

Ji, R., Sheng, Y., Chen, L., Li, X. and Shao, J. 2020. Genetic structure of *Polygonatum cyrtonema* in Anhui Province from eastern China. – Nordic Journal of Botany 2020: e02643

Appendix 1

Table A1. The genetic diversity level of *Polygonatum* with 9 loci screening. Number of alleles (N_A), observed heterozygosity (H_O), expected heterozygosity (H_E), gene diversity within population (H_S), gene diversity due to differences among populations (G_{ST}) and polymorphic information content(PIC).

| Locus | N_A | H_O | H_E | H_S | G_{ST} | PIC |
|-------|--------|-------|-------|-------|----------|-------|
| Pc11 | 42 | 0.539 | 0.938 | 0.853 | 0.094 | 0.933 |
| Pc30 | 9 | 0.512 | 0.569 | 0.468 | 0.188 | 0.535 |
| Pc14 | 11 | 0.574 | 0.56 | 0.516 | 0.105 | 0.508 |
| Pc17 | 45 | 0.646 | 0.957 | 0.909 | 0.05 | 0.954 |
| Pc25 | 21 | 0.339 | 0.614 | 0.416 | 0.267 | 0.578 |
| Pc28 | 21 | 0.483 | 0.663 | 0.528 | 0.196 | 0.635 |
| Pc33 | 32 | 0.572 | 0.954 | 0.875 | 0.082 | 0.951 |
| Pc34 | 19 | 0.897 | 0.852 | 0.674 | 0.22 | 0.835 |
| Mean | 25.667 | 0.563 | 0.772 | 0.663 | 0.150 | 0.751 |

Table A2. The genetic diversity of the 17 studied populations of *Polygonatum*. Number of alleles (N_A), number of effective alleles (N_E), observed heterozygosity (H_O), expected heterozygosity (H_E), inbreeding coefficient (F_{IS}), allelic richness (A_R), Shannones's information index (I). Asterisks denote significant differences (***) ($p < 0.001$).

| Population code | N_A | N_E | H_O | H_E | F_{IS} | A_R | I |
|---------------------|--------|-------|-------|-------|----------|-------|-------|
| <i>P. cyrtonema</i> | | | | | | | |
| MC | 9.333 | 4.964 | 0.573 | 0.697 | 0.194*** | 5.672 | 1.599 |
| FLS | 11.111 | 4.710 | 0.601 | 0.726 | 0.187*** | 6.214 | 1.741 |
| BJS | 7.000 | 3.721 | 0.678 | 0.658 | -0.014 | 4.635 | 1.370 |
| HHGD | 7.889 | 4.752 | 0.497 | 0.682 | 0.296*** | 5.537 | 1.517 |
| JHGS | 5.778 | 3.752 | 0.652 | 0.630 | 0.000 | 4.726 | 1.303 |
| JHHS | 7.889 | 4.915 | 0.595 | 0.696 | 0.162*** | 5.465 | 1.547 |
| YLC | 6.778 | 3.423 | 0.464 | 0.632 | 0.287*** | 4.852 | 1.352 |
| HG | 8.222 | 4.942 | 0.491 | 0.616 | 0.217*** | 5.080 | 1.405 |
| HGGS | 6.111 | 3.617 | 0.496 | 0.559 | 0.138*** | 4.568 | 1.209 |
| HT | 7.444 | 4.208 | 0.502 | 0.579 | 0.151*** | 4.734 | 1.284 |
| TTZ | 9.667 | 6.221 | 0.507 | 0.708 | 0.313*** | 6.933 | 1.734 |
| YLP | 11.444 | 6.089 | 0.483 | 0.665 | 0.292*** | 6.654 | 1.713 |
| TZS | 5.111 | 3.532 | 0.472 | 0.537 | 0.163*** | 4.500 | 1.136 |
| <i>P. filipes</i> | | | | | | | |
| flsC | 11.333 | 5.999 | 0.680 | 0.761 | 0.124*** | 6.760 | 1.867 |
| hgC | 5.444 | 3.486 | 0.524 | 0.566 | 0.105 | 4.327 | 1.172 |
| <i>P. odoratum</i> | | | | | | | |
| ttzY | 5.111 | 3.453 | 0.750 | 0.648 | -0.091 | 5.111 | 1.320 |
| jhsY | 4.111 | 3.000 | 0.681 | 0.583 | -0.134 | 3.713 | 1.092 |

Table A3. The leaf length, leaf width, ratio of blade length to blade width and fruit stem length of the three groups of the *Polygonatum cyrtonema*. Group I is (MC, FLS, BJS, HHGD, JHGS, JHHS), group II is (YLC, HG, HGGS, HT) and group III is (TTZ, YLP, TZS). Values followed by different letters in a column show differ significantly (post-hoc test), asterisks denote significant differences (**p < 0.01, ***p<0.001).

| Groups | Leaf length (mm) | Leaf width (mm) | Ratio of blade length to blade width | Fruit stem length (mm) |
|--------|----------------------------|--------------------------|--------------------------------------|--------------------------|
| I | 116.64±25.85 ^a | 37.89±8.59 ^a | 3.15±0.65 ^b | 10.79±3.69 ^a |
| II | 137.82±39.14 ^{bc} | 54.54±15.49 ^b | 2.61±0.62 ^a | 32.44±15.23 ^b |
| III | 126.05±36.81 ^{ab} | 33.10±6.43 ^a | 3.83±0.93 ^c | 28.35±11.73 ^b |
| F | 6.244 ^{**} | 41.210 ^{***} | 21.855 ^{***} | 33.856 ^{***} |

Table A4. The paired FST estimates for the 17 *Polygonatum* populations are below the diagonal. FST values were tested by permutation of genotypes among the populations (1000 randomizations). All pairwise FST values yielded p < 0.01 even when corrected by a sequential Bonferroni check.

| | MC | FLS | BJS | HHGD | JHGS | JHHS | YLC | HG | HGGS | HT | TTZ | YLP | TZS | flsC | hgC | ttzY |
|------|-------|-------|--------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| FLS | 0.044 | | | | | | | | | | | | | | | |
| BJS | 0.043 | 0.058 | | | | | | | | | | | | | | |
| HHGD | 0.036 | 0.059 | 0.058 | | | | | | | | | | | | | |
| JHGS | 0.055 | 0.069 | 0.051 | 0.045 | | | | | | | | | | | | |
| JHHS | 0.043 | 0.091 | 0.099 | 0.053 | 0.078 | | | | | | | | | | | |
| YLC | 0.132 | 0.153 | 0.135 | 0.133 | 0.147 | 0.163 | | | | | | | | | | |
| HG | 0.151 | 0.175 | 0.148 | 0.172 | 0.17 | 0.184 | 0.046 | | | | | | | | | |
| HGGS | 0.166 | 0.184 | 0.153 | 0.196 | 0.198 | 0.190 | 0.094 | 0.074 | | | | | | | | |
| HT | 0.169 | 0.192 | 0.1589 | 0.206 | 0.191 | 0.196 | 0.094 | 0.052 | 0.034 | | | | | | | |
| TTZ | 0.087 | 0.111 | 0.099 | 0.097 | 0.094 | 0.115 | 0.093 | 0.103 | 0.138 | 0.126 | | | | | | |
| YLP | 0.114 | 0.140 | 0.120 | 0.126 | 0.111 | 0.141 | 0.092 | 0.092 | 0.128 | 0.109 | 0.008 | | | | | |
| TZS | 0.145 | 0.173 | 0.152 | 0.167 | 0.139 | 0.171 | 0.130 | 0.105 | 0.171 | 0.146 | 0.061 | 0.051 | | | | |
| flsC | 0.117 | 0.122 | 0.148 | 0.118 | 0.152 | 0.131 | 0.140 | 0.154 | 0.199 | 0.189 | 0.078 | 0.113 | 0.151 | | | |
| hgC | 0.130 | 0.172 | 0.200 | 0.150 | 0.212 | 0.144 | 0.197 | 0.231 | 0.272 | 0.268 | 0.149 | 0.167 | 0.218 | 0.114 | | |
| ttzY | 0.167 | 0.165 | 0.176 | 0.174 | 0.181 | 0.194 | 0.164 | 0.159 | 0.204 | 0.219 | 0.132 | 0.153 | 0.209 | 0.156 | 0.255 | |
| jhsY | 0.229 | 0.232 | 0.235 | 0.223 | 0.237 | 0.249 | 0.212 | 0.205 | 0.252 | 0.250 | 0.169 | 0.178 | 0.209 | 0.194 | 0.275 | 0.161 |

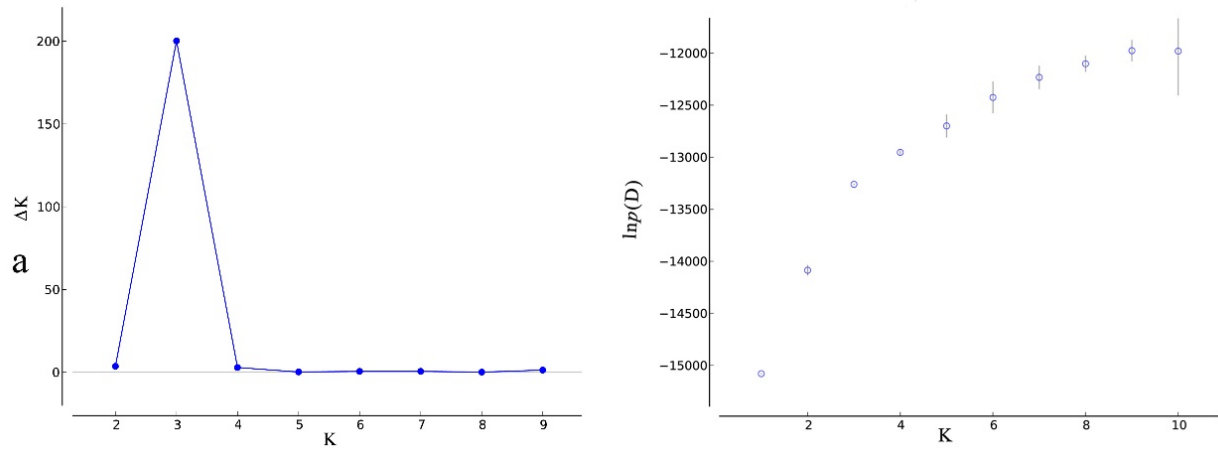


Figure A1. The results of genetic structure analyzed with STRUCTURE software. (a) The corresponding ΔK statistics calculated according to Evanno et al. (2005) (b). Plot of mean posterior probability $\ln P(D)$ values of each K .