

Population study

Tomimatsu H. & Ohara M. (2003): Genetic diversity and local population structure of fragmented populations of *Trillium camschatcense* (Trilliaceae). *Biological Conservation* 109: 249–258.



Reasons for the study

- fragmentation – decrease of population size
 - genetic drift, inbreeding
 - reduced heterozygosity – decreased fitness
 - loss of allelic diversity – elimination of possible future advantages
- positive correlation of genetic diversity, heterozygosity and population size
- what is the genetic effect of fragmentation ?

Description of landscape and species

- highly fragmented, many small forests
- *Trillium* – continuous populations (> 5 ha)
- *self-incompatible*
- outbred seeds only
- diploid ($2n=10$)
- long-lived – at least 20 years
- reproduced only by seeds

Methods

- 12 populations from eastern Hokkaido
- 40 samples per population (leaves)
- samples on dry ice (- 80 °C)
- 14 enzyme systems tested, 6 selected
- 11 putative loci

Data analysis

FSTAT

- percentage of polymorphic loci (P)
- average number of alleles per polymorphic locus (A_p)
- average number of alleles per locus (A)
- expected heterozygosity (H_E)
- observed heterozygosity (H_O)
- F-statistics (F_{IT}, F_{ST}, F_{IS})
- *gene flow*
- standardised genetic distance – Nei
- neighbour-joining dendrogram + bootstrapping

Results (Table 2)

- $P = 90.9\%$
 - 18.2 – 81.8 %
- $A = 2.55$
- $H_O < H_E$
- F_{IS} – higher in relatively smaller populations
- $F_{ST} = 0.130$
- Aat-1, Aat-2 – correlation with latitude
- NJ – separation of N and S populations (lower F_{ST} within groups)

Relationship of A , P and population size

- significant relationship
- reduced genetic diversity in smaller populations
- 46% of alleles are rare – not found in smaller populations
- F_{IS} and heterozygosity – no correlations

Discussion

- genetic bottleneck during fragmentation
 - reduction of population size
 - loss of alleles
- low seed dispersal between N and S populations – barrier for gene flow
 - limited dispersal ability (ants – up to 3.3 m)
 - limited pollinator availability
- low genetic differentiation within group – relatively high migration
 - estimate of historical gene flow under migration/drift equilibrium
 - gene flow increases with decreasing population size

Conclusions for nature conservation

- for conservation of allelic diversity at least 550 flowering individuals per population is necessary
- in the long view we need bigger populations to avoid allelic loss
 - allelic richness might be correlated with adaptive traits
- historically two genetically unconnected areas
 - both regions must be conserved

Systematic study

Ritland K., Meagher L.D., Edwards D.G.W. & El-Kassaby Y.A. (2005): Isozyme variation and the conservation genetics of Garry oak. *Canadian Journal of Botany* 83: 1478-1487



Reasons for the study

- disjunct and scattered distribution
- baseline information about genetic variation needed
- anthropogenic factors forming genetic structure?
- infer level of inbreeding (mating among related individuals)
- more effective conservation strategies

Studied species

- Garry oak (Oregon white oak) – deciduous, native to western North America
- climax on dry sites, periodic fire regimes
- fragmented “Garry oak meadows” – less than 8% left unmodified
- acorns dispersed by animals, also food resource for indigenous people

Methods

- 28 populations from British Columbia
- 14 populations from the USA
- buds from at least 30 trees per population
- mating system analyses
 - 2 populations
 - acorns from 25 trees
 - 10 progeny from each family
- 15 enzymatic systems, 23 loci (10 loci for outcrossing rate analysis)

Methods II.

- expected heterozygosity (H)
- average number of alleles per locus (N_a)
- proportion polymorphic loci (PPL)
- inbreeding coefficient (F)
- genetic distance (D) and Nei's G_{st} between populations – dendrogram (+ SE of branch length)
- mating system parameters (program MLTR)
 - single-locus and multilocus estimates of outcrossing (single-locus higher in case of biparental inbreeding)
 - correlation of paternity
 - pollen and egg gene frequencies

Results

- diversity and inbreeding statistics (Table 1)
- lower measures of diversity in northern populations (Fig. 3)
- dendrogram of genetic distances (Fig. 4)
 - BC island + Yale
 - mainland in the center
 - other – no meaningful pattern (remoteness)
- nine alleles only in USA populations, eight others only in BC populations

Results II.

- significant relationship between genetic and physical distance (Fig. 5)
- mating system analysis (Tables 2 and 3)
 - lack of informative loci
 - pollen and egg frequencies significantly deviated
 - multilocus outcrossing rate 1.006 and 0.918
 - single-locus estimates lower (0.941)
 - significant level of “correlated mating” (6%)

Discussion and conclusions

- $H_e=0.17$ and $N_a=1.84$ – one-half of values found in other white oak species – limited potential for adaptive response
- outcrossing rate to be near to 100% - inbreeding should not be a significant concern for management
- low but significant level of “correlated mating” – siblings share mother and father
- pollen pool is heterogenous (probably due to synchronous flowering and low population density)
- two major genetic group based on dendrogram and presence of unique alleles – two different refugia during last glaciation, cpDNA markers needed to confirm this pattern
- two isolated BC populations (Sumas, Yale) – genetically distinct, less diverse – likely due to long-term genetic drift