*Article*

# Epigenetic Patterns and Geographical Parthenogenesis in the Alpine Plant Species *Ranunculus kuepferi* (Ranunculaceae)

**Christoph C. F. Schinkel, Eleni Syngelaki, Bernhard Kirchheimer, Stefan Dullinger, Simone Klatt and Elvira Hörandl**

The following supplementary material is available for this article:

**Table S1.** Results of molecular variance analyses (AMOVA) of epiloci. df: Degrees of freedom, p: p-value.

| Source of variation | df | Non-methylated | | | F statistics | |
| --- | --- | --- | --- | --- | --- | --- |
| | | Variance components | $p$ | % variation | | |
| Among combined groups | 3 | 11.510 | <0.001 | 42.95 | $F_{ST}$: | 0.526 |
| Within groups | 119 | 15.287 | <0.001 | 57.05 | | |
| Among cytotypes | 1 | 7.375 | <0.001 | 27.11 | $F_{ST}$: | 0.533 |
| Within cytotypes | 121 | 19.828 | <0.001 | 72.89 | | |
| Among reproduction modes | 2 | 7.129 | <0.001 | 26.14 | $F_{ST}$: | 0.534 |
| Within reproduction modes | 120 | 20.149 | <0.001 | 73.86 | | |

| Source of variation | df | Internally-methylated | | | F statistics | |
| --- | --- | --- | --- | --- | --- | --- |
| | | Variance components | $p$ | % variation | | |
| Among groups | 3 | 10.900 | <0.001 | 32.98 | $F_{ST}$: | 0.448 |
| Within groups | 119 | 22.151 | <0.001 | 67.02 | | |
| Among cytotypes | 1 | 11.501 | <0.001 | 32.15 | $F_{ST}$: | 0.491 |
| Within cytotypes | 121 | 24.275 | <0.001 | 67.85 | | |
| Among reproduction modes | 2 | 10.515 | <0.001 | 29.57 | $F_{ST}$: | 0.487 |
| Within reproduction modes | 120 | 25.047 | <0.001 | 70.43 | | |

| Source of variation | df | Externally-methylated | | | F statistics | |
| --- | --- | --- | --- | --- | --- | --- |
| | | Variance components | $p$ | % variation | | |
| Among groups | 3 | 8.526 | <0.001 | 27.68 | $F_{ST}$: | 0.366 |
| Within groups | 119 | 22.278 | <0.001 | 72.32 | | |
| Among cytotypes | 1 | 5.011 | <0.001 | 16.23 | $F_{ST}$: | 0.367 |
| Within cytotypes | 121 | 25.859 | <0.001 | 83.77 | | |
| Among reproduction modes | 2 | 4.531 | <0.001 | 14.74 | $F_{ST}$: | 0.365 |
| Within reproduction modes | 120 | 26.216 | <0.001 | 85.26 | | |

**Table S2.** Geary's C values correlated to environmental variables.

| Population | Group | Altitude | Mean Annual Temp. | Annual Precipitation |
|---|---|---|---|---|
| 3 | 2xS | 2.550 | 2.577 | 2.232 |
| 23 | 2xS | 0.676 | 1.869 | 2.464 |
| 24 | 2xS | 0.081 | 0.055 | 0.021 |
| 25 | 2xS | 2.164 | 0.366 | 0.001 |
| 26 | 2xS | 1.948 | 0.279 | 0.021 |
| 27 | 2xS | 2.019 | 0.464 | 0.010 |
| 29 | 2xS | 0.391 | 0.378 | 0.072 |
| 33 | 2xS | 2.992 | 3.090 | 2.613 |
| 31 | 2xS | 0.108 | 0.695 | 0.696 |
| 233 | 2xS | 1.481 | 1.499 | 1.008 |
| 235 | 2xS | 0.092 | 0.055 | 0.021 |
| 202 | 2xS | 0.003 | 0.090 | 0.218 |
| 203 | 2xS | 0.014 | 0.221 | 0.371 |
| 204 | 2xS | 0.278 | 0.596 | 0.768 |
| 206 | 2xS | 0.532 | 1.149 | 1.008 |
| 201 | 2xS | 0.414 | 0.378 | 0.153 |
| 207 | 2xS | 0.073 | 0.214 | 0.153 |
| 112 | 2xS | 0.618 | 1.475 | 2.094 |
| 115 | 2xS | 0.027 | 0.000 | 0.010 |
| 117 | 2xS | 0.585 | 1.666 | 2.464 |
| 26 | 2xM | 1.948 | 0.279 | 0.021 |
| 31 | 2xM | 0.108 | 0.695 | 0.696 |
| 204 | 2xM | 0.278 | 0.596 | 0.768 |
| 207 | 2xM | 0.073 | 0.214 | 0.153 |
| 201 | 4xM | 0.027 | 0.108 | 3.264 |
| 36 | 4xM | 0.158 | 0.404 | 0.288 |
| 37 | 4xM | 0.332 | 0.336 | 0.342 |
| 40 | 4xM | 3.285 | 1.067 | 0.609 |
| 48 | 4xM | 0.018 | 0.108 | 0.010 |
| 54 | 4xM | 0.112 | 0.108 | 2.012 |
| 58 | 4xM | 0.321 | 0.057 | 1.876 |
| 75 | 4xM | 4.632 | 3.252 | 0.860 |
| 17 | 4xM | 0.356 | 0.016 | 0.535 |
| 17 | 4xM | 0.356 | 0.016 | 0.535 |
| 79 | 4xM | 0.050 | 2.140 | 0.116 |
| 83 | 4xM | 0.032 | 0.612 | 0.060 |
| 81 | 4xM | 2.004 | 2.140 | 0.152 |
| 204 | 4xM | 8.287 | 7.480 | 1.618 |
| 205 | 4xM | 0.023 | 0.562 | 0.022 |
| 114 | 4xM | 0.259 | 0.124 | 0.059 |
| 20 | 4xA | 0.027 | 0.108 | 3.264 |
| 36 | 4xA | 0.158 | 0.404 | 0.288 |
| 48 | 4xA | 0.018 | 0.108 | 0.010 |
| 54 | 4xA | 0.112 | 0.108 | 2.012 |
| 75 | 4xA | 4.632 | 3.252 | 0.860 |
| 17 | 4xA | 0.356 | 0.016 | 0.535 |
| 79 | 4xA | 0.050 | 2.140 | 0.116 |
| 83 | 4xA | 0.032 | 0.612 | 0.060 |

| 205 | 4xA | 0.023 | 0.562 | 0.022 |
| 104 | 4xA | 0.096 | 0.148 | 1.056 |
| 114 | 4xA | 0.259 | 0.124 | 0.059 |
| 111 | 4xA | 0.002 | 0.336 | 0.085 |
| 81  | 4xA | 2.004 | 2.140 | 0.152 |

**Table S3.** Candidate loci and environmental correlations as revealed by Samßada. NON = nonmethylated.M = internally methylated.EXT = externally methylated.Env = environmental variable: ALT = elevation, MEAN = Mean annual temperature. Error code (0 if success). AIC = Akaike information criterion, BIC = Bayesian information criterion; Beta_0 = constant parameter (corresponding to marker), Beta_1 = parameter corresponding to environmental variable.

| Marker | Env | Loglikelihood | Gscore | WaldScore | NumError | AIC | BIC | Beta_0 | Beta_1 |
|--------|-----|---------------|--------|-----------|----------|-----|-----|--------|--------|
| EXT154 | ALT | -57.493 | 45.430 | 29.094 | 0 | 118.986 | 134.235 | 9.932 | -0.005 |
| EXT17 | ALT | -55.971 | 41.720 | 28.377 | 0 | 115.942 | 131.191 | 9.077 | -0.005 |
| EXT197 | ALT | -52.083 | 36.847 | 26.700 | 0 | 108.167 | 123.415 | 8.171 | -0.005 |
| EXT199 | ALT | -65.634 | 35.643 | 24.769 | 0 | 135.268 | 150.517 | 8.588 | -0.004 |
| EXT210 | ALT | -45.748 | 35.387 | 25.682 | 0 | 95.495 | 110.744 | 8.067 | -0.005 |
| EXT235 | ALT | -65.402 | 35.384 | 24.791 | 0 | 134.804 | 150.053 | 8.479 | -0.004 |
| EXT241 | ALT | -55.319 | 36.274 | 26.438 | 0 | 114.638 | 129.887 | 8.080 | -0.004 |
| EXT248 | ALT | -55.858 | 31.345 | 24.159 | 0 | 115.717 | 130.965 | 7.246 | -0.004 |
| EXT33 | ALT | -50.375 | 55.833 | 31.731 | 0 | 104.749 | 119.998 | 11.722 | -0.006 |
| EXT351 | ALT | -54.694 | 56.009 | 30.682 | 0 | 113.389 | 128.637 | 12.356 | -0.006 |
| EXT358 | ALT | -59.037 | 34.016 | 25.298 | 0 | 122.074 | 137.323 | 7.749 | -0.004 |
| EXT52 | ALT | -66.965 | 34.750 | 24.005 | 0 | 137.930 | 153.179 | 8.630 | -0.004 |
| EXT74 | ALT | -55.339 | 41.413 | 28.331 | 0 | 114.677 | 129.926 | 8.998 | -0.005 |
| EXT86 | ALT | -55.145 | 51.261 | 30.437 | 0 | 114.290 | 129.538 | 11.075 | -0.006 |
| EXT95 | ALT | -53.405 | 49.772 | 30.557 | 0 | 110.811 | 126.059 | 10.575 | -0.006 |
| M92 | ALT | -67.984 | 34.538 | 22.872 | 0 | 139.968 | 155.216 | 9.183 | 0.004 |
| NON129 | ALT | -65.708 | 37.264 | 24.969 | 0 | 135.416 | 150.665 | 9.102 | -0.004 |
| NON168 | ALT | -55.070 | 50.276 | 30.350 | 0 | 114.140 | 129.389 | 10.825 | -0.006 |
| NON173 | ALT | -57.027 | 41.105 | 28.087 | 0 | 118.055 | 133.304 | 9.001 | -0.005 |
| NON180 | ALT | -62.894 | 33.423 | 24.666 | 0 | 129.787 | 145.036 | 7.796 | -0.004 |
| NON250 | ALT | -46.971 | 32.941 | 24.647 | 0 | 97.942 | 113.190 | 7.637 | -0.005 |
| NON47 | ALT | -57.493 | 38.676 | 27.245 | 0 | 118.986 | 134.235 | 8.557 | -0.005 |
| EXT137 | MEAN | -49.271 | 33.416 | 23.118 | 0 | 102.541 | 117.790 | -3.160 | 0.064 |
| EXT154 | MEAN | -44.554 | 71.307 | 35.385 | 0 | 93.109 | 108.358 | -3.272 | 0.099 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| EXT159 | MEAN | -48.665 | 37.026 | 24.752 | 0 | 101.329 | 116.578 | -3.236 | 0.067 |
| EXT17 | MEAN | -46.162 | 61.338 | 33.658 | 0 | 96.324 | 111.573 | -3.327 | 0.089 |
| EXT186 | MEAN | -52.844 | 43.028 | 28.485 | 0 | 109.688 | 124.936 | -2.845 | 0.069 |
| EXT197 | MEAN | -46.092 | 48.829 | 29.175 | 0 | 96.185 | 111.434 | -3.492 | 0.080 |
| EXT199 | MEAN | -58.851 | 49.209 | 31.336 | 0 | 121.702 | 136.951 | -2.041 | 0.069 |
| EXT210 | MEAN | -42.494 | 41.895 | 24.998 | 0 | 88.988 | 104.237 | -3.883 | 0.079 |
| EXT216 | MEAN | -53.510 | 39.891 | 27.152 | 0 | 111.021 | 126.269 | -2.803 | 0.066 |
| EXT227 | MEAN | -49.330 | 35.694 | 24.262 | 0 | 102.661 | 117.910 | -3.170 | 0.066 |
| EXT235 | MEAN | -56.363 | 53.462 | 32.581 | 0 | 116.726 | 131.974 | -2.221 | 0.074 |
| EXT24 | MEAN | -48.821 | 34.316 | 23.471 | 0 | 101.641 | 116.890 | -3.205 | 0.065 |
| EXT241 | MEAN | -47.142 | 52.627 | 31.015 | 0 | 98.285 | 113.534 | -3.346 | 0.082 |
| EXT248 | MEAN | -49.344 | 44.373 | 28.291 | 0 | 102.689 | 117.938 | -3.175 | 0.073 |
| EXT33 | MEAN | -42.905 | 70.772 | 34.984 | 0 | 89.811 | 105.060 | -3.539 | 0.100 |
| EXT351 | MEAN | -40.373 | 84.652 | 34.728 | 0 | 84.745 | 99.994 | -3.392 | 0.117 |
| EXT358 | MEAN | -52.835 | 46.420 | 29.958 | 0 | 109.670 | 124.919 | -2.813 | 0.071 |
| EXT52 | MEAN | -62.764 | 43.152 | 29.102 | 0 | 129.528 | 144.777 | -1.720 | 0.063 |
| EXT56 | MEAN | -66.457 | 33.275 | 24.867 | 0 | 136.913 | 152.162 | -1.657 | 0.053 |
| EXT74 | MEAN | -45.653 | 60.783 | 33.338 | 0 | 95.307 | 110.555 | -3.403 | 0.089 |
| EXT76 | MEAN | -52.246 | 40.537 | 27.218 | 0 | 108.491 | 123.740 | -2.914 | 0.067 |
| EXT86 | MEAN | -43.512 | 74.527 | 35.525 | 0 | 91.025 | 106.273 | -3.315 | 0.103 |
| EXT95 | MEAN | -44.856 | 66.870 | 34.715 | 0 | 93.713 | 108.962 | -3.368 | 0.095 |
| M228 | MEAN | -60.558 | 40.436 | 25.154 | 0 | 125.116 | 140.364 | 0.618 | -0.065 |
| M290 | MEAN | -64.360 | 34.891 | 23.684 | 0 | 132.721 | 147.970 | 0.594 | -0.057 |
| M32 | MEAN | -56.806 | 55.526 | 30.159 | 0 | 117.612 | 132.861 | 1.359 | -0.080 |
| M92 | MEAN | -60.708 | 49.091 | 30.271 | 0 | 125.415 | 140.664 | 1.530 | -0.069 |
| NON129 | MEAN | -56.764 | 55.152 | 32.641 | 0 | 117.529 | 132.778 | -2.039 | 0.076 |
| NON131 | MEAN | -56.839 | 47.873 | 31.013 | 0 | 117.678 | 132.927 | -2.360 | 0.069 |
| NON157 | MEAN | -51.815 | 33.033 | 23.407 | 0 | 107.629 | 122.878 | -2.945 | 0.061 |
| NON168 | MEAN | -44.356 | 71.704 | 35.403 | 0 | 92.712 | 107.961 | -3.289 | 0.099 |
| NON171 | MEAN | -64.642 | 32.267 | 24.342 | 0 | 133.284 | 148.533 | -1.883 | 0.052 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| NON173 | MEAN | -47.307 | 60.545 | 33.732 | 0 | 98.614 | 113.863 | -3.198 | 0.087 |
| NON180 | MEAN | -54.399 | 50.412 | 31.727 | 0 | 112.798 | 128.046 | -2.578 | 0.073 |
| NON250 | MEAN | -44.612 | 37.659 | 23.936 | 0 | 93.223 | 108.472 | -3.625 | 0.072 |
| NON47 | MEAN | -49.710 | 54.242 | 32.306 | 0 | 103.420 | 118.669 | -3.033 | 0.080 |

**Table S4.** List of the 123 individuals used for MSAP analyses with individual code (population number_plotnumber_individual number) provenances, ploidy level, respective reproductive group, and percentage of sexual seeds with n = 5-10 (data from Schinkel et al. 2016). 2x = diploid, 4x = tetraploid, 2xM = diploid mixed, 2xS = diploid obligate sexual, 4xA = tetraploid obligate apomictic, 4xM = tetraploid mixed.

| | Geographic Coordinates (WGS84) | | | | | |
|---|---|---|---|---|---|---|
| Individual | North | East | Elevation [m.a.s.l.] | Cytotype | Reproduction mode | % sexual seeds |
| 14_2_2 | 4.435.489 | 6.505.583 | 1880 | 2x | 2xM | 80 |
| 26_2_1 | 4.490.033 | 5.469 | 1456 | 2x | 2xM | 80 |
| 31_3_2 | 4.419.522 | 7.659.222 | 1937 | 2x | 2xM | 40 |
| 32_2_3 | 4.420.667 | 71.475 | 2320 | 2x | 2xM | 90 |
| 204_1_1 | 4.415.725 | 6.729.195 | 1640 | 2x | 2xM | 40 |
| 207_3_1 | 4.430.108 | 6.567.389 | 1921 | 2x | 2xM | 20 |
| 3_3_1 | 4.420.028 | 715.639 | 2291 | 2x | 2xS | 100 |
| 3_3_2 | 4.420.028 | 715.639 | 2291 | 2x | 2xS | 100 |
| 23_2_1 | 4.374.931 | 6.657.444 | 1616 | 2x | 2xS | 100 |
| 23_2_2 | 4.374.931 | 6.657.444 | 1616 | 2x | 2xS | 100 |
| 24_3_1 | 4.415.083 | 6.543.611 | 1925 | 2x | 2xS | 100 |
| 24_4_2 | 4.415.083 | 6.543.611 | 1925 | 2x | 2xS | 100 |
| 25_2_1 | 4.490.128 | 5.476.167 | 1435 | 2x | 2xS | 100 |
| 25_3_3 | 4.490.128 | 5.476.167 | 1435 | 2x | 2xS | 100 |
| 25_4_3 | 4.490.128 | 5.476.167 | 1435 | 2x | 2xS | 100 |
| 26_3_2 | 4.490.033 | 5.469 | 1456 | 2x | 2xS | 100 |
| 27_1_1 | 4.483.933 | 5.424.222 | 1449 | 2x | 2xS | 100 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 27_2_1 | 4.483.933 | 5.424.222 | 1449 | 2x | 2xS | 100 |
| 27_2_3 | 4.483.933 | 5.424.222 | 1449 | 2x | 2xS | 100 |
| 29_1_1 | 4.423.111 | 7.617.222 | 2020 | 2x | 2xS | 100 |
| 29_2_3 | 4.423.111 | 7.617.222 | 2020 | 2x | 2xS | 100 |
| 31_2_3 | 4.419.522 | 7.659.222 | 1937 | 2x | 2xS | 100 |
| 33_3_1 | 4.421.305 | 7.146.667 | 2328 | 2x | 2xS | 100 |
| 33_3_3 | 4.421.305 | 7.146.667 | 2328 | 2x | 2xS | 100 |
| 112_1_2 | 438.525 | 6.352.778 | 1626 | 2x | 2xS | 100 |
| 112_2_3 | 438.525 | 6.352.778 | 1626 | 2x | 2xS | 100 |
| 112_4_1 | 438.525 | 6.352.778 | 1626 | 2x | 2xS | 100 |
| 114_4_3 | 4.472.089 | 6.919.861 | 2339 | 2x | 2xS | 100 |
| 115_3_2 | 44.245 | 6.756.111 | 1891 | 2x | 2xS | 100 |
| 115_3_3 | 44.245 | 6.756.111 | 1891 | 2x | 2xS | 100 |
| 117_2_2 | 4.374.556 | 6.655.833 | 1632 | 2x | 2xS | 100 |
| 117_3_3 | 4.374.556 | 6.655.833 | 1632 | 2x | 2xS | 100 |
| 118_3_3 | 4.423.161 | 7.628.333 | 1636 | 2x | 2xS | 100 |
| 201_2_2 | 4.408.044 | 66.375 | 2025 | 2x | 2xS | 100 |
| 201_2_3 | 4.408.044 | 66.375 | 2025 | 2x | 2xS | 100 |
| 202_1_1 | 44.159 | 6.714.611 | 1829 | 2x | 2xS | 100 |
| 202_4_2 | 44.159 | 6.714.611 | 1829 | 2x | 2xS | 100 |
| 203_1_3 | 4.416.294 | 6.710.805 | 1840 | 2x | 2xS | 100 |
| 203_3_1 | 4.415.725 | 6.729.195 | 1840 | 2x | 2xS | 100 |
| 204_4_2 | 4.415.725 | 6.729.195 | 1640 | 2x | 2xS | 100 |
| 206_1_2 | 442.468 | 66.988 | 2049 | 2x | 2xS | 100 |
| 206_3_1 | 442.468 | 66.988 | 2049 | 2x | 2xS | 100 |
| 207_1_3 | 4.430.108 | 6.567.389 | 1921 | 2x | 2xS | 100 |
| 233_1_1 | 4.412.946 | 696.878 | 2185 | 2x | 2xS | 100 |
| 233_1_2 | 4.412.946 | 696.878 | 2185 | 2x | 2xS | 100 |
| 235_1_1 | 4.416.689 | 670.763 | 1930 | 2x | 2xS | 100 |
| 235_1_3 | 4.416.689 | 670.763 | 1930 | 2x | 2xS | 100 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 17_1_2 | 4.505.069 | 6.390.778 | 2357 | 4x | 4xA | 0 |
| 17_3_1 | 4.505.069 | 6.390.778 | 2357 | 4x | 4xA | 0 |
| 17_4_3 | 4.505.069 | 6.390.778 | 2357 | 4x | 4xA | 0 |
| 20_1_2 | 4.634.719 | 7.724.111 | 2200 | 4x | 4xA | 0 |
| 20_2_1 | 4.634.719 | 7.724.111 | 2200 | 4x | 4xA | 0 |
| 20_4_2 | 4.634.719 | 7.724.111 | 2200 | 4x | 4xA | 0 |
| 36_1_3 | 4.538.542 | 7.043.722 | 2152 | 4x | 4xA | 0 |
| 36_3_2 | 4.538.542 | 7.043.722 | 2152 | 4x | 4xA | 0 |
| 48_1_1 | 4.647.153 | 9.728.889 | 2262 | 4x | 4xA | 0 |
| 48_1_3 | 4.647.153 | 9.728.889 | 2262 | 4x | 4xA | 0 |
| 48_4_1 | 4.647.153 | 9.728.889 | 2262 | 4x | 4xA | 0 |
| 54_2_2 | 4.627.239 | 1.057.506 | 2303 | 4x | 4xA | 0 |
| 54_3_1 | 4.627.239 | 1.057.506 | 2303 | 4x | 4xA | 0 |
| 54_3_2 | 4.627.239 | 1.057.506 | 2303 | 4x | 4xA | 0 |
| 54_4_3 | 4.627.239 | 1.057.506 | 2303 | 4x | 4xA | 0 |
| 75_1_2 | 4.652.845 | 9.811.194 | 2678 | 4x | 4xA | 0 |
| 79_1_2 | 4.698.753 | 1.035.919 | 2280 | 4x | 4xA | 0 |
| 79_2_2 | 4.698.753 | 1.035.919 | 2280 | 4x | 4xA | 0 |
| 81_1_10 | 4.698.753 | 1.032.303 | 2526 | 4x | 4xA | 0 |
| 81_1_12 | 4.698.753 | 1.032.303 | 2526 | 4x | 4xA | 0 |
| 83_3_2 | 470.407 | 1.269.105 | 2271 | 4x | 4xA | 0 |
| 104_1_3 | 4.645.142 | 1.030.158 | 2298 | 4x | 4xA | 0 |
| 104_2_1 | 4.645.142 | 1.030.158 | 2298 | 4x | 4xA | 0 |
| 111_2_1 | 44.279 | 6.719.222 | 2243 | 4x | 4xA | 0 |
| 111_3_1 | 44.279 | 6.719.222 | 2243 | 4x | 4xA | 0 |
| 114_2_1 | 4.472.089 | 6.919.861 | 2339 | 4x | 4xA | 0 |
| 114_2_3 | 4.472.089 | 6.919.861 | 2339 | 4x | 4xA | 0 |
| 114_3_1 | 4.472.089 | 6.919.861 | 2339 | 4x | 4xA | 0 |
| 200_2_3 | 4.418.431 | 7.603.472 | 1390 | 4x | 4xA | 0 |
| 205_1_3 | 4.423.711 | 6.704.778 | 2265 | 4x | 4xA | 0 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 235_2_1 | 4.416.689 | 670.763 | 1930 | 4x | 4xA | 0 |
| 4_4_2 | 4.417.528 | 689.806 | 2050 | 4x | 4xM | 20 |
| 17_1_3 | 4.505.069 | 6.390.778 | 2357 | 4x | 4xM | 20 |
| 17_2_3 | 4.505.069 | 6.390.778 | 2357 | 4x | 4xM | 40 |
| 17_3_2 | 4.505.069 | 6.390.778 | 2357 | 4x | 4xM | 40 |
| 17_4_2 | 4.505.069 | 6.390.778 | 2357 | 4x | 4xM | 40 |
| 20_1_3 | 4.634.719 | 7.724.111 | 2200 | 4x | 4xM | 20 |
| 34_2_2 | 4.524.244 | 6.951.889 | 2120 | 4x | 4xM | 20 |
| 36_1_1 | 4.538.542 | 7.043.722 | 2152 | 4x | 4xM | 20 |
| 36_1_2 | 4.538.542 | 7.043.722 | 2152 | 4x | 4xM | 20 |
| 36_4_1 | 4.538.542 | 7.043.722 | 2152 | 4x | 4xM | 40 |
| 36_4_2 | 4.538.542 | 7.043.722 | 2152 | 4x | 4xM | 20 |
| 37_3_1 | 4.561.622 | 7.552.611 | 2115 | 4x | 4xM | 40 |
| 37_3_2 | 4.561.622 | 7.552.611 | 2115 | 4x | 4xM | 40 |
| 40_1_3 | 460.825 | 70.125 | 1860 | 4x | 4xM | 40 |
| 40_2_1 | 460.825 | 70.125 | 1860 | 4x | 4xM | 60 |
| 40_2_2 | 460.825 | 70.125 | 1860 | 4x | 4xM | 40 |
| 45_1_3 | 4.657.119 | 8.410.556 | 2400 | 4x | 4xM | 40 |
| 47_1_3 | 4.654.628 | 9.211.389 | 2211 | 4x | 4xM | 20 |
| 48_1_2 | 4.647.153 | 9.728.889 | 2262 | 4x | 4xM | 80 |
| 53_1_2 | 4.654.856 | 1.043.431 | 2456 | 4x | 4xM | 20 |
| 54_1_1 | 4.627.239 | 1.057.506 | 2303 | 4x | 4xM | 40 |
| 54_1_2 | 4.627.239 | 1.057.506 | 2303 | 4x | 4xM | 20 |
| 54_2_1 | 4.627.239 | 1.057.506 | 2303 | 4x | 4xM | 20 |
| 54_2_3 | 4.627.239 | 1.057.506 | 2303 | 4x | 4xM | 20 |
| 54_4_1 | 4.627.239 | 1.057.506 | 2303 | 4x | 4xM | 20 |
| 54_4_2 | 4.627.239 | 1.057.506 | 2303 | 4x | 4xM | 60 |
| 58_1_1 | 4.645.667 | 1.188.814 | 2117 | 4x | 4xM | 20 |
| 58_1_2 | 4.645.667 | 1.188.814 | 2117 | 4x | 4xM | 20 |
| 58_1_3 | 4.645.667 | 1.188.814 | 2117 | 4x | 4xM | 40 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 58_2_2 | 4.645.667 | 1.188.814 | 2117 | 4x | 4xM | 20 |
| 58_2_3 | 4.645.667 | 1.188.814 | 2117 | 4x | 4xM | 20 |
| 59_1_7 | 4.666.434 | 1.218.316 | 2391 | 4x | 4xM | 60 |
| 73_1_3 | 4.721.906 | 1.031.961 | 2180 | 4x | 4xM | 20 |
| 75_1_3 | 4.652.845 | 9.811.194 | 2678 | 4x | 4xM | 20 |
| 77_3_1 | 4.636.692 | 7.652.778 | 2259 | 4x | 4xM | 20 |
| 79_3_2 | 4.698.753 | 1.035.919 | 2280 | 4x | 4xM | 20 |
| 79_4_1 | 4.698.753 | 1.035.919 | 2280 | 4x | 4xM | 60 |
| 81_1_4 | 4.698.753 | 1.032.303 | 2526 | 4x | 4xM | 20 |
| 81_1_5 | 4.698.753 | 1.032.303 | 2526 | 4x | 4xM | 20 |
| 83_4_1 | 470.407 | 1.269.105 | 2271 | 4x | 4xM | 20 |
| 114_3_3 | 4.472.089 | 6.919.861 | 2339 | 4x | 4xM | 20 |
| 114_4_2 | 4.472.089 | 6.919.861 | 2339 | 4x | 4xM | 20 |
| 204_2_3 | 4.415.725 | 6.729.195 | 1640 | 4x | 4xM | 20 |
| 204_3_1 | 4.415.725 | 6.729.195 | 1640 | 4x | 4xM | 20 |
| 205_4_1 | 4.423.711 | 6.704.778 | 2265 | 4x | 4xM | 20 |

**Table S5.** Adapter and primer sequences.

| Adaptor | | Sequence |
|---|---|---|
| EcoRI F | 5'- | CTCGTAGACTGCGTACC |
| EcoRI R | 5'- | AATTGGTACGCAGTC |
| MspI/HpaII F | 5'- | GATCATGAGTCCTGCT |
| MspI/HpaII R | 5'- | CGAGCAGGACTCATGA |

**Table S6.** RawGeno input parameters and actuating factors, and resulting no. of markers per primer.

| Primer | | | | Sequence |
|---|---|---|---|---|
| *Preselective* | | | | |
| EcoRI | | 5' | - | GACTGCGTACCAATTCA |
| MspI/HpaII | | 5' | - | ATCATGAGTCCTGCTCGG |
| *Selective* | | | | |
| EcoRI | | 5' | - | GACTGCGTACCAATTCAAC |
| MspI/HpaII 1 | 5'- | [FAM] | - | ATCATGAGTCCTGCTCGGCTCG |
| MspI/HpaII 2 | 5'- | [HEX] | - | ATCATGAGTCCTGCTCGGCTGA |
| MspI/HpaII 3 | 5'- | [NED] | - | ATCATGAGTCCTGCTCGGCATA |

**Table S7.** Raw binary data resulted from the RawGeno package. Check the Supplementary excel file.

| Dye | Bin Size | | Thresholds | | Estimation | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | *Min* | *Max* | *RFU* | *Repr.* | $N_{Bins}$ | *Repr.* | *Error$_{Bonnin}$* | *Polym.* | *No.* |
| Blue | 1.5 | 1.7 | 200 | 90 | 100 | 85.15 | < 0.01 | 0.77 | 139 |
| Green | 1.6 | 2.0 | 250 | 90 | 110 | 77.78 | < 0.00 | 0.76 | 187 |
| Yellow | 1.5 | 2.0 | 150 | 95 | 108 | 92.21 | < 0.01 | 0.79 | 186 |

**Methods S1.** Flow cytometric seed screening (all methods and data from [45]):

To quantify the main mode of reproduction, we determined ploidies of both endosperm and embryo per single seed for each individual. Since many tetraploid plants had a poor seed set, as reported previously [45], we had to restrict the sampling to 551 individuals, which formed each a minimum of five well-developed seeds per flower. Five seeds per plant from at least three plants per population were analyzed with a slightly modified FCSS method. Seeds were placed in 2 ml Eppendorf tubes together with two 0.23 cm steel beads (QIAGEN, Hilden, Germany) and ground in a TissueLyser II mill (QIAGEN, Hilden, Germany) with a stroke rate of 30 Hz for 7 seconds. Further preparation was realized using a two-step procedure described by performing (1) a nuclei isolation step with Otto I buffer: 0.1 M citric acid monohydrate, 0.5% v/v Tween 20 (Sigma-Aldrich Munich, Germany), ddH$_2$O, and (2) a separate staining step with Otto II buffer: 0.4 M Na$_2$HPO4, ddH$_2$O and charged with 3 ng/ml 4',6-diamidinophenyl-indole (Sigma-Aldrich, Munich, Germany). Macerated seeds were incubated for 5 minutes with 200 µl ice-cold Otto I buffer. Suspensions were filtered through 40 µm mesh tubes (Partec, Münster, Germany). 800 µl Otto II buffer were then added and incubated for another 15 minutes before analysis. Ploidy levels of all mother plants were determined on fresh leaves from the cultivated plants using the same methods as described above, except for a slightly prolonged grinding time in the TissueLyser (15 seconds).

All analyses were performed on a CyFlow Space flow cytometer (Partec, Münster, Germany). Histograms were taken and analyzed with the supplied FloMAX Software version 2.2.0 (Quantum Analysis GmbH, Münster, Germany). Leaf material of *Zea mays* (CE-777 strain, provided by Doležel J.) and a diploid tested plant of *R. kuepferi* were used as external reference standard to adjust the gain level of the UV LED lamp. All subsequent analyses were conducted with the same parameters.

Peak ranges for embryo (em) and endosperm (es) were set manually in FloMAX and values of DNA content were calculated as Gaussian means. Ratios of es:em ploidies were calculated to determine whether a seed has been produced sexually (3:2 ratio) or via apomixis (3:1, 2.5:1, 2:1 ratio). Interpretation of all plausible pathways for development and fertilization of seeds of *R. kuepferi* have been adopted from the studies by [45, 52], and provided the basis for our classification: A threshold of 1.65 es:em ratio was set to discriminate between sexual (lower values) and asexual (higher values) cases. Those with ratio values between 1.85 and 2.15 were interpreted as autonomous endosperm development since the second peak was always distinct and as high as the endosperm peak in other pathways. Hence, we interpreted it as endosperm peak, and we excluded the possibility that it could represent just a G2 peak of the growing embryo (G2 peaks are usually much smaller than the respective G1 peak, as only few cells are in the respective stage of the cell cycle). Representative flow cytometric histograms are shown in [45]. We categorized every individual as obligate sexual (only sexual seeds), obligate apomictic (only apomictic seeds) or mixed (sexual as well as apomictic seeds = facultative apomixis) by pooling the results of the analyzed seeds, and calculated percentages (see above in Table S1).

**Methods S2.** DNA Extraction

For standardized DNA preparation and high yields 1 cm$^2$ leaf material per sample was disrupted using a QIAGEN TissueLyser II (QIAGEN, Hilden, Germany) with 2 steel beads (diameter: 5 mm) in 2 ml Eppendorf tubes, operating at 25 Hz for 2 mins. Isolation of DNA was realized with QIAGEN DNeasy Plant Mini Kit (QIAGEN, Hilden, Germany) using a slightly modified protocol. During lipid cleansing (step 2) a reduced amount of 360 µl AP1 Buffer was used while 40 µl 2.6% polyvinylpyrrolidone (PVP; Carl Roth GmbH & Co. KG, Karlsruhe, Germany) solution was added to attenuate detrimental influence of high polyphenolic compound content in our samples (Healey et al. 2014). Incubation times for lipid cleansing and elution (step 3, step 12 and 13) were prolonged to 30 mins with preheated elution buffer. Elution of isolated DNA (step 12 and 13) was performed with reduced amount of elution buffer (50 µl each) to gain higher concentrations. Isolate quality and quantity was checked on 1.5% agarose gel (Carl Roth GmbH & Co. KG, Karlsruhe, Germany) and NanoDrop 2000 (Thermo Fisher Scientific, Waltham, MA, USA). Only samples without impurities and a DNA content of at least 20 ng/µl were processed further.
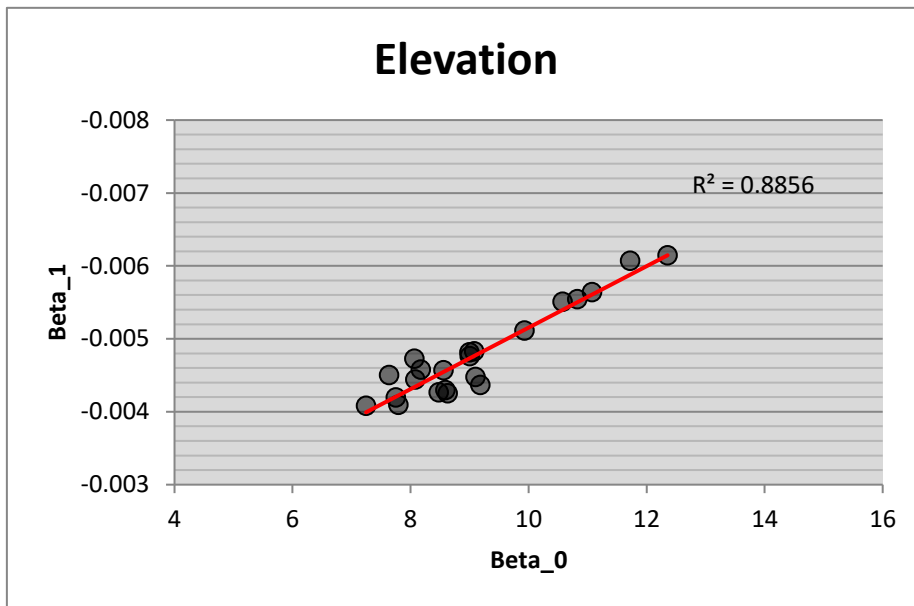
**Figure S1.** Scatterplot of univariate logistic regression using SamßadaBeta parameters (see Supplementary Table S6) of 22 candidate epilocifor altitude.
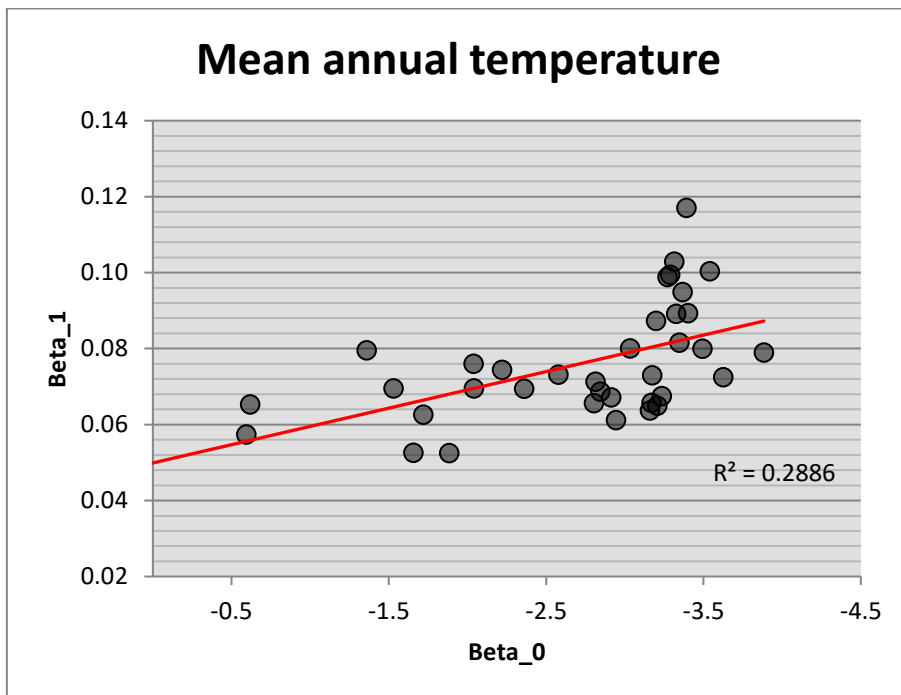


**Figure S2.** Scatterplot of univariate logistic regression using SamßadaBeta parameters (see Supplementary Table S6) of 36 candidate epilocifor mean annual temperature.