Investigation of genetic structure in van cats using microsatellite markers

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Animal biotechnology can help produce farm and companion animals as well as conserving endangered species as being native genetic resources. Using molecular markers, it is possible to preserve the genetics of endangered species, therefore, generating increased genetic diversity. The Van cats are one of the endemic species, living around Lake Van region and endangered. Microsatellite markers are widely used for estimating genetic diversity and genetic differentiation in a population.

The aim of this study was to characterize genetic structure and detect genetic differentiation of the Van cat population under a conservation programme based on eye colors, fur length and a three spot on head. 25 male and 41 female cats were selected and 4 microsatellite loci (FCA176, 478, 547, 688) were chosen throughout the domestic cat genome. Heterozyosity (H) and Polymorphism Information Content (PIC) were estimated as 0.446 and 0.347; 0.425 and 0.335; 0.204 and 0.183; 0.495 and 0.372 for each loci, respectively. As a result, combining phenotype and marker data, no genetic relations in pedigree were obtained. Moreover, there were no statistical evidences among marker loci and phenotypes but statistical relationships between FCA176, FCA478 loci and three head spots and fur length were detected, respectively, ($p = 0.0734$ and $p = 0.0651$).

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Development of effective population size methods for genetic parameter estimation

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The reliability of genetic parameter estimations depends on sufficiency of sample size. In this study, it was aimed to determine the effective population size (EPS) for genetic parameter estimate using pedigree information for cattle, sheep and goat breeds in different heritability levels. For this aim, methods depend on sex ratio, variance of progeny size and inbreeding rate were compared and models were improved including heritability and it's standard error to determine the sample size. Interested methods evaluated only the demographic status of population to calculate the EPS. It is clear that these methods should also be approached in terms of sampling theory when the genetic parameter estimation is evaluated. To determine the relationship among the methods, size levels within genotypes of estimated EPS were examined by Spearman rank correlation. In order to compare the effectiveness of the methods, R^2 and MSE were used as criteria on the regression models where; estimated EPS was used as the outcome variable and heritability, its standard error and genotypes were used as explanatory variables. Results indicated that the methods depend on variance of progeny size was suggestible and improved methods were more reliable to estimate sample size because of taking into consideration the heritability.

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Biocatalysis/Biotransformation

Use of mixed-cultures of *Yarrowia lipolytica* mutant strains for γ-decalactone production from castor oil

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Natural aroma additives request increases every year due to consumer demand, thus the biotechnological production of such compounds have gained increased importance. γ-Decalactone is a peach-like aroma widely used in many industrial applications (food, cosmetics, detergents, etc.). γ-Decalactone production by *Yarrowia lipolytica* from castor oil (CO) has been studied by many authors in order to improve strains by genetic engineering, as well as to optimize cultures performance by selecting bioreactor operating conditions. In this work, the use of co-cultures (mixed cultures) of two mutant strains derived from *Y. lipolytica* wild-type W29, MTLY40-2P strain overexpressing POX2 gene and JMY3010 that overexpresses LIP2 gene, was evaluated and compared with pure cultures of each strain. For batch co-culture (mixed culture of both strains) higher γ-decalactone concentration ($1844 \pm 46\ mg\ L^{-1}$) and productivity ($80 \pm 5\ mg\ L^{-1}\ h^{-1}$) were obtained, when compared with pure cultures of each strain. The lipase production by JMY310 strain accelerates the CO hydrolysis and the use of MTLY40-2P strain, minimize γ-decalactone re-consumption. The optimization of the co-culture performance was further performed at different cellular and CO concentrations in order to maximize aroma productivity.

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