

Genetic status of golden lion tamarin (glt)



**ASSIGN
BUSTER**

Golden Lion Tamarin (GLT)

1. In assessing the genetic status of GLT, the information given about the pedigree shows that firstly, all the individuals within the population have very low mean kinship (MK) hence it shows that the animals are genetically important. Secondly, the observed heterozygosity H_o among the individuals is high which shows that there is a lot of genetic variability in the population. Thirdly, the sex ratio of males to females in the population is 35 : 30 respectively, this suggest that mating among the population follows a monogamous pattern of one male to one female, except for one case in the pedigree where one female (3025) mated with two males (3429 and 2457). Overall, I think that the population is well managed however, there are some factors like missing information for some Sire and Dam in the early generations and a breeding status of false for most of the population which suggests some work need to be done to keep data management in check
2. The five breeding pairs I would give priority to include:
 - Pair 3(3358, 3713): not related, female have no offspring, male have one offspring and low MK (0. 035, 0. 026)
 - Pair 4(3875, 3493): not related, both have no offspring and low MK (0. 035, 0. 03)
 - Pair 5(3954, 3560): not related, both have no offspring and low MK (0. 033, 0. 026)
 - Pair 12(3799, 3729): not related, both have no offspring, rare allele present in female and low MK (0. 033, 0. 023)

- Pair 13(3946, 3759): both have no offspring, rare alleles and low Mean Kinship (0.028, 0.021)

The selection of the pairs were based on evidence provided in the pedigree data that the individuals are not related and they share a few alleles identical by descent with the rest of the population (low mean kinship).

Therefore, they have the highest genetic value due to the presence of those unique alleles. Mean kinship however doesn't always optimize genetic diversity, it is dependent on the population structure

Often times, increasing offspring production and reducing the loss of population genetic variation can be seen as separate and competing goals(Fiumera, Porter et al. 2004). Preserving genetic variations and avoiding inbreeding in order to maximize the long-term viability of captive populations is the primary goal of genetic management (National Research Council Institute for Laboratory Animal 2003). I recommend when planning breeding, inbreeding avoidance by ensuring that the relatives don't mate should be a priority. Also, individuals with low mean kinship and high heterozygosity and who carry rare alleles should be selected. A reduction in the rate of loss of rare alleles helps to maximize the effective population size and this in turn helps to maintain genetic variability(Kimura and Ohta 1969).

3. In terms of genetic variance, the populations from the four different zoos are assessed below:

- Zoo one (focal) have a low MK (0.031), high effective allelic diversity A_e (5.01), high average observed heterozygosity (0.63) and high F_{IS} (0.131) which demonstrates that the population somewhat genetically

healthy because even though it has a low MK, the high inbreeding coefficient suggests that inbreeding occurs within the population which means that they are not well managed. The presence of only one unique allele also suggest that the population is endangered.

- Zoo two (pop_2) have a low Mean Kinship (0. 020) among individuals, high effective allelic diversity A_e (5. 47), two unique allele, high average observed heterozygosity (0. 83), low F_{IS} (0. 027) and a P-value (0. 345) which demonstrates that the population is genetically healthy and well managed.
- Zoo three (pop_3) shows a high MK (0. 103) among individuals, a really low allelic diversity A_e (3. 19), low observed heterozygosity (0. 56) and very high F_{IS} (0. 327) and a P-value (0. 004) which demonstrates a genetically unhealthy population. These characteristics suggests that inbreeding is high, p-value also indicates a statistically differentiated population showing that they are not well managed.
- Zoo four (pop_4) have the characteristics of a population that is genetically healthy. This include a very low MK (0. 007), a high effective allelic diversity A_e (6. 71), high average observed heterozygosity (0. 87) and five unique alleles which demonstrates that the population is well managed compared to the other populations.

The genetic divergence among populations in the four zoos shows that there is a great genetic differentiation 0. 15-0. 25 between population 3 and 4 as well as a statistical significance between population 3 and 4. For the rest of the populations, there is a moderate genetic differentiation 0. 05-0. 15 and no statistical significance between them. Furthermore, Frankham et al.

(2010), states that $F_{ST} > 0.15$ shows a biologically significant differentiation thus, the F_{ST} between population 3 and 4 is 0.21 which means that there is a biologically significant differentiation among the populations. Similarly, the p value is 0.0133 which is < 0.05 that means that there is a statistical significance among the population therefore we reject the null hypothesis since we have statistical support that allele frequencies are differentiated among the two population.

4. My recommendations for future management of gene flow among the populations are;

Dobson and May (1986), stated that gene flow by exchanging animals or potential gametes and embryos among subdivided populations is advantageous for protection against diseases and catastrophes. Hedrick (1995) has also shown that 20% of gene flow from source population shouldn't be exceeded when augmenting translocation into a recipient population in order to reduce detrimental genetic load without uniquely adapted alleles. I would therefore recommend moving $< 20\%$ of individuals from population 4 to 3. This is because population 4 has proved to be both biologically and statistically significant hence an introduction to population 3 would help to boost both the population size while maintaining the genetic diversity of the population. I also suggest that genetic capture be carried out on population 1 by translocating 20-50 individuals in order to capture $> 95\%$ of the standing genetic variations within the source population because they have the least number of unique alleles.

References

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