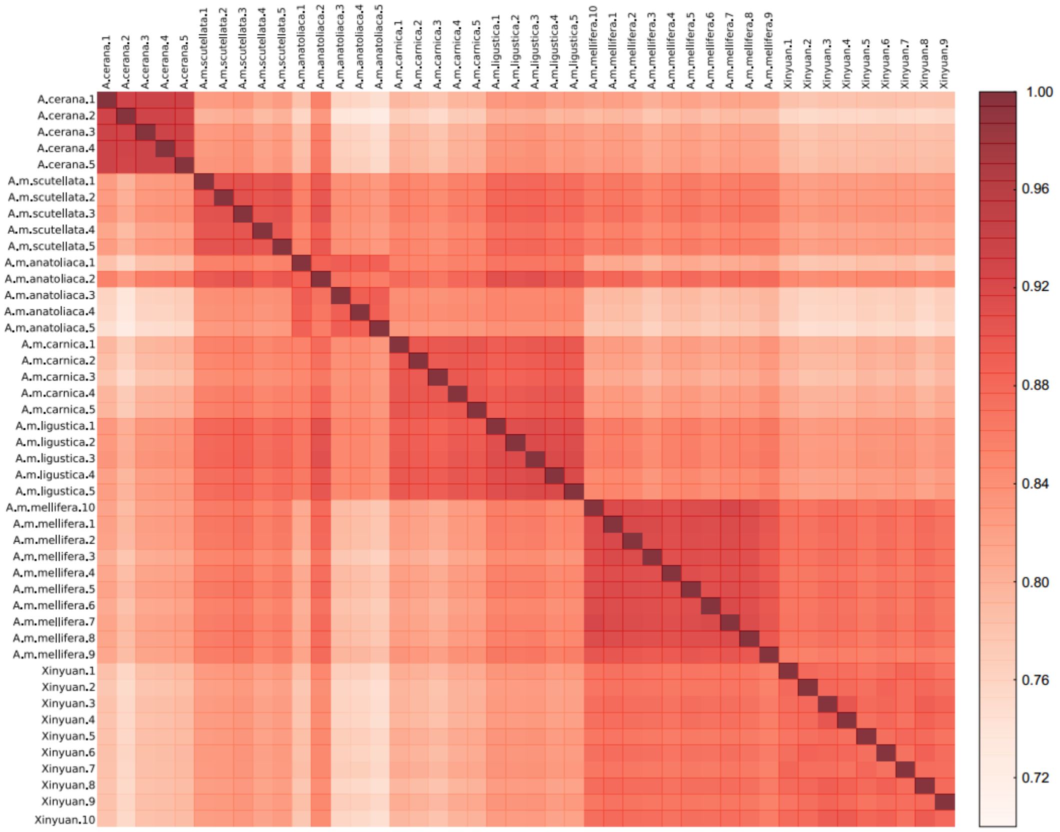
Supplementary Fig. 2. Principal component analysis (PCA) plot of (A) the first two components (PC1 and PC2); (B) PC1 and PC3; (C) PC2 and PC3. The points of Xinyuan bees (*A. m. sinisxinyuan*) are in close proximity to that of the *A. m. mellifera* individuals in the three figures.



(A)

(B)

Supplementary Fig. 3. Taxonomic status of the Xinyuan honey bees. (A) Principle component analysis of the Xinyuan honey bees and subspecies from the C-, O- and A-lineages. Factor 1 is plotted against factor 2. Each symbol represents one colony sample. (B) Phylogenetic tree of the mitochondrial DNA fragment (tRNA ILE and part of the ND2 gene).



Supplementary Fig. 4. The similarity score of the individuals in pairwise comparisons. Heat map colors indicate identity scores (IS). The IS of each pair of individuals within group are lower than between groups. IS are lower between *A. m. carnica* and *A. m. ligustica* than between Xinyuan bees (*A. m. sinisxinyuan*) and *A. m. mellifera*.

Supplementary Tables

Supplementary Table 1. Statistics of genomic sequencing of Xinyuan bees (*A. m. sinisxinyuan*).

Sample	Individual ID	Raw reads	Raw data (bp)	Effective Rate(%)	Clean reads	Clean Data (bp)	Proportion of Q20 (%)	Proportion of Q30 (%)	Proportion of GC (%)
Xinyuan	Xinyuan.1	16,412,010	1,641,201,000	94.48	15,506,452	1,550,645,200	96.15	89.69	35.83
	Xinyuan.2	25,315,236	2,531,523,600	94.32	23,877,762	2,387,776,200	96.28	90.01	34.86
	Xinyuan.3	18,409,458	1,840,945,800	95.02	17,492,766	1,749,276,600	96.45	90.36	34.93
	Xinyuan.4	17,555,088	1,755,508,800	94.84	16,648,888	1,664,888,800	96.47	90.32	35.52
	Xinyuan.5	21,073,228	2,107,322,800	93.90	19,788,184	1,978,818,400	96.14	89.68	35.64
	Xinyuan.6	16,594,726	1,659,472,600	93.44	15,505,778	1,550,577,800	95.99	89.38	35.89
	Xinyuan.7	18,646,258	1,864,625,800	93.21	17,380,082	1,738,008,200	95.84	89.08	35.39
	Xinyuan.8	18,951,110	1,895,111,000	93.97	17,808,028	1,780,802,800	96.02	89.46	35.14
	Xinyuan.9	18,102,432	1,810,243,200	91.39	16,544,256	1,654,425,600	95.87	89.57	35.38
	Xinyuan.10	20,076,588	2,007,658,800	91.36	18,340,974	1,834,097,400	95.95	89.77	34.73

Supplementary Table 2. Information for honey bee populations included in the analyses.

Population	Source of data	Number of individuals	Lineage
Xinyuan bees (*A. m. sinisxinyuan*)	This study	10	M
A. m. mellifera	Download from NCBI	10	M
A. m. scutellata	Download from NCBI	5	A
A. m. ligustica	Download from NCBI	5	C
A. m. carnica	Download from NCBI	5	C
A. m. anatoliaca	Download from NCBI	5	O
A. cerana	Download from NCBI	5	

Supplementary Table 3. Summary of mapping and coverage rate of Xinyuan bees (*A. m. sinisxinyuan*).

Sample	clean bases(bp)	mapping rate	mismatch rate	Average depth	Coverage 1X
Xinyuan.1	1,550,645,200	97.87%	1.77%	7.56	86.78%
Xinyuan.2	2,387,776,200	97.61%	1.76%	10.15	92.62%
Xinyuan.3	1,749,276,600	97.89%	1.78%	7.80	90.84%
Xinyuan.4	1,664,888,800	96.87%	1.78%	7.55	89.79%
Xinyuan.5	1,978,818,400	97.47%	1.76%	8.75	91.20%
Xinyuan.6	1,550,577,800	97.55%	1.79%	7.34	87.79%
Xinyuan.7	1,738,008,200	97.78%	1.76%	7.95	89.86%
Xinyuan.8	1,780,802,800	97.57%	1.81%	8.01	90.10%
Xinyuan.9	1,654,425,600	97.62%	1.79%	7.61	88.87%
Xinyuan.10	1,834,097,400	97.63%	1.83%	8.11	90.79%

Supplementary Table 4. The functional annotation statistics of SNP in bees by ANNOVAR.

Sample	Exonic				Intronic	Splicing	Upstream	Downstream	upstream/downstream	Intergenic	ts	tv	ts/tv	Het rate (‰)	Total
	Stop gain	Stop loss	Synonymous	Non-synonymous											
A.cerana.1	64	8	98,974	25,070	213,096	55	17,749	13,143	1,915	191,709	455,348	113,497	4.011	0.056	568,845
A.cerana.2	95	7	130,154	34,570	296,706	83	24,507	18,756	2,773	264,336	625,453	155,675	4.017	0.088	781,128
A.cerana.3	71	6	94,813	23,949	203,588	59	17,118	13,065	1,964	182,572	436,301	107,600	4.054	0.054	543,901
A.cerana.4	76	3	91,270	22,938	192,595	59	15,979	11,909	1,745	174,042	414,025	102,905	4.023	0.05	516,930
A.cerana.5	68	6	86,468	21,474	179,784	46	15,131	11,066	1,775	162,745	388,207	96,343	4.029	0.043	484,550
A.m.scutellata.1	45	6	23,564	6,613	260,043	36	9,524	7,687	899	222,004	444,164	87,994	5.047	0.787	532,158
A.m.scutellata.2	54	1	21,373	6,242	238,125	35	8,680	7,514	845	205,154	408,265	81,382	5.016	0.7	489,647
A.m.scutellata.3	31	3	20,167	5,651	213,003	32	7,746	6,529	701	182,676	365,587	72,533	5.04	0.594	438,120
A.m.scutellata.4	41	8	25,996	7,312	301,805	36	11,002	9,233	1,072	258,348	514,722	102,143	5.039	0.964	616,865
A.m.scutellata.5	49	5	23,209	6,539	252,795	33	9,064	7,566	845	216,039	432,031	85,882	5.03	0.76	517,913
A.m.anatoliaca.1	37	2	15,981	5,460	217,440	33	7,673	6,618	756	185,101	370,202	70,116	5.279	0.518	440,318
A.m.anatoliaca.2	4	1	3,951	1,269	42,212	7	1,603	1,340	133	37,163	74,079	13,885	5.335	0.036	87,964
A.m.anatoliaca.3	32	3	20,496	6,891	283,136	33	9,825	8,382	923	241,565	480,927	91,816	5.237	0.738	572,743
A.m.anatoliaca.4	50	5	20,962	7,059	287,251	41	9,974	8,523	944	244,509	488,085	92,719	5.264	0.872	580,804
A.m.anatoliaca.5	54	5	23,471	7,893	329,853	39	11,236	9,482	1,028	280,644	559,063	106,297	5.259	0.985	665,360
A.m.carnica.1	31	1	12,105	4,277	156,896	23	5,375	4,664	505	133,699	266,849	51,795	5.152	0.423	318,644

A.m.carnica.2	32	6	12,943	4,654	173,619	29	5,898	5,136	530	149,554	296,269	57,326	5.168	0.492	353,595
A.m.carnica.3	38	4	13,701	5,089	191,291	38	6,658	5,781	692	166,595	327,125	64,000	5.111	0.547	391,125
A.m.carnica.4	32	4	11,390	4,070	146,516	23	5,171	4,317	512	127,264	251,428	48,857	5.146	0.373	300,285
A.m.carnica.5	24	1	12,039	4,094	151,830	22	5,354	4,624	543	130,651	259,700	50,487	5.143	0.401	310,187
A.m.ligustica.1	18	0	8,985	2,923	102,775	11	3,494	2,939	306	90,198	177,707	34,704	5.12	0.276	212,411
A.m.ligustica.2	19	1	8,886	2,823	99,232	13	3,465	3,003	323	87,167	172,212	33,423	5.152	0.261	205,635
A.m.ligustica.3	14	0	7,736	2,416	85,958	16	3,196	2,634	295	74,101	148,322	28,745	5.159	0.174	177,067
A.m.ligustica.4	17	1	9,309	3,121	104,633	16	3,894	3,163	398	91,590	181,442	35,511	5.109	0.212	216,953
A.m.ligustica.5	18	0	9,155	3,002	102,357	14	3,797	3,061	337	88,805	177,110	34,183	5.181	0.201	211,293
A.m.mellifera.10	30	4	20,261	6,302	247,197	35	9,072	7,730	823	209,064	419,871	82,250	5.104	0.336	502,121
A.m.mellifera.1	40	6	19,366	6,000	236,133	28	8,631	7,292	776	199,416	400,679	78,592	5.098	0.305	479,271
A.m.mellifera.2	34	4	20,229	6,384	249,469	36	9,127	7,806	870	209,924	423,030	82,483	5.128	0.321	505,513
A.m.mellifera.3	40	7	24,144	7,952	328,101	45	11,970	10,342	1,130	277,654	554,775	108,573	5.109	0.532	663,348
A.m.mellifera.4	40	9	24,182	8,041	311,323	42	11,355	9,613	1,010	264,398	528,597	103,372	5.113	0.89	631,969
A.m.mellifera.5	36	3	20,067	6,380	248,559	26	8,998	7,757	870	209,701	421,530	82,436	5.113	0.367	503,966
A.m.mellifera.6	39	7	21,943	7,050	290,981	31	10,527	9,044	986	245,366	491,729	96,049	5.119	0.469	587,778
A.m.mellifera.7	32	5	21,012	6,634	254,509	33	9,299	7,943	810	214,661	431,995	84,679	5.101	0.367	516,674
A.m.mellifera.8	32	6	21,404	6,741	257,273	31	9,416	8,048	866	214,835	435,329	85,159	5.111	0.404	520,488
A.m.mellifera.9	32	6	20,992	6,619	268,010	28	9,543	8,446	902	227,173	454,623	88,791	5.12	0.884	543,414
Xinyuan.1	42	12	31,047	10,107	580,211	50	20,332	17,815	1,974	499,498	966,597	196,940	4.908	1.856	1,163,537
Xinyuan.2	48	14	33,807	11,409	676,190	49	25,428	21,792	2,659	597,801	1,137,678	234,198	4.857	2.238	1,371,876
Xinyuan.3	45	14	31,618	10,392	617,408	52	22,682	19,890	2,355	538,025	1,032,820	212,225	4.866	1.677	1,245,045

Xinyuan.4	49	12	30,322	9,989	590,522	49	21,221	18,521	2,179	514,427	986,704	203,022	4.86	1.394	1,189,726
Xinyuan.5	41	14	32,840	10,918	639,471	58	23,475	19,960	2,327	564,623	1,075,895	220,497	4.879	2.344	1,296,392
Xinyuan.6	38	9	30,149	9,931	578,052	47	20,231	17,395	1,984	503,099	965,458	197,860	4.879	1.623	1,163,318
Xinyuan.7	36	10	31,376	10,322	610,683	54	21,864	18,763	2,222	532,787	1,020,764	209,900	4.863	2.103	1,230,664
Xinyuan.8	52	11	31,281	10,572	605,959	51	22,527	19,249	2,308	536,703	1,021,337	209,903	4.865	1.46	1,231,240
Xinyuan.9	47	12	30,902	10,398	594,356	44	21,352	18,605	2,197	521,536	997,394	204,584	4.875	1.892	1,201,978
Xinyuan.10	45	12	31,836	10,732	625,093	42	23,202	20,189	2,395	550,958	1,051,068	216,006	4.865	1.643	1,267,074

Supplementary Table 5. The functional annotation statistics of indel in bees by ANNOVAR.

Sample	Exonic						Intronic	Splicing	Upstream	Upstream/Downstream	Intergenic	Insertion	Deletion	Het Rate (‰)	Total
	Stop gain	Stop loss	Frameshift deletion	Frameshift insertion	Non-frameshift deletion	Non-frameshift insertion									
A.cerana.1	3	0	93	39	403	214	34,958	57	1,834	213	30,305	12,261	58,499	0.004	70,760
A.cerana.2	7	3	137	77	583	317	49,953	80	2,716	320	43,428	17,971	83,574	0.007	101,545
A.cerana.3	3	1	91	45	408	201	33,123	46	1,806	205	28,653	11,720	55,505	0.004	67,225
A.cerana.4	7	2	102	38	337	191	31,454	45	1,605	186	27,675	11,045	52,944	0.003	63,989
A.cerana.5	4	3	88	29	335	196	29,194	44	1,603	181	25,572	10,215	49,246	0.003	59,461
A.m.scutellata.1	6	3	90	56	131	123	38,829	25	1,330	129	31,059	33,708	39,635	0.095	73,343
A.m.scutellata.2	3	1	91	55	137	107	34,662	27	1,247	117	27,936	30,484	35,305	0.081	65,789
A.m.scutellata.3	2	1	97	52	99	106	31,172	18	1,089	96	25,142	27,413	31,729	0.068	59,142
A.m.scutellata.4	2	1	113	82	138	132	45,405	43	1,612	165	36,367	39,979	45,957	0.117	85,936
A.m.scutellata.5	4	2	66	69	96	114	37,442	27	1,280	116	29,966	32,701	37,935	0.09	70,636
A.m.anatoliaca.1	5	3	55	62	124	77	32,369	26	1,157	114	26,145	26,254	35,177	0.055	61,431
A.m.anatoliaca.2	1	1	16	10	17	15	5,661	2	193	24	4,731	4,779	6,119	0.003	10,898
A.m.anatoliaca.3	7	1	92	79	153	107	45,055	31	1,592	137	36,234	36,870	48,335	0.088	85,205
A.m.anatoliaca.4	5	2	97	74	154	103	45,553	36	1,577	147	36,744	36,866	49,403	0.104	86,269
A.m.anatoliaca.5	5	3	109	96	188	132	54,847	43	1,869	167	44,183	44,819	58,950	0.126	103,769

A.m.carnica.1	2	3	42	58	104	56	23,839	15	798	63	19,383	17,367	27,947	0.046	45,314
A.m.carnica.2	6	2	51	58	111	53	26,972	23	916	78	21,813	19,910	31,231	0.056	51,141
A.m.carnica.3	4	2	53	61	130	62	29,936	22	1,064	93	24,535	21,994	35,159	0.062	57,153
A.m.carnica.4	3	1	55	45	90	39	22,453	11	780	65	18,252	16,322	26,379	0.041	42,701
A.m.carnica.5	3	2	47	49	94	60	22,973	20	832	70	18,591	17,006	26,674	0.043	43,680
A.m.ligustica.1	0	1	26	23	51	41	14,331	10	475	44	11,769	10,406	16,865	0.028	27,271
A.m.ligustica.2	2	1	28	40	76	40	13,984	8	487	44	11,511	10,176	16,625	0.027	26,801
A.m.ligustica.3	0	1	26	30	61	27	12,228	9	494	41	9,981	8,435	14,945	0.018	23,380
A.m.ligustica.4	4	1	67	37	74	35	15,619	10	564	57	12,890	10,777	19,240	0.024	30,017
A.m.ligustica.5	1	1	43	39	69	42	15,211	16	563	51	12,504	10,538	18,618	0.022	29,156
A.m.mellifera.10	3	3	50	67	130	83	38,483	26	1,318	129	30,587	32,359	40,000	0.036	72,359
A.m.mellifera.1	1	3	59	65	122	68	36,525	30	1,278	109	28,882	30,621	37,960	0.032	68,581
A.m.mellifera.2	1	3	65	68	124	87	39,134	26	1,363	114	31,015	32,993	40,577	0.034	73,570
A.m.mellifera.3	5	4	88	107	173	116	52,881	38	1,865	181	42,058	44,570	55,015	0.061	99,585
A.m.mellifera.4	1	3	99	93	191	131	51,756	39	1,811	144	41,753	43,857	54,158	0.133	98,015
A.m.mellifera.5	3	3	77	64	137	75	38,959	32	1,347	120	30,733	32,690	40,358	0.039	73,048
A.m.mellifera.6	3	4	62	90	156	106	45,606	42	1,554	137	36,213	38,343	47,420	0.051	85,763
A.m.mellifera.7	4	2	77	68	144	98	40,188	30	1,388	114	31,732	33,877	41,525	0.039	75,402
A.m.mellifera.8	2	2	57	67	150	111	40,117	26	1,405	121	31,457	33,630	41,464	0.042	75,094
A.m.mellifera.9	3	3	63	69	124	90	40,519	42	1,360	149	32,850	34,813	42,067	0.104	76,880
Xinyuan.1	9	4	106	121	320	233	108,142	57	3,692	356	87,466	93,227	111,572	0.251	204,799
Xinyuan.2	8	5	122	142	382	258	133,542	77	4,985	521	110,176	116,912	139,046	0.326	255,958

Xinyuan.3	7	5	115	139	337	240	119,352	63	4,416	461	96,626	104,176	122,611	0.227	226,787
Xinyuan.4	6	7	110	122	320	253	114,337	59	4,079	402	92,430	99,475	117,286	0.182	216,761
Xinyuan.5	8	6	106	143	353	269	123,558	67	4,511	428	101,013	107,397	128,110	0.331	235,507
Xinyuan.6	9	4	99	133	300	226	108,991	65	3,835	344	88,352	94,561	112,081	0.218	206,642
Xinyuan.7	5	4	107	121	309	235	114,750	65	4,100	418	93,925	99,244	119,415	0.291	218,659
Xinyuan.8	4	5	107	134	323	231	118,886	69	4,414	453	96,889	104,171	122,307	0.197	226,478
Xinyuan.9	4	5	106	127	315	236	111,974	69	3,986	400	91,594	97,242	116,084	0.254	213,326
Xinyuan.10	7	6	107	135	296	247	121,154	65	4,507	455	99,467	106,315	125,333	0.22	231,648

Supplementary Table 6. Tracy-Widom statistics of the top ten eigenvalues from PCA analysis of 45 individuals.

Number	**Eigenvalue**	**TW**	***P-value***
1	10.628857	6.212	1.12E-06
2	9.283494	11.911	9.51E-14
3	3.648300	1.754	1.56E-02
4	3.345304	1.892	1.24E-02
5	3.184757	3.108	1.38E-03
6	2.663874	0.980	4.99E-02
7	2.540443	1.798	1.45E-02
8	2.369168	2.217	7.18E-03
9	2.365180	5.012	2.22E-05
10	1.904863	1.727	1.63E-02

Supplementary Table 7. Comparative characteristics of *A. m. sinisxinyuan*, *A. m. mellifera*, *A. m. carnica*, *A. m. ligustica*, *A. m. caucasica*, and *A. m. pomonella*. Values are presented as means ± standard deviations of samples, with each sample representing one colony. N = number of sampled colonies. Measurements of size are in units of 1:100 mm; wing venation angles are in degrees. Characters of pigmentation: 0 =completely dark, 9 = completely bright (yellow). Measurements were taken according to Ruttner (1988).

	sinisxinyuan (N = 20)	***mellifera*** (N = 9)	***carnica*** (N = 20)	***ligustica*** (N = 12)	***caucasica*** (N = 12)	***pomonella*** (N = 31)
hairlength	49.89 ± 2.41	43.47 ± 4.77	29.57 ± 3.74	27.92 ± 2.35	33.22 ± 1.96	26.85 ± 1.95
proboscis	595.00 ± 11.02	607.15 ± 13.12 (N = 4)	640.87 ± 7.51 (N = 18)	635.94 ± 7.86	706.64 ± 15.06	641.16 ± 17.96
body size	409.95 ± 7.19	463.02 ± 9.58	453.44 ± 6.25	436.93 ± 7.8	456.62 ± 7.76	449.49 ± 14.04
cubital index	1.67 ± 0.16	1.82 ± 0.2	2.69 ± 0.18	2.52 ± 0.12	2.14 ± 0.12	2.24 ± 0.20
sternite 6 index	68.96 ± 1.31	77.99 ± 2.92	83.81 ± 1.2	84.14 ± 1.49	82.14 ± 1.14	78.18 ± 3.03 (N = 29)
tarsus index	54.11 ± 1.26	54.86 ± 1.64	55.31 ± 1.37	55.24 ± 0.68	57.81 ± 0.75	56.78 ± 1.35
pigmentation tergite 2	1.71 ± 1.68	2.1 ± 0.74	1.39 ± 0.95 (N = 15)	7.87 ± 0.4	3.92 ± 0.27	5.65 ± 1.12
tomentum index	1.26 ± 0.12	1.63 ± 0.57	2.07 ± 0.26	2.2 ± 0.54	2.76 ± 0.21	2.05 ± 0.39

Supplementary Table 8. GO enrichment of the selective sweep genes in *A. m. sinisxinyuan* & *A. m. mellifera* compared to *A. m. scutellata*.

GO_accession	**Description**	**Term type**	***P*-value**	**Gene (#)**
GO:0051899	membrane depolarization	BP	9.64E-05	4
GO:0042417	dopamine metabolic process	BP	0.001131	4
GO:0017150	tRNA dihydrouridine synthase activity	MF	0.001251	3
GO:0010883	regulation of lipid storage	BP	0.001981	5
GO:0007629	flight behavior	BP	0.002020	5
GO:0007626	locomotory behavior	BP	0.003594	13
GO:0003254	regulation of membrane depolarization	BP	0.003615	2
GO:0010644	cell communication by electrical coupling	BP	0.003615	2
GO:0016264	gap junction assembly	BP	0.003615	2
GO:0005355	glucose transmembrane transporter activity	MF	0.003826	6
GO:0015149	hexose transmembrane transporter activity	MF	0.003826	6
GO:0045199	maintenance of epithelial cell apical/basal polarity	BP	0.004169	2
GO:0048047	mating behavior, sex discrimination	BP	0.004309	2
GO:0031080	nuclear pore outer ring	CC	0.004454	3
GO:0008280	cohesin core heterodimer	CC	0.004633	2
GO:0007488	histoblast morphogenesis	BP	0.004694	3
GO:0004617	phosphoglycerate dehydrogenase activity	MF	0.004798	2
GO:0005921	gap junction	CC	0.004822	3
GO:0030534	adult behavior	BP	0.004855	11
GO:0031638	zymogen activation	BP	0.005234	2

Supplementary Table 9. KEGG enrichment of the selective sweep genes in *A. m. sinisxinyuan* & *A. m. mellifera* relative to *A. m. scutellata*.

ID	#Term	*P*-value	Gene (#)
ame00230	Purine metabolism	0.00056654	13
ame03013	RNA transport	0.00067975	13
ame00511	Other glycan degradation	0.00242878	4
ame01100	Metabolic pathways	0.00255971	43
ame03050	Proteasome	0.01634206	5
ame00520	Amino sugar and nucleotide sugar metabolism	0.01634206	5
ame04145	Phagosome	0.02180289	6
ame00900	Terpenoid backbone biosynthesis	0.03462671	3
ame03015	mRNA surveillance pathway	0.03817694	6
ame04391	Hippo signaling pathway - fly	0.03995289	5
ame04122	Sulfur relay system	0.04380862	2
ame00512	Mucin type O-Glycan biosynthesis	0.04380862	2
ame03450	Non-homologous end-joining	0.04380862	2

Supplementary Table 10. KEGG enrichment of the selective sweep genes in *A. m. sinisxinyuan* relative to *A. m. mellifera*.

ID	#Term	*P*-value	Gene (#)
ame00983	Drug metabolism - other enzymes	0.025161	2
ame04130	SNARE interactions in vesicular transport	0.030699	2
ame04391	Hippo signaling pathway - fly	0.038240	3
ame03008	Ribosome biogenesis in eukaryotes	0.065188	3
ame00740	Riboflavin metabolism	0.080605	1
ame03030	DNA replication	0.092758	2

Supplementary note

Materials and methods

Morphometric analysis

Fifteen workers from each colony were dissected and analyzed for morphometric measurement according to the methods described by Ruttner et al (1988). A total of 39 morphometric characters were measured, among which wing venation angles and characters of size were measured using a stereomicroscope and a computer-aided measuring system that based on a CCD system, with a measuring program system developed by the Institute of Environment and Sustainable Development in Agriculture, Chinese Academy of Agricultural Sciences (CAAS).

Mitochondrial analysis

Total DNA was extracted from the thorax muscle tissue of each individual from each colony. An mtDNA region that encompasses the tRNA ILE and part of the ND2 gene were amplified using the primer set: ILE: 5' –TGATAAAAGAAATATTTTGA -3'; and L1: 5' –GAATCTAATTAATAAAAAA -3'. The amplifications were carried out following the procedure in Arias and Sheppard (1996). PCR products sequenced on an ABI377 automated sequencer in the North Molecular Research Core Facility of Beijing Genomics Institute.

References

Ruttner F. 1988. Biogeography and taxonomy of honeybees. Berlin: Springer-Verlag.