*Article*

Gene Expression Analysis Reveals Potential Response Factors to Temperature in *Bemisia tabaci* Mediterranean

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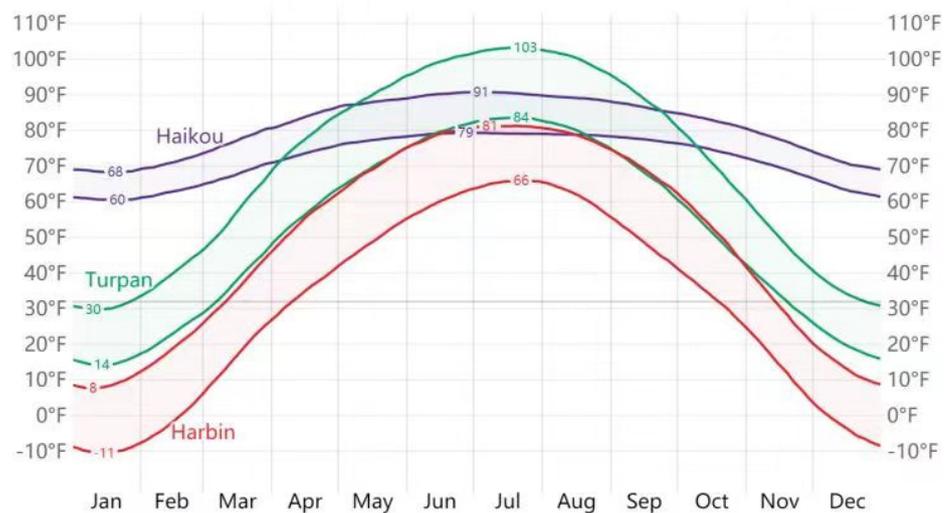
Supplementary Figure S1.: The daily average high and low air temperatures at two meters above the ground (© WeatherSpark.com).
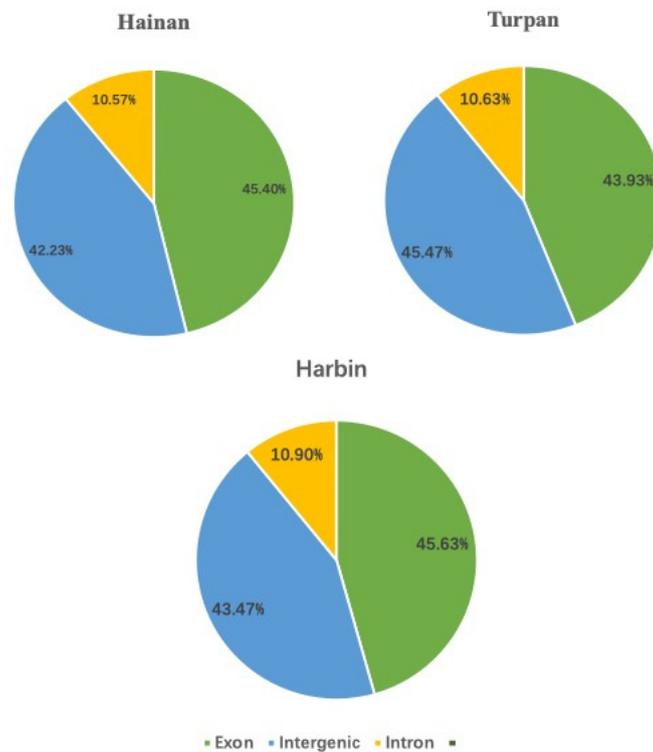
Supplementary Figure S2. The distribution of reads mapped to reference genome from three *Bemisia tabaci* geographic populations
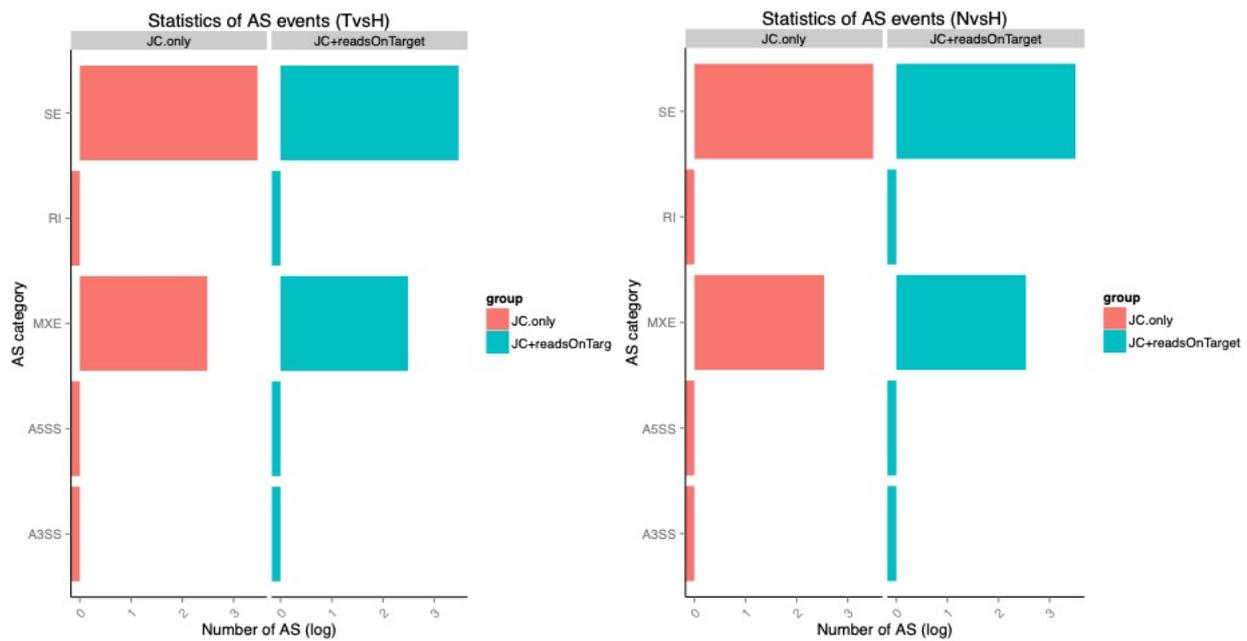
Supplementary Figure S3. Classification and Counting of Alternative splicing Events from two comparisons (T: Turpan; H: Harbin; N: Hainan)

* SE：Skipped exon; MXE: Mutually exclusive exon; A5SS: Alternative 5' splice site; A3SS: Alternative 3' splice site; RI: Retained intron

Supplementary Table S1 Summary of the quality of data output

Sample name	Raw reads	Clean reads	clean bases	Error rate(%)	Q20(%)	Q30(%)	GC content(%)
T_1	42000720	39894888	5.98G	0.02	95.55	89.44	37.15
T_2	44783106	42276006	6.34G	0.02	94.9	88.34	36.64
T_3	46750216	44541656	6.68G	0.02	95.51	89.23	37.25
H_1	46525472	44139430	6.62G	0.02	95.62	89.66	37.59
H_2	52915098	49816812	7.47G	0.02	95.28	88.73	37.59
H_3	59508372	56266916	8.44G	0.02	95.29	88.79	37.4
N_1	49765444	47823190	7.17G	0.02	95.74	89.75	38.41
N_2	44400592	41869522	6.28G	0.02	95.85	90.17	37.57
N_3	45833748	44061888	6.61G	0.02	95.68	89.83	36.48

Supplementary Table S2 List of reads and reference genome alignment

Sample name	T_1	T_2	T_3	H_1	H_2	H_3	N_1	N_2	N_3
Total reads	39894888	42276006	44541656	44139430	49816812	56266916	47823190	41869522	44061888
Total mapped	28626392	28610618	32632565	31263253	36536167	39056824	35329405	30139913	30301158
	(71.75%)	(67.68%)	(73.26%)	(70.83%)	(73.34%)	(69.41%)	(73.88%)	(71.99%)	(68.77%)
Multiple mapped	3686583	3812385	4289457	4302940	4926232	5439613	4676941	4134175	4141156
	(9.24%)	(9.02%)	(9.63%)	(9.75%)	(9.89%)	(9.67%)	(9.78%)	(9.87%)	(9.4%)
Uniquely mapped	24939809	24798233	28343108	26960313	31609935	33617211	30652464	26005738	26160002
	(62.51%)	(58.66%)	(63.63%)	(61.08%)	(63.45%)	(59.75%)	(64.1%)	(62.11%)	(59.37%)
Read-1	12708964	12656388	14411048	13722653	16106051	17066394	15598975	13217681	13326529
	(31.86%)	(29.94%)	(32.35%)	(31.09%)	(32.33%)	(30.33%)	(32.62%)	(31.57%)	(30.25%)
Read-2	12230845	12141845	13932060	13237660	15503884	16550817	15053489	12788057	12833473
	(30.66%)	(28.72%)	(31.28%)	(29.99%)	(31.12%)	(29.41%)	(31.48%)	(30.54%)	(29.13%)
Reads map to '+'	12451550	12384769	14152379	13461663	15793250	16799527	15316235	12989965	13064610
	(31.21%)	(29.3%)	(31.77%)	(30.5%)	(31.7%)	(29.86%)	(32.03%)	(31.02%)	(29.65%)
Reads map to '-'	12488259	12413464	14190729	13498650	15816685	16817684	15336229	13015773	13095392
	(31.3%)	(29.36%)	(31.86%)	(30.58%)	(31.75%)	(29.89%)	(32.07%)	(31.09%)	(29.72%)
Non-splice reads	19298666	19758616	21579613	20405033	23657048	25770124	22564645	19814815	20511928
	(48.37%)	(46.74%)	(48.45%)	(46.23%)	(47.49%)	(45.8%)	(47.18%)	(47.33%)	(46.55%)
Splice reads	5641143	5039617	6763495	6555280	7952887	7847087	8087819	6190923	5648074
	(14.14%)	(11.92%)	(15.18%)	(14.85%)	(15.96%)	(13.95%)	(16.91%)	(14.79%)	(12.82%)

Supplementary Table S3 Classification and quantity statistics of Alternative splicing events in comparison between Turpan and Harbin

Event Type	Num Events. JC. only	Sig Events. JC. only	Num Events. JC. + reads On Target	Sig Events. JC. + readsOn Target
Skipped exon	2927	185 (107:78)	2981	195 (113:82)
Mutually exclusive exon	306	67 (34:33)	306	71 (38:33)
Alternative 5' splice site	0	0 (0:0)	0	0 (0:0)
Alternative 3' splice site	0	0 (0:0)	0	0 (0:0)
Retained intron	0	0 (0:0)	0	0 (0:0)

* Num Events. JC. only: total number of alternative splicing events detected only by junction counts; Sig Events. JC. only: total number of differential alternative splicing events detected only by Junction Counts (the number of up-regulated alternative splicing events: the number of down-regulated alternative splicing events); Num Events. JC. + reads On Target: total number of alternative splicing events detected using both junction counts and reads on target. Sig Events. JC. + reads On Target: total number of differential alternative splicing events detected using both junction counts and reads on target (the number of up-regulated alternative splicing events: the number of down-regulated alternative splicing events).

Supplementary Table S4 Classification and quantity statistics of Alternative splicing events in comparison between Hainan and Harbin 11

Event Type	NumEvents.JC.only	SigEvents.JC.only	NumEvents.JC.+readsOnTarget	SigEvents.JC.+readsOnTarget
Skipped exon	3159	159(76:83)	3212	168 (78:90)
Mutually exclusive exon	345	73 (35:38)	345	80 (41:39)
Alternative 5' splice site	0	0 (0:0)	0	0 (0:0)
Alternative 3' splice site	0	0 (0:0)	0	0 (0:0)
Retained intron	0	0 (0:0)	0	0 (0:0)

*Same as supplementary Table 3.   12

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Supplementary Table S5 Distribution of differential expressed genes in GO terms enriched in biological processes, cell components, and molecular functions

Go terms	NvsH	TvsH	TvsN
Biological process	62.43%	58.44%	62.15%
Cellular component	11.29%	14.46%	11.46%
Molecular function	26.28%	27.10%	26.39%