

Table S1. Genotype information and least square means (standard error in parenthesis) of all traits in the original scale.

Genotype	Subspecies	Geography	In 19 subset	Latitude	Longitude	Instantaneous WUE dry	Instantaneous WUE wet	Long-term $\Delta^{13}C$ dry	Long-term $\Delta^{13}C$ wet	Bolting time
BNK	East	Allopatric	Yes	44.79	-113.31	4.028 (0.248)	3.988 (0.317)	-30.068 (0.215)	-30.459 (0.191)	29.312 (0.539)
ECMF	East	Allopatric	Yes	44.54	-112.62	4.028 (0.248)	4.460 (0.309)	-30.520 (0.215)	-31.456 (0.191)	26.479 (0.528)
HMC	East	Allopatric	Yes	44.52	-112.19	4.028 (0.248)	3.817 (0.384)	-30.335 (0.215)	-30.935 (0.191)	34.671 (0.801)
MAH	East	Allopatric	No	44.18	-113.74	4.028 (0.248)	4.076 (0.309)	-30.431 (0.215)	-30.722 (0.191)	26.725 (0.528)
MIL	East	Allopatric	No	44.37	-113.36	4.028 (0.248)	4.051 (0.312)	-29.856 (0.215)	-30.528 (0.191)	29.839 (0.528)
PCS	East	Allopatric	Yes	44.03	-113.45	4.028 (0.248)	5.589 (0.309)	-31.578 (0.215)	-32.048 (0.191)	34.100 (0.528)
BHS	East	Sympatric	Yes	44.41	-114.41	4.506 (0.260)	4.253 (0.318)	-31.966 (0.215)	-31.023 (0.191)	30.345 (0.539)
EGM	East	Sympatric	Yes	45.54	-113.83	4.506 (0.260)	4.226 (0.499)	-30.614 (0.215)	-31.108 (0.191)	34.457 (1.670)
FLF	East	Sympatric	Yes	44.80	-113.80	4.506 (0.260)	4.730 (0.310)	-31.352 (0.215)	-31.052 (0.191)	29.355 (0.528)
JAM	East	Sympatric	No	44.97	-114.09	4.506 (0.260)	4.541 (0.317)	-30.942 (0.215)	-31.074 (0.191)	29.281 (0.551)
MFP	East	Sympatric	Yes	44.96	-114.66	4.506 (0.260)	4.244 (0.370)	-30.908 (0.215)	-30.769 (0.191)	29.211 (0.735)
PAR	East	Sympatric	No	44.62	-114.52	4.506 (0.260)	4.492 (0.310)	-30.951 (0.215)	-31.656 (0.191)	31.240 (0.528)
BSC	West	Allopatric	Yes	44.42	-115.47	4.116 (0.249)	4.729 (0.333)	-30.099 (0.215)	-32.086 (0.191)	33.553 (0.606)
BVC	West	Allopatric	Yes	44.41	-115.37	4.116 (0.249)	4.384 (0.310)	-29.997 (0.215)	-31.475 (0.191)	38.054 (0.528)
DDW	West	Allopatric	Yes	44.30	-115.48	4.116 (0.249)	4.750 (0.310)	-30.455 (0.215)	-32.182 (0.191)	37.644 (0.528)
THT	West	Allopatric	Yes	44.37	-115.14	4.116 (0.249)	4.480 (0.309)	-30.042 (0.215)	-31.469 (0.191)	33.219 (0.528)
VNH	West	Allopatric	Yes	44.41	-115.29	4.116 (0.249)	4.775 (0.309)	-30.684 (0.215)	-31.477 (0.191)	38.381 (0.528)
WHC	West	Allopatric	Yes	44.57	-115.54	4.116 (0.249)	4.592 (0.368)	-31.155 (0.215)	-31.242 (0.191)	36.963 (0.763)
BHM	West	Sympatric	Yes	44.41	-114.38	3.911 (0.242)	4.473 (0.309)	-30.092 (0.215)	-30.781 (0.191)	32.116 (0.528)
BVM	West	Sympatric	Yes	44.79	-113.78	3.911 (0.242)	5.035 (0.309)	-30.152 (0.215)	-30.916 (0.191)	36.787 (0.528)
IRF	West	Sympatric	Yes	44.94	-114.12	3.911 (0.242)	4.457 (0.308)	-30.569 (0.215)	-31.655 (0.191)	37.443 (0.528)
LTM	West	Sympatric	Yes	45.71	-113.99	3.911 (0.242)	4.469 (0.308)	-30.264 (0.215)	-30.931 (0.191)	38.344 (0.528)
Ruby	West	Sympatric	No	45.55	-113.76	3.911 (0.242)	4.706 (0.311)	-30.336 (0.215)	-30.878 (0.191)	50.800 (0.528)
UpSil	West	Sympatric	Yes	44.91	-114.39	3.911 (0.242)	4.151 (0.309)	-30.250 (0.215)	-31.349 (0.191)	38.344 (0.528)

Genotype	Flowering time	Flowering duration	Flowering rosette width	Flowering height	Flowering leaf number	Flowering rosette number	Flowering stalk number	Main stalk diameter
BNK	9.758 (0.689)	17.200 (1.299)	103.066 (2.640)	192.020 (8.342)	46.959 (2.342)	1.074 (0.109)	1.034 (0.078)	2.751 (0.072)
ECMF	9.225 (0.676)	12.932 (1.272)	81.178 (2.592)	318.143 (8.195)	68.943 (2.302)	1.223 (0.107)	1.142 (0.077)	2.713 (0.071)
HMC	13.696 (1.027)	20.194 (1.931)	110.855 (3.785)	248.553 (11.975)	48.137 (3.334)	1.070 (0.158)	1.073 (0.110)	2.931 (0.098)
MAH	6.900 (0.676)	18.116 (1.272)	94.336 (2.592)	215.978 (8.195)	55.038 (2.302)	2.287 (0.107)	1.724 (0.077)	2.331 (0.071)
MIL	9.225 (0.676)	14.861 (1.272)	113.433 (2.592)	234.663 (8.195)	66.300 (2.302)	1.527 (0.107)	1.505 (0.077)	2.749 (0.071)
PCS	11.142 (0.676)	17.111 (1.272)	111.027 (2.592)	161.935 (8.195)	84.270 (2.302)	1.071 (0.107)	1.069 (0.077)	3.180 (0.071)
BHS	11.209 (0.689)	14.963 (1.299)	101.569 (2.641)	141.910 (8.343)	58.474 (2.342)	1.842 (0.109)	1.534 (0.078)	2.150 (0.072)
EGM	11.861 (2.117)	14.346 (3.829)	109.594 (6.784)	192.419 (23.218)	50.042 (6.589)	1.303 (0.277)	1.209 (0.179)	2.402 (0.181)
FLF	10.453 (0.676)	18.501 (1.272)	98.293 (2.593)	244.439 (8.196)	70.760 (2.303)	2.114 (0.107)	1.661 (0.077)	2.774 (0.071)
JAM	8.079 (0.704)	11.902 (1.327)	112.695 (2.694)	230.686 (8.506)	55.544 (2.386)	1.259 (0.112)	1.084 (0.080)	2.484 (0.073)
MFP	9.691 (0.942)	15.009 (1.774)	105.510 (3.508)	216.182 (11.062)	42.128 (3.082)	1.301 (0.147)	1.085 (0.103)	2.336 (0.092)
PAR	9.923 (0.676)	16.049 (1.272)	120.029 (2.593)	156.448 (8.196)	69.622 (2.303)	1.582 (0.107)	1.443 (0.077)	2.634 (0.071)
BSC	9.532 (0.776)	20.251 (1.462)	103.459 (2.941)	119.810 (9.270)	66.803 (2.593)	1.023 (0.122)	1.002 (0.087)	3.272 (0.079)
BVC	14.181 (0.676)	21.436 (1.272)	101.364 (2.592)	68.249 (8.195)	64.800 (2.302)	1.094 (0.107)	1.003 (0.077)	3.435 (0.071)
DDW	13.610 (0.676)	22.039 (1.272)	107.031 (2.592)	60.436 (8.195)	67.564 (2.302)	1.018 (0.107)	1.003 (0.077)	3.271 (0.071)
THT	12.427 (0.676)	21.757 (1.272)	101.947 (2.592)	153.783 (8.195)	94.967 (2.302)	1.246 (0.107)	1.003 (0.077)	3.410 (0.071)
VNH	14.467 (0.676)	31.241 (1.272)	102.723 (2.592)	91.928 (8.195)	68.052 (2.302)	1.056 (0.107)	1.003 (0.077)	3.392 (0.071)
WHC	13.349 (0.979)	21.813 (1.931)	94.201 (3.625)	124.135 (11.444)	68.767 (3.186)	1.787 (0.152)	1.145 (0.106)	3.055 (0.098)
BHM	8.315 (0.675)	18.746 (1.272)	95.140 (2.591)	143.647 (8.195)	62.243 (2.302)	1.047 (0.107)	1.000 (0.077)	3.270 (0.071)
BVM	13.863 (0.675)	22.363 (1.272)	111.947 (2.591)	113.122 (8.195)	63.625 (2.302)	1.123 (0.107)	1.000 (0.077)	3.223 (0.071)
IRF	15.291 (0.675)	21.666 (1.299)	91.064 (2.591)	106.437 (8.195)	64.398 (2.302)	1.009 (0.107)	1.000 (0.077)	2.960 (0.072)
LTM	18.758 (0.675)	21.117 (1.272)	101.350 (2.591)	113.162 (8.195)	62.121 (2.302)	1.009 (0.107)	1.000 (0.077)	2.871 (0.071)
Ruby	32.832 (0.675)	50.734 (1.272)	108.842 (2.591)	91.295 (8.195)	98.590 (2.302)	1.123 (0.107)	1.000 (0.077)	4.096 (0.071)
UpSil	14.190 (0.675)	24.694 (1.272)	111.365 (2.591)	81.671 (8.195)	71.106 (2.302)	1.313 (0.107)	1.000 (0.077)	3.272 (0.071)

Genotype	Reproductive branch number	Main stalk height	Stalk height containing branch	Internode between branch	Rosette width	Rosette height	Rosette volume
BNK	20.021 (0.975)	547.591 (16.907)	256.439 (9.896)	13.598 (0.322)	171.306 (7.758)	128.054 (4.110)	1039527.330 (72353.119)
ECMF	23.199 (0.958)	523.641 (16.630)	211.237 (9.719)	9.366 (0.315)	125.862 (7.758)	102.801 (4.110)	451124.529 (72353.119)
HMC	18.898 (1.374)	609.620 (23.590)	269.797 (13.995)	15.259 (0.479)	134.886 (7.758)	99.422 (4.110)	503740.771 (72353.119)
MAH	16.773 (0.958)	537.162 (16.630)	243.053 (9.719)	15.762 (0.315)	138.915 (7.758)	95.688 (4.110)	497262.932 (72353.119)
MIL	21.070 (0.958)	555.126 (16.630)	219.303 (9.719)	10.878 (0.315)	151.485 (7.758)	93.554 (4.110)	580697.239 (72353.119)
PCS	20.385 (0.958)	490.880 (16.630)	220.654 (9.719)	11.300 (0.315)	103.946 (7.758)	78.082 (4.110)	237861.173 (72353.119)
BHS	11.825 (0.976)	391.289 (16.915)	143.953 (9.905)	12.724 (0.322)	139.292 (7.758)	91.389 (4.110)	466005.940 (72353.119)
EGM	14.285 (2.352)	500.284 (41.111)	188.118 (23.559)	13.946 (0.973)	157.019 (7.758)	109.172 (4.110)	736484.176 (72353.119)
FLF	19.079 (0.959)	513.228 (16.637)	217.509 (9.727)	12.249 (0.316)	133.168 (7.758)	81.252 (4.110)	381746.907 (72353.119)
JAM	13.604 (0.995)	582.651 (17.225)	205.532 (10.100)	16.319 (0.329)	151.539 (7.758)	89.255 (4.110)	551394.510 (72353.119)
MFP	11.331 (1.279)	519.104 (21.968)	178.295 (13.032)	17.707 (0.440)	138.809 (7.758)	95.835 (4.110)	488522.943 (72353.119)
PAR	18.015 (0.959)	462.889 (16.637)	222.874 (9.727)	13.037 (0.316)	128.173 (7.758)	80.897 (4.110)	349626.709 (72353.119)
BSC	26.355 (1.081)	375.217 (18.653)	173.157 (10.994)	6.850 (0.362)	155.607 (7.758)	106.256 (4.110)	713541.445 (72353.119)
BVC	19.607 (0.958)	253.868 (16.631)	101.220 (9.719)	5.302 (0.315)	132.402 (7.758)	92.563 (4.110)	428893.977 (72353.119)
DDW	20.139 (0.958)	281.104 (16.631)	149.582 (9.719)	7.655 (0.315)	148.516 (7.758)	91.674 (4.110)	559464.415 (72353.119)
THT	23.903 (0.958)	372.084 (16.631)	155.172 (9.719)	6.762 (0.315)	123.216 (7.758)	75.313 (4.110)	312526.141 (72353.119)
VNH	21.166 (0.958)	321.977 (16.631)	134.161 (9.719)	6.577 (0.315)	155.124 (7.758)	103.589 (4.110)	673660.943 (72353.119)
WHC	26.201 (1.369)	389.527 (23.486)	184.113 (13.947)	7.270 (0.478)	134.335 (7.758)	84.205 (4.110)	401803.703 (72353.119)
BHM	22.476 (0.958)	372.986 (16.629)	159.491 (9.717)	7.566 (0.315)	171.124 (7.758)	96.622 (4.110)	748954.235 (72353.119)
BVM	19.244 (0.958)	356.838 (16.629)	141.294 (9.717)	7.787 (0.315)	160.972 (7.758)	97.867 (4.110)	672675.083 (72353.119)
IRF	16.037 (0.975)	328.344 (16.904)	122.690 (9.893)	8.335 (0.322)	149.691 (7.758)	89.864 (4.110)	549117.862 (72353.119)
LTM	17.115 (0.958)	287.840 (16.629)	92.969 (9.717)	5.703 (0.315)	173.058 (7.758)	102.846 (4.110)	826456.977 (72353.119)
Ruby	21.449 (0.958)	251.834 (16.629)	104.563 (9.717)	4.707 (0.315)	148.080 (7.758)	95.199 (4.110)	559439.024 (72353.119)
UpSil	16.164 (0.958)	295.219 (16.629)	104.750 (9.717)	6.729 (0.315)	147.274 (7.758)	98.401 (4.110)	553895.833 (72353.119)

Genotype	Rosette leaf number	Rosette fresh weight	Rosette dry weight	Rosette water weight	Rosette water proportion	Rosette leaf area	Rosette leaf packing
BNK	25.839 (3.107)	1982.394 (284.576)	283.625 (44.103)	1701.250 (242.063)	0.857 (0.004)	83.753 (11.893)	0.095 (0.016)
ECMF	24.269 (3.107)	1660.232 (284.576)	239.169 (44.103)	1420.705 (242.063)	0.862 (0.004)	68.857 (11.893)	0.150 (0.016)
HMC	22.308 (3.107)	1533.702 (284.576)	228.302 (44.103)	1303.198 (242.063)	0.853 (0.004)	64.231 (11.893)	0.123 (0.016)
MAH	26.885 (3.107)	1660.446 (284.576)	231.365 (44.103)	1429.592 (242.063)	0.866 (0.004)	71.576 (11.893)	0.149 (0.016)
MIL	40.745 (3.107)	2220.347 (284.576)	325.513 (44.103)	1898.411 (242.063)	0.850 (0.004)	96.103 (11.893)	0.188 (0.016)
PCS	19.954 (3.107)	1261.680 (284.576)	185.427 (44.103)	1072.245 (242.063)	0.863 (0.004)	53.116 (11.893)	0.194 (0.016)
BHS	27.269 (3.107)	1815.608 (284.576)	274.932 (44.103)	1540.043 (242.063)	0.849 (0.004)	76.153 (11.893)	0.162 (0.016)
EGM	23.608 (3.107)	2084.845 (284.576)	309.312 (44.103)	1777.580 (242.063)	0.850 (0.004)	84.858 (11.893)	0.131 (0.016)
FLF	29.100 (3.107)	1745.861 (284.576)	251.223 (44.103)	1494.950 (242.063)	0.861 (0.004)	77.090 (11.893)	0.200 (0.016)
JAM	27.662 (3.107)	1848.178 (284.576)	268.215 (44.103)	1580.858 (242.063)	0.857 (0.004)	74.663 (11.893)	0.142 (0.016)
MFP	28.969 (3.107)	1811.215 (284.576)	273.055 (44.103)	1537.630 (242.063)	0.848 (0.004)	77.828 (11.893)	0.161 (0.016)
PAR	27.792 (3.107)	1668.294 (284.576)	256.063 (44.103)	1410.139 (242.063)	0.846 (0.004)	68.991 (11.893)	0.192 (0.016)
BSC	28.796 (3.107)	3148.146 (284.576)	459.659 (44.103)	2694.160 (242.063)	0.854 (0.004)	143.832 (11.893)	0.223 (0.016)
BVC	22.127 (3.107)	2487.000 (284.576)	392.185 (44.103)	2092.035 (242.063)	0.834 (0.004)	112.422 (11.893)	0.259 (0.016)
DDW	21.735 (3.107)	2564.354 (284.576)	359.584 (44.103)	2207.457 (242.063)	0.864 (0.004)	118.136 (11.893)	0.232 (0.016)
THT	23.042 (3.107)	1999.096 (284.576)	329.354 (44.103)	1662.165 (242.063)	0.825 (0.004)	91.605 (11.893)	0.258 (0.016)
VNH	21.342 (3.107)	2593.602 (284.576)	365.709 (44.103)	2230.607 (242.063)	0.864 (0.004)	119.117 (11.893)	0.185 (0.016)
WHC	23.958 (3.107)	2451.002 (284.576)	365.709 (44.103)	2084.575 (242.063)	0.853 (0.004)	109.958 (11.893)	0.271 (0.016)
BHM	22.385 (3.107)	3043.016 (284.576)	456.333 (44.103)	2587.654 (242.063)	0.848 (0.004)	130.738 (11.893)	0.182 (0.016)
BVM	22.646 (3.107)	2729.210 (284.576)	389.748 (44.103)	2340.243 (242.063)	0.864 (0.004)	118.802 (11.893)	0.173 (0.016)
IRF	22.515 (3.107)	3043.551 (284.576)	458.013 (44.103)	2586.337 (242.063)	0.847 (0.004)	133.472 (11.893)	0.255 (0.016)
LTM	22.123 (3.107)	2933.307 (284.576)	431.833 (44.103)	2502.513 (242.063)	0.853 (0.004)	132.543 (11.893)	0.171 (0.016)
Ruby	19.769 (3.107)	2502.078 (284.576)	364.260 (44.103)	2135.950 (242.063)	0.860 (0.004)	109.228 (11.893)	0.182 (0.016)
UpSil	20.162 (3.107)	2563.039 (284.576)	376.213 (44.103)	2185.103 (242.063)	0.856 (0.004)	110.299 (11.893)	0.189 (0.016)

Genotype	Rosette fresh weight / area	Rosette dry weight / area	Rosette water weight / area	Leaf shape Y1	Leaf shape Y2	Leaf shape Y3	Leaf shape Y4	Leaf shape Y5
BNK	23.657 (0.443)	3.381 (0.128)	20.302 (0.374)	0.894 (0.035)	0.853 (0.039)	0.872 (0.070)	1.054 (0.183)	1.882 (0.314)
ECMF	23.589 (0.443)	3.277 (0.128)	20.332 (0.374)	0.894 (0.035)	0.853 (0.039)	0.868 (0.070)	1.006 (0.183)	1.895 (0.314)
HMC	23.184 (0.443)	3.398 (0.128)	19.789 (0.374)	0.894 (0.035)	0.859 (0.039)	0.913 (0.070)	1.133 (0.183)	1.993 (0.314)
MAH	22.919 (0.443)	3.079 (0.128)	19.818 (0.374)	0.894 (0.035)	0.859 (0.039)	0.907 (0.070)	1.208 (0.183)	2.349 (0.314)
MIL	23.440 (0.443)	3.493 (0.128)	19.967 (0.374)	0.894 (0.035)	0.857 (0.039)	0.866 (0.070)	1.090 (0.183)	2.389 (0.314)
PCS	22.447 (0.443)	3.080 (0.128)	19.320 (0.374)	0.894 (0.035)	0.859 (0.039)	0.903 (0.070)	1.027 (0.183)	1.700 (0.314)
BHS	23.781 (0.443)	3.593 (0.128)	20.185 (0.374)	0.923 (0.035)	0.921 (0.039)	0.925 (0.070)	1.321 (0.183)	2.786 (0.314)
EGM	24.821 (0.443)	3.731 (0.128)	21.146 (0.374)	0.923 (0.035)	0.919 (0.039)	0.903 (0.070)	1.032 (0.183)	2.353 (0.314)
FLF	22.398 (0.443)	3.110 (0.128)	19.195 (0.374)	0.923 (0.035)	0.921 (0.039)	0.922 (0.070)	1.246 (0.183)	2.682 (0.314)
JAM	25.038 (0.443)	3.611 (0.128)	21.491 (0.374)	0.923 (0.035)	0.921 (0.039)	0.925 (0.070)	1.202 (0.183)	2.410 (0.314)
MFP	23.152 (0.443)	3.506 (0.128)	19.607 (0.374)	0.923 (0.035)	0.923 (0.039)	0.927 (0.070)	1.204 (0.183)	2.432 (0.314)
PAR	24.056 (0.443)	3.702 (0.128)	20.370 (0.374)	0.923 (0.035)	0.921 (0.039)	0.911 (0.070)	1.112 (0.183)	2.325 (0.314)
BSC	21.979 (0.443)	3.232 (0.128)	18.766 (0.374)	0.973 (0.035)	1.031 (0.039)	1.258 (0.070)	2.202 (0.183)	4.456 (0.314)
BVC	21.754 (0.443)	3.570 (0.128)	18.203 (0.374)	0.973 (0.035)	1.034 (0.039)	1.297 (0.070)	2.631 (0.183)	5.368 (0.314)
DDW	21.368 (0.443)	2.927 (0.128)	18.418 (0.374)	0.973 (0.035)	1.034 (0.039)	1.250 (0.070)	2.261 (0.183)	5.015 (0.314)
THT	20.860 (0.443)	3.597 (0.128)	17.236 (0.374)	0.973 (0.035)	1.036 (0.039)	1.266 (0.070)	2.360 (0.183)	4.980 (0.314)
VNH	21.451 (0.443)	2.938 (0.128)	18.495 (0.374)	0.973 (0.035)	1.030 (0.039)	1.216 (0.070)	2.053 (0.183)	4.651 (0.314)
WHC	22.162 (0.443)	3.268 (0.128)	18.925 (0.374)	0.973 (0.035)	1.033 (0.039)	1.265 (0.070)	2.323 (0.183)	4.938 (0.314)
BHM	23.379 (0.443)	3.559 (0.128)	19.863 (0.374)	0.915 (0.035)	0.941 (0.039)	1.114 (0.070)	2.069 (0.183)	4.689 (0.314)
BVM	22.767 (0.443)	3.128 (0.128)	19.635 (0.374)	0.915 (0.035)	0.944 (0.039)	1.132 (0.070)	2.076 (0.183)	4.762 (0.314)
IRF	22.712 (0.443)	3.453 (0.128)	19.263 (0.374)	0.915 (0.035)	0.946 (0.039)	1.216 (0.070)	2.565 (0.183)	5.685 (0.314)
LTM	22.021 (0.443)	3.218 (0.128)	18.763 (0.374)	0.915 (0.035)	0.943 (0.039)	1.138 (0.070)	2.248 (0.183)	5.062 (0.314)
Ruby	22.341 (0.443)	3.137 (0.128)	19.178 (0.374)	0.915 (0.035)	0.943 (0.039)	1.138 (0.070)	1.956 (0.183)	4.888 (0.314)
UpSil	23.167 (0.443)	3.339 (0.128)	19.853 (0.374)	0.915 (0.035)	0.945 (0.039)	1.165 (0.070)	2.179 (0.183)	4.969 (0.314)

Genotype	Leaf shape Y6	Leaf shape Y7	Leaf shape Y8	Leaf shape Y9
BNK	3.754 (0.393)	5.423 (0.403)	6.179 (0.362)	4.814 (0.276)
ECMF	3.957 (0.393)	5.939 (0.403)	6.758 (0.362)	5.110 (0.276)
HMC	4.105 (0.393)	6.119 (0.403)	6.792 (0.362)	4.999 (0.276)
MAH	4.736 (0.393)	6.482 (0.403)	7.097 (0.362)	5.326 (0.276)
MIL	4.676 (0.393)	6.736 (0.403)	7.485 (0.362)	6.369 (0.276)
PCS	3.863 (0.393)	6.573 (0.403)	7.543 (0.362)	6.226 (0.276)
BHS	5.156 (0.393)	6.920 (0.403)	7.303 (0.362)	5.787 (0.276)
EGM	4.628 (0.393)	6.572 (0.403)	6.909 (0.362)	5.616 (0.276)
FLF	5.611 (0.393)	7.515 (0.403)	7.961 (0.362)	6.346 (0.276)
JAM	5.145 (0.393)	6.666 (0.403)	6.852 (0.362)	5.036 (0.276)
MFP	4.754 (0.393)	6.393 (0.403)	6.682 (0.362)	4.994 (0.276)
PAR	4.899 (0.393)	7.132 (0.403)	7.617 (0.362)	6.120 (0.276)
BSC	7.461 (0.393)	9.654 (0.403)	10.382 (0.362)	8.496 (0.276)
BVC	8.556 (0.393)	11.049 (0.403)	10.973 (0.362)	7.646 (0.276)
DDW	8.749 (0.393)	11.142 (0.403)	11.335 (0.362)	9.148 (0.276)
THT	8.456 (0.393)	10.699 (0.403)	11.120 (0.362)	8.597 (0.276)
VNH	8.125 (0.393)	10.854 (0.403)	11.315 (0.362)	9.016 (0.276)
WHC	8.990 (0.393)	11.454 (0.403)	11.831 (0.362)	9.201 (0.276)
BHM	7.661 (0.393)	9.653 (0.403)	9.872 (0.362)	7.509 (0.276)
BVM	8.204 (0.393)	10.665 (0.403)	10.741 (0.362)	8.575 (0.276)
IRF	9.048 (0.393)	10.968 (0.403)	11.286 (0.362)	8.297 (0.276)
LTM	8.182 (0.393)	10.337 (0.403)	10.705 (0.362)	8.290 (0.276)
Ruby	8.058 (0.393)	10.082 (0.403)	10.156 (0.362)	7.373 (0.276)
UpSil	8.493 (0.393)	10.601 (0.403)	10.965 (0.362)	8.825 (0.276)

Table S2. Trait divergence between subspecies. For all traits in 19 genotypes, shown are trait, category, P -value for subspecies in ANOVA, the subspecies with higher trait value, Q_{ST} , P -value of Q_{ST} compared to empirical F_{ST} distribution, and the correlation with discriminant function analysis (DFA) score from each trait category.

Trait	Category	P -value ^a	Higher ^b	Q_{ST}	$Q_{ST} P^c$	DFA-cor ^d
Instantaneous WUE dry	Physiology	0.346	EAST	-	-	-
Instantaneous WUE wet	Physiology	0.670	WEST	0.00	1.000	-
Long-term $\Delta^{13}C$ dry	Physiology	0.038	WEST	0.33	0.270	-
Long-term $\Delta^{13}C$ wet	Physiology	0.071	WEST	0.26	0.314	-
Bolting time	Phenology	0.001	WEST	0.66	0.128	0.84
Flowering time	Phenology	0.065	WEST	0.29	0.290	0.44
Flowering duration	Phenology	< 0.001	WEST	0.75	0.103	0.63
Flowering rosette width	Phenology	0.983	EAST	0.00	1.000	0.09
Flowering height	Phenology	< 0.001	EAST	0.74	0.107	-0.83
Flowering leaf number	Phenology	0.072	WEST	0.29	0.315	0.28
Flowering rosette number	Phenology	0.096	EAST	0.06	0.614	-0.29
Flowering stalk number	Phenology	0.010	EAST	0.31	0.276	-0.39
Main stalk diameter	Morph-stalk	< 0.001	WEST	0.66	0.123	0.65
Reproductive branch number	Morph-stalk	0.044	WEST	0.18	0.406	0.22
Main stalk height	Morph-stalk	< 0.001	EAST	0.82	0.062	-0.78
Stalk height containing branch	Morph-stalk	0.002	EAST	0.59	0.157	-0.55
Internode between branch	Morph-stalk	< 0.001	EAST	0.88	0.048	-0.87
Rosette width	Morph-rosette	0.149	WEST	0.11	0.501	0.27
Rosette height	Morph-rosette	0.618	EAST	0.00	1.000	-0.12
Rosette volume	Morph-rosette	0.400	WEST	0.00	1.000	0.17
Rosette leaf number	Morph-rosette	0.743	EAST	0.00	1.000	-0.03
Rosette fresh weight	Morph-rosette	0.001	WEST	0.72	0.107	0.53
Rosette dry weight	Morph-rosette	< 0.001	WEST	0.77	0.088	0.52
Rosette water weight	Morph-rosette	0.001	WEST	0.71	0.109	0.52
Rosette water proportion	Morph-rosette	0.468	EAST	0.00	1.000	-0.16
Rosette leaf area	Morph-rosette	< 0.001	WEST	0.79	0.071	0.60
Rosette leaf packing	Morph-rosette	0.004	WEST	0.56	0.167	0.60
Rosette fresh weight / area	Morph-rosette	0.025	EAST	0.42	0.216	-0.40
Rosette dry weight / area	Morph-rosette	0.631	EAST	0.00	1.000	-0.10
Rosette water weight / area	Morph-rosette	0.019	EAST	0.42	0.215	-0.43
Leaf shape Y1	Morph-leaf	0.392	WEST	0.00	1.000	0.11
Leaf shape Y2	Morph-leaf	0.042	WEST	0.50	0.185	0.30
Leaf shape Y3	Morph-leaf	< 0.001	WEST	0.87	0.061	0.53
Leaf shape Y4	Morph-leaf	< 0.001	WEST	0.94	0.029	0.80
Leaf shape Y5	Morph-leaf	< 0.001	WEST	0.93	0.029	0.87
Leaf shape Y6	Morph-leaf	< 0.001	WEST	0.93	0.029	0.91
Leaf shape Y7	Morph-leaf	< 0.001	WEST	0.93	0.029	0.94
Leaf shape Y8	Morph-leaf	< 0.001	WEST	0.94	0.028	0.95
Leaf shape Y9	Morph-leaf	< 0.001	WEST	0.92	0.029	0.93

- a. Boldface denotes significant P -values after sequential Bonferroni correction within each trait category.
- b. This column denotes which subspecies has the higher trait value.
- c. Empirical P -values, based on the proportion of polymorphic SNPs with F_{ST} higher than or equal to Q_{ST} for this trait. Boldface denotes values less than 0.05.
- d. Pearson's correlation coefficient between trait value and the DFA score of each trait category. DFA is not available for physiology traits.

Table S3. Divergence of the ‘composite trait’ from each trait category. This table shows the data from 19 genotypes. For DFA scores from each trait category, this table shows the subspecies effect P -value in univariate ANOVA, the Q_{ST} , and the empirical P value of Q_{ST} compared to genome-wide distribution of SNP F_{ST} .

Trait category	ANOVA P	Q_{ST}	P vs. F_{ST}
Phenology	< 0.001	0.87	0.061
Morphology – stalk	< 0.001	0.91	0.029
Morphology – rosette	< 0.001	0.97	0.028
Morphology – leaf	< 0.001	0.97	0.028

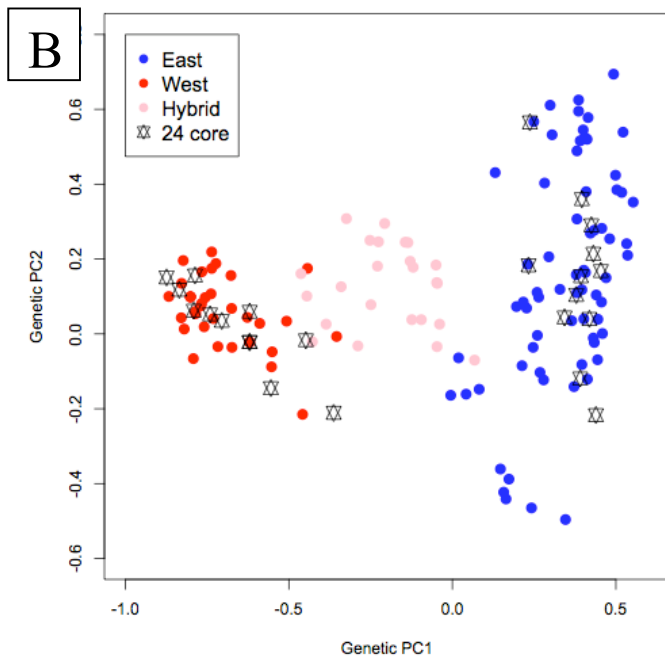
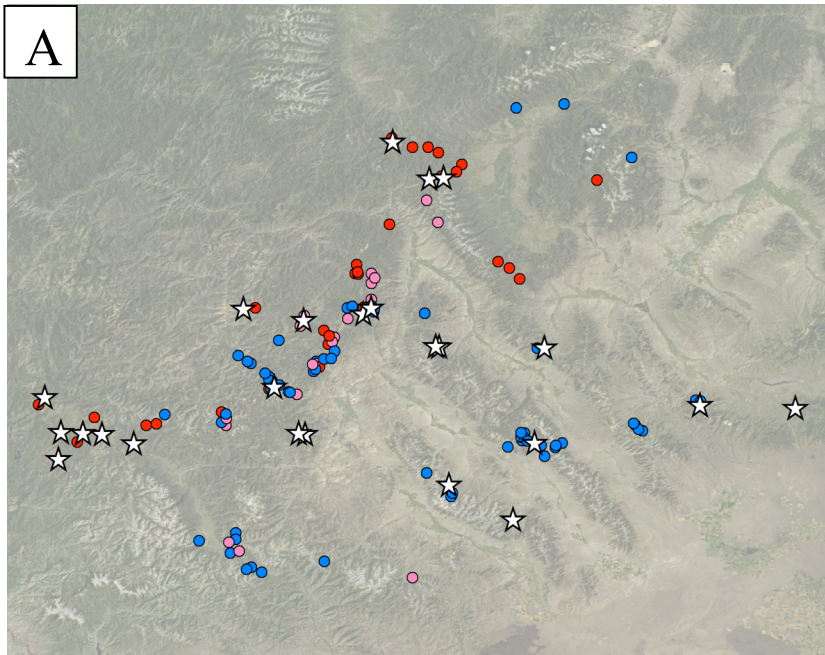
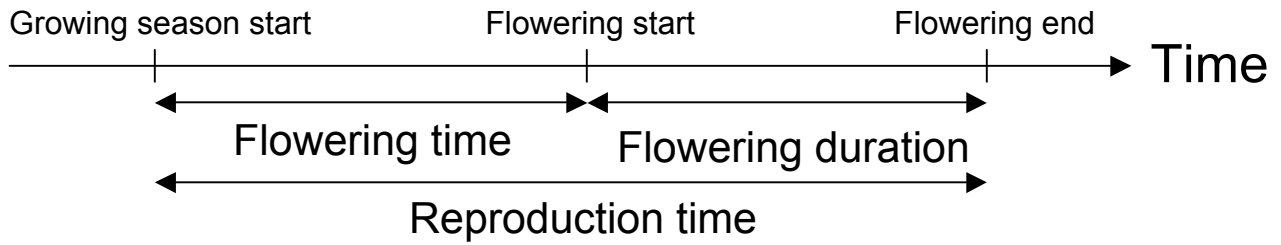
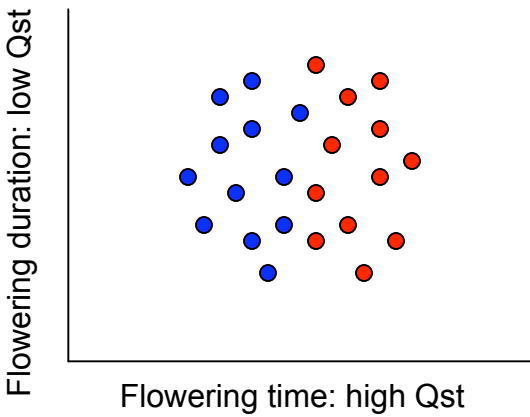


Figure S1. The 24 genotypes represent most of the (A) geographical and (B) genetic variation among all *Boecheera stricta* accessions in our study area (Latitude: 43.50 to 46.00 N, Longitude: 111.00 to 116.00 W). In both panels, white stars represent 24 core genotypes used in this study, blue dots represent EASTERN genotypes, red dots represent WESTERN genotypes, and pink dots represent hybrids. All data are obtained from Lee and Mitchell-Olds (2011). Genetic groups (EAST/WEST/hybrid) were assigned by STRUCTURE.

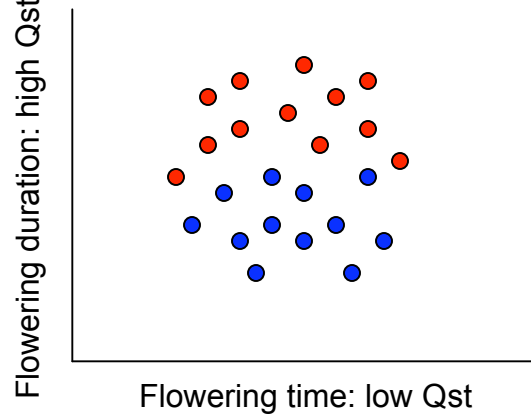
A



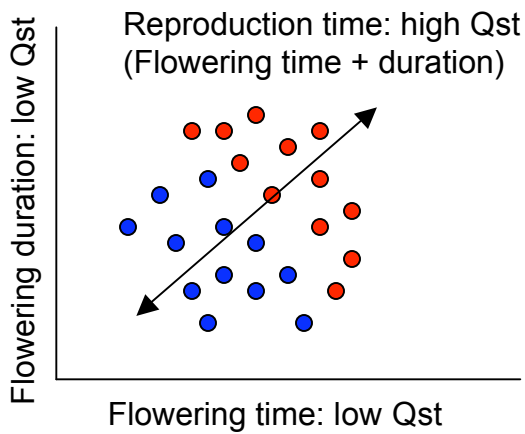
B



C



D



E

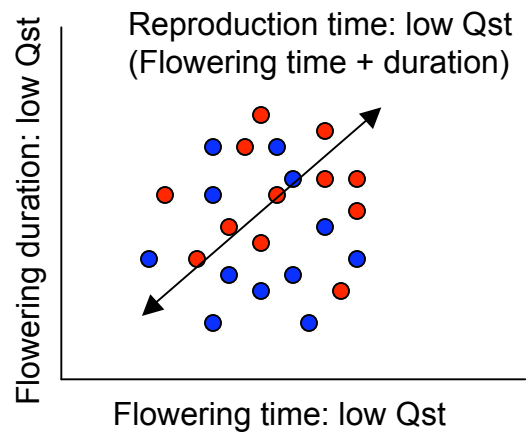


Figure S2: Example of multivariate trait divergence in phenology, assuming natural selection favors the divergence in 'total reproduction time' between the red and blue population. Each point represents one genotype. (A) This trait, although not directly measured, is a linear combination of flowering time and duration. The two populations may diverge in either flowering time (B), duration (C), or both (D). In examples (B) and (C), the traits under divergent selection could be identified via their high Q_{st} . In case (D), however, no univariate trait has Q_{st} higher than the significance threshold, and the divergent selection on phenology as a whole might not be identified. Nevertheless, these three examples all have the same amount of divergence in total reproduction time. In case (D), the composite trait under strongest divergent selection (and therefore its Q_{st}) could be identified via discriminant function analysis or MANOVA between the two populations. Notice that this method only involves a rotation of axis and does not produce an upward bias in multivariate Q_{st} . Finally, in (E) if none of the univariate or multivariate traits has diverged, the multivariate Q_{st} also will be low.

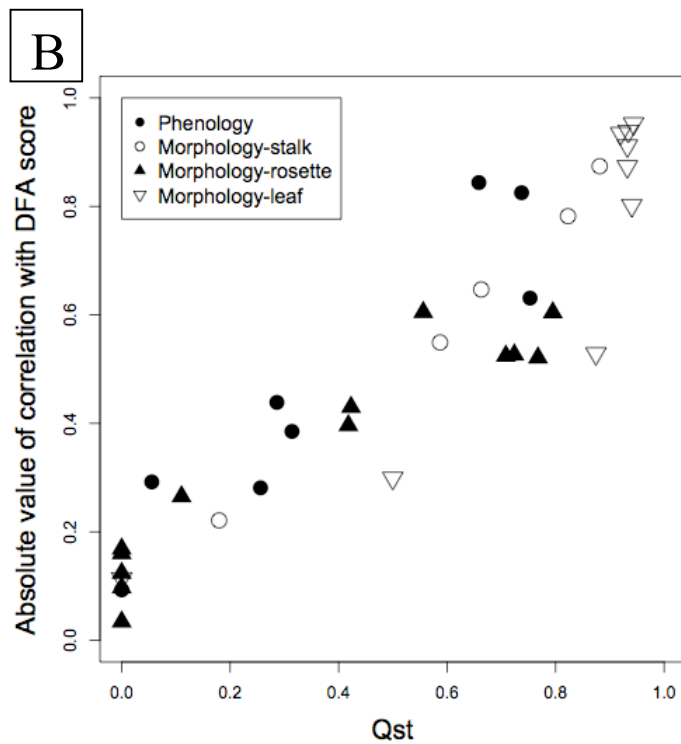
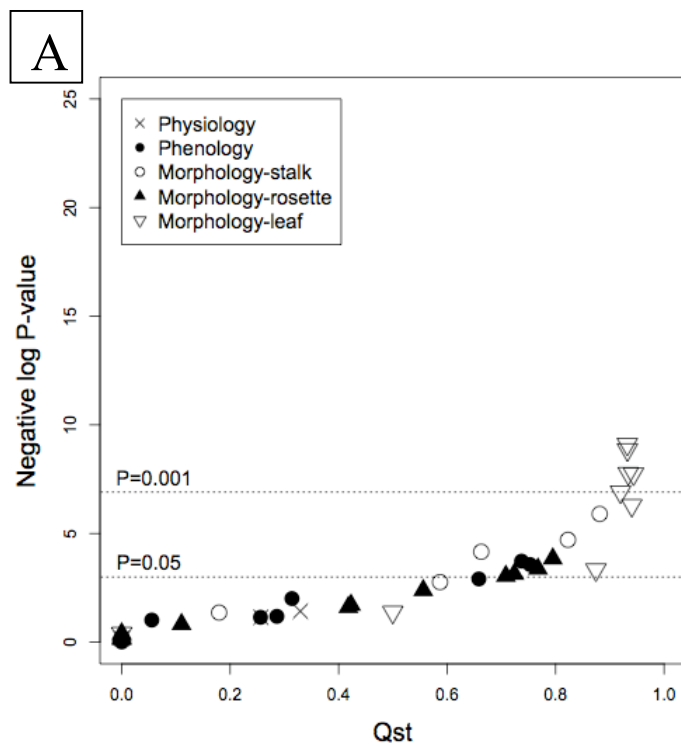


Figure S3. Relationship between trait Q_{ST} and (A) P value of subspecies effect in ANOVA (B) absolute value of correlation with discriminant function analysis (DFA) score from each trait category. Shown are data from 19 genotypes. All axes and scales are equivalent to Figure 3.