* Island Anolis lizards are threatened by rats
* Lost of genetic diversity after rats invasion – loss of alleles and heterozygosity
* Effect of inbreeding - Loss of heterozygosity advantage and unmasking of deleterious recessive alleles – loss of fitness – inbreeding depression
* Inbreeding isn’t necessarily inbreeding depression – inbreeding depression only when there is a loss of fitness
* Measuring fitness in the wild population is difficult
* Most animals outbred
* When have inbreeding, increase in mortality
* Purging – we are all carrying deleterious mutation – mutation load is the proportion of variance that is deleterious and they tend to be recessive because if they are dominant, they get selected out of the population rapidly
* Purging – selection is most effective in large population – following bottleneck – small population – higher heterozygosity and masking of deleterious alleles
* Purging is not always true
* These populations (in green – white tiger slide) may have their proportion of deleterious alleles purged out
* Inbreeding should be concerned about in conservation
* Pedigree – inbreeding loob – slide 14 – C is the common ancestor – we want to calculate the inbreeding coefficient for individual I
* Inbreeding coefficient is measuring how likely is an individual to receive the alleles twice from an ancestor – inherit allele twice – homozygote – measure probability of being homozygous at a loci that is inherited from a common ancestor – identical by descent
* F is inbreeding depression
* Slide 16 – 2 breeding loop – U and V are the common ancestor of Z – count number of linkages – 4 for loop 1 and 4 for loop 2 – if got diploid individuals, 2 alleles that is one from dad one from mom – at linkage 50% chance of one allele being passed on – 2 loops for half to the power 4 and time 2 for each
* Slide 19 – 1 inbreeding loop – common ancestor C – C has 2 different alleles – probab of red passed to A is half, B is half, B and A to I are both half so half^4 – probab of blue also the same so 1/16 + 1/16 = 1/8
* Pedigree is usually the circle and square (not the second year inbreeding loop) – shade means phenotype is present
* Slide 24 - Calculate inbreeding depression from pedigree – find the inbreeding in the pedigree – identify the nodes – between outbred parents and full siblings – interested in inbreeding depression for F2 – will be told who we are calculating the inbreeding coefficient for
* At population level – earlier was individual – heterozygosity observed vs expected – observed is measured – expected is H-W
* If observed much higher than expect – F will be close to -1
* Measure heterozygosity a different time period – look at change of heterozygosity to find F
* Overtime, when higher F, heterozygosity will be lost at a faster rate
* F=0.43 means that there is a 43% chance of inheriting the same allele twice from a common ancestor
* If F negative, meaning excess outbreeding – rare – sample family group where there is strong inbreeding avoidance and preference for outbreeding – need to account for genetic structure
* can be sampling error – genetic structure – genetic component in one population may not be found in another population (find excess inbreeding)
* Problems of inbreeding have been identified in plants and animals
* Genetic rescue – a lot of data show the success of genetic rescue – measuring fitness relating to that
* Fear of outbreeding depression – if you mix individuals together and they are too divergent, locally adapt individuals, the resulting individuals will be less fit – natural population has narrow hybrid zone – hybrids selected out because low fitness, outbreeding depression – BUT habit fragmentation, low genetic variation, genetic rescue is the rescue – outbreeding depression is rarely seen
* Problems if major chromosomal differences (eg. horse and donkey), long isolation – population isolated for longer than 500 years because that was when anthropogenic events appear, adaptive differentiation (different environment which has higher risk of outbreeding depression)