Genetic structure among sexually derived populations

1. BEARS(*URSUS*)

**Data from:**

Cronin MA, Rincon G, Meredith RW, MacNeil MD, Islas-Trejo A, Canovas A, Medrano JF (2014) Data from: Molecular phylogeny and SNP variation of polar bears (Ursus maritimus), brown bears (U. arctos) and black bears (U. americanus) derived from genome sequences. Dryad Digital Repository. <http://dx.doi.org/10.5061/dryad.1qp80>

**General description:**

SNP loci (162) were scored for 336 bears from Alaska and Montana. Samples were collected from 12 sites involving black (3 sites), brown (6 sites) and polar (3 sites) bears. The three species were discriminated by FLOCK at the top level but only the Brown bear cluster split further into geographical sub-clusters.

ii) BALSAM POPLARS(*POPULUS BALSAMIFERA*)

**Data from:**

Keller SR, Olson MS, Silim S, Schroeder W, Tiffin P (2010) Data from: Genomic diversity, population structure, and migration following rapid range expansion in the balsam poplar, Populus balsamifera. Dryad Digital Repository. <http://dx.doi.org/10.5061/dryad.1164>

**General description:**

Individuals (474) were sampled from 34 populations covering most of Canadian territory including Northern (West), Central and Eastern areas. Genotypes were scored for 412 SNP markers. FLOCK found two clusters (refs) at the top-level: (North + Central) and East. The (North + Central) cluster was further separated into (mostly) North and (mostly) Central sub-clusters.

Admixture mapping: CHICKADEES(*POECILE*)

**Data from:**

Taylor SA, White TA, Hochachka WM, Ferretti V, Curry RL, Lovette I (2014) Data from: Climate-mediated movement of an avian hybrid zone. Dryad Digital Repository. <http://dx.doi.org/10.5061/dryad.7gg47>

**General description:**

Here Flock is used to map the levels of admixture between black-capped (Poecile atricapillus) and Carolina (Poecile carolinensis) chickadees based on genotypes of 1425 SNPs for 167 individuals. Samples were collected from five sites in Eastern North America. The number of clusters (refs) was known a priori (K = 2) and this was confirmed by the output, based on plateau analysis. The map of LLODs shows where hybridization of the two species is likely to have taken place.

Genetic structure among clonal populations: COGONGRASS (*IMPERATA CYLINDRICA*)

**Data from:**

Burrell AM, Pepper AE, Hodnett G, Goolsby JA, Overholt WA, Racelis AE, Diaz R, Klein PE (2015) Data from: Exploring origins, invasion history and genetic diversity of Imperata cylindrica (L.) P. Beauv. (Cogongrass) in the United States using genotyping by sequencing. Dryad Digital Repository. <http://dx.doi.org/10.5061/dryad.k2d05>

**General description:**

In clonal populations, the assumption of HWE is violated (Kamvar et al. 2014) and loci show linkage disequilibrium (de Meeus & Balloux 2004). FLOCK is a non-modeled based cluster program and therefore it is expected to do as well on clonal as on sexually generated clusters. Here FLOCK was tested to identify clonal lineages among 238 genotypes collected from 17 populations (sites) that showed highly significant deviations from HWE (Burrell et al. 2015).The number of available SNP loci was 2320, but after verifying that the first 1500 loci did not bring any extra resolution over 1000, only the first 1000 were used. A tree representation shows hierarchical structure among the clonal lineages.