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Genetic characterization of F_0 outbred and F_1 inbred Swiss albino mice using microsatellite markers and their performance evaluation

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ABSTRACT

Swiss albino mice have been widely utilized in various biological researches worldwide. Phenotypic and fitness related traits of F_0 and F_1 inbred mice were estimated on 918 and 707 individual offsprings, respectively. The influence of fixed effects (litter size and sex) on birth weight (BW), weaning weight (WW) and adult body weight (ABW) in both the generations were found to be statistically significant. Genetic characterization of F_0 outbred and the F_1 inbred strain of Swiss albino mice were evaluated by using 10 microsatellites markers. The results indicated that total number of alleles per locus ranged from 3 (D2Mit61, D3Mit55, D8Mit14, D9Mit27, D10Mit180, D11Mit167) to 4 (D1Mit15, D2Mit51, D5Mit18, D7Mit323) in F_0 and F_1 inbred population, with a mean value of 3.4 indicating polymorphism in all 10 loci. The mean of effective number of alleles was 2.935 and 2.733 in F_0 and F_1 population, respectively. Estimates of the F_{IS} ranged from 0.139 (D10Mit180) to 0.999 (D9Mit27); and from 0.109 (D3Mit55) to 0.679 (D2Mit51) in F_0 and F_1 inbred population, respectively. The estimated mean marker-based F_{IS} was 0.294 and 0.372 in F_0 and F_1 populations, respectively. The mean values of observed heterozygosity (H_o) and expected heterozygosity (H_e) were 0.460 and 0.654, respectively for F_0 and 0.390 and 0.627, respectively for F_1 inbred mice population. Slight reduction in heterozygosity and 7.8% increase in inbreeding coefficient were observed in F_1 inbred in comparison to F_0 population. The results suggested that genome wide microsatellite genotyping might be more useful for accurate measuring and reliable estimation of population genetic parameters and inbreeding coefficient.

Keywords: Genetic characterization, Inbreeding coefficient, Microsatellite marker, Population genetic parameters, Swiss albino mice

The laboratory mice are often used as an outstanding research model in various areas of biological research. The biggest advantage of using mice in research is the ability to control genetics and environment (Arends *et al.* 2018). They are characterized by many features including small size, short generation interval, easy laboratory reproduction and low maintenance costs (Danneman *et al.* 2012). A strain is considered to be inbred if it is developed using brother × sister or parent × offspring mating of at least 20 consecutive generations (F_{20}) and can be traced in a single ancestral reproductive pair in generation 20 or later. On an average, at 20th generation, at least 98.6% of each loci of mouse are homozygous (Beck *et al.* 2000). An inbred strain of mice is known for their unique and identical genotypes and phenotypes. They were used in several biological studies worldwide. An inbred strain provides more strength and requires fewer animals per experiment, thus limiting the noise caused by the separation of genetic variations (Casellas 2010, Danneman *et al.* 2012).

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Genetic characterization refers to the detection of variation due to differences in either DNA sequences or specific genes or modifying factors (de Vicente *et al.* 2006). It also helps to determine species breeding behaviour, individual reproductive success, and gene flow existence (Papa and Gepts 2003). Microsatellites are highly polymorphic tract of repetitive DNA in which some DNA motifs of 1–6 base pairs (bp) are repeated in length, typically 5–50 times (Gulcher 2012). Microsatellites are regarded as an ideal DNA marker for deciphering genetic variability (Das *et al.* 2016).

Inbreeding depression occurs primarily in all populations and for almost all characters (Frankham *et al.*2002). If there is no availability of detailed pedigree records, inbreeding coefficient estimation by using a panel of microsatellite markers approach is more convenient and more reliable than conventional pedigree based approach (Amos *et al.* 2001, Selvaggi *et al.* 2010). Microsatellite approach exploits the fact that inbreeding leads to heterozygosity reduction, so it can be used to estimate inbreeding coefficient of an individual and, in addition to estimate population inbreeding levels (Naghavian *et al.* 2016).

Despite widespread utilization in research in the region, only very limited genetic studies has been performed on Swiss albino mice. Therefore, considering the importance of inbred strain of mice, the present study was undertaken with the objective of evaluating the phenotypic performance and genetics of the F_0 outbred and the F_1 inbred strain of Swiss albino mice using a panel of microsatellite markers to obtain various population genetic parameters.

MATERIALS AND METHODS

Swiss albino mice maintained at Laboratory Animal Research (LAR) Section, Animal Genetics Division, ICAR-Indian Veterinary Research Institute, Izatnagar, Uttar Pradesh were used for the present study. Breeding pairs (55) were randomly selected from out bred Swiss albino mice to produce F_0 stock. Full sib breeding pairs (75) of F_0 were selected and full sib mating was practiced for the production of F_1 inbred of Swiss albino mice. The selection criterion for choosing of F_0 full sib breeding pairs were the minimum body weight of the adult (≥ 30 g), apparently healthy and litter size at birth (≥ 8). The selected mice were provided with an *ad lib.* access to food and water. These mice were reared under similar feeding and management conditions throughout the experimental period. Sexing of mice was done at weaning age (28 days). Subsequently, until further mating, males and females were housed separately.

Phenomics and sample collection: Phenotypic traits were recorded for F_0 and F_1 inbred mice. Birth weights (BW), weaning weight (WW) and adult body weight (ABW) were recorded in grams (g) at age of 0, 28 and 70 days, respectively. Fitness traits, i.e. litter size at birth (LSB) and litter size at weaning (LSW) were also recorded. Approval was taken from Institute Animal Ethics Committee (IAEC) of ICAR-IVRI, Izatnagar and tail tissues (1–1.5 cm in size) were randomly collected from 100 F_0 and 100 F_1 inbred Swiss albino mice in a sterile 1.5 ml eppendorf tube and kept in ice until transferred to the laboratory for DNA extraction.

DNA extraction: Genomic DNA was isolated from the tail tissue of mice using DNA isolation kit (Qiagen DNeasy Blood and Tissue Kit) as per the manufacturer conditions. DNA concentration and purity (A260/A280 ratio) for each sample was assessed using a spectrophotometer and by 0.8% agarose gel electrophoresis. The measured DNA samples were stored at –20°C until further analysis.

PCR- microsatellite analysis: Ten microsatellite loci, viz. (D1Mit15, D2Mit51, D2Mit61, D3Mit55, D5Mit18, D7Mit323, D8Mit14, D9Mit27, D10Mit180 and D11Mit167) were used in the present study. Detailed information about each microsatellite locus along with primer sequence, annealing temperature, and amplicon size is given in Table 1. Primer sequences of the microsatellite loci were used according to the Mouse Locus List (http://www.informatics.jax.org). The forward and reverse primers working solutions were prepared to obtain a final concentration of 10 pmol of each primer. Final reaction mix (25 µl) comprised of Forward primer (1.0 µl of 10 pm/µl), Reverse primer (1.0 µl of 10 pm/µl), 10X Dream Taq Green buffer (2.5 µl), dNTPs mix (0.5 µl of 10 mM), Taq polymerase (0.2 µl of 5 U/µl), DNA template (2 µl) and Nuclease Free Water (17.8 µl). PCR was carried out in a 25 µl reaction volume, which was kept constant for all reactions using thermo cycler (Bio-Rad, USA).

Table 1. Microsatellite loci along with primer sequence, annealing temperature (AT), and amplicon size (AS) of each locus

Loci	Primer sequence (5′ → 3′)	AT (°C)	AS (bp)
D1Mit15-F	TCCACAGAACTGTCCCTCAA	52.5	154–188
D1Mit15-R	ATACACTCACACCACCCCGT		
D2Mit51-F	GTGAGGGGTCAATGCCAC	56.6	170–190
D2Mit51-R	GGCTCAGTTGTAAGCACAAGG		
D2Mit61-F	AAAGTCAACTGCTTTCAGTTACCC	56.6	122–158
D2Mit61-R	CACAGAAGTGCCCTTGCATA		
D3Mit55-F	CTGGGACCACCAGTAGTACCA	57.5	116–144
D3Mit55-R	TCAGGACTGCAACTGAGGC		
D5Mit18-F	CTGTAGTGGGTGGTTTTAAAATTG	57.5	220–238
D5Mit18-R	ATGCCACTGGTGCTCTCTG		
D7Mit323-F	TTTCACCTTCTAATCCTACTTCCTG	59.7	125–178
D7Mit323-R	TGTCCAGAACAGGAAATAGAGTACC		
D8Mit14-F	TTTTCACACTCACGTGTGCG	58.0	130–167
D8Mit14-R	GTCTCTCCTTCCTGGCGCTG		
D9Mit27-F	TAGATTTCTCAGGCAAGGAAGC	58.0	158–194
D9Mit27-R	TCCACTCTGAGCTTGGTGG		
D10Mit180-F	GACCTTCCTTTATACACAAGTCATAGC	62.9	108–206
D10Mit180-R	GTGGTACAGAACTTAGGTGTTTAATTG		
D11Mit167-F	TCGGATGCTAAGGAAATTGC	56.6	134–150
D11Mit167-R	GACACTCAGTGTTGACCTCTGG		

The optimization of appropriate annealing temperature with respect to each primer was determined by gradient PCR. The PCR conditions involved initial denaturation at 95°C for 5 min, followed by 40 cycles with denaturation at 94°C for 1 min, annealing temperature ranges from 52.5°C and 62°C for 45 sec to specifically amplify a target region 1 and 2 respectively, extension at 72°C for 1 min followed by a final extension at 72°C for 5 min. For genotyping of microsatellites, the amplified products were first run on 2.5% (w/v) agarose gel electrophoresis for checking their amplification. The products were then resolved on ultra-high-resolution agarose (4%; at 70–80 V; for 3–5 h) to differentiate alleles as per their length (in bp). Visualization of each gel was performed under Gel Doc (Genesnap, Syngene) system and size of allele was determined by using the software Gel Analyzer (2010).

Statistical analysis: Fixed effects of LSB, LSW, generation (Gen) and sex on phenotypic traits of F_0 and F_1 inbred Swiss albino mice were computed using following PROC GLM module of SAS 9.3.

$$Y_{ijklm} = \mu + LSB_i + LSW_j + Gen_k + Sex_l + e_{ijklm}$$

where, Y_{ijklm}, Phenotypic observation on m^{th} mouse; μ, overall mean; LSB_i, effect of i^{th} LSB; LSW_j, effect of j^{th} LSW; Gen_k, effect of k^{th} Gen; Sex_l, effect of l^{th} Sex; e_{ijklm}, random error ~ NID (0, e^2).

Observed heterozygosity (H_o) and expected heterozygosity (H_e), allele frequencies, observed number of alleles per locus (N_a), effective number of alleles (N_e), polymorphic information content (PIC), allelic diversity, Wright's F-statistic (F_{IS}) and Hardy Weinberg equilibrium were estimated using POPGENE 32 (Yeh *et al.* 1999) software. The inbreeding coefficient (F_{IS}) was calculated as deviation of the observed heterozygosity of an individual relative to the heterozygosity expected under random mating (Keller and Waller 2002) which was derived as:

$$F_{IS} = 1 - (H_o/H_e)$$

where, F_{IS}, coefficient of inbreeding; H_o, observed frequency of heterozygous individuals; H_e, expected frequency of heterozygous individuals in the population.

RESULTS AND DISCUSSION

Phenotypic and fitness related traits of F_0 and F_1 inbred mice were estimated on 918 and 707 individual off-springs, respectively. The BW, WW and ABW were recorded in grams (g) at the age of 0, 28 and 70 days, respectively. Fitness traits, i.e. LSB and LSW were recorded at the age of 0 and 28 days, respectively. The estimated phenotypic parameters (BW, WW, ABW, LWB and LSW) were found to be in concurrence with the general mice vital statistics (Table 3).

Effect of LSB and LSW on BW, WW and ABW in F_0 and F_1 inbred mice: All the LSB and LSW were classified into 3 groups (Table 2). The influence of fixed effects (litter size) on BW, WW and ABW in both the generation was found to be statistically significant ($p<0.05$) (Table 2). It was observed that BW, WW and ABW of LSB (1–5) group were significantly higher ($p<0.05$) than LSB (6–10) and LSB (≥ 11) groups in both the generations of mice (Table 2). Similarly, WW and ABW of LSW (1–5) group were

Table 2. Effect of LSB and LSW on BW, WW and ABW in F_0 and F_1 inbred mice

Generation	Effect	BW (g)	WW (g)	ABW (g)	Effects	WW (g)	ABW (g)
	LSB	Mean±SE (N)	Mean±SE (N)	Mean±SE (N)	LSW	Mean±SE (N)	Mean±SE (N)
F_0	1–5	2.11^a±0.11 (58)	19.26^a±0.66 (43)	36.08^a±1.15 (20)	1–5	19.18^a±0.59 (48)	36.08^a±1.15 (20)
	6–10	1.71^b±0.01 (572)	13.38^b±0.16 (439)	34.00^b±0.32 (260)	6–8	13.61^b±0.18(347)	33.54^b±0.36 (211)
	≥11	1.55^c±0.02 (288)	11.8^c±0.25 (159)	30.40^c±0.78 (77)	≥9	11.94^c±0.19 (246)	32.56^b±0.58 (126)
F_1	1–5	2.06^a±0.06 (91)	21.01^a±0.39 (55)	34.00^a±0.52 (55)	1–5	20.96^a±0.36 (73)	34.68^a±0.51 (58)
	6–10	1.62^b±0.01 (436)	16.78^b±0.19 (324)	32.00^b±0.27 (382)	6–8	17.02^b±0.21(245)	32.49^b±0.32 (212)
	≥11	1.41^c±0.01 (180)	13.94^c±0.25 (142)	30.00^c±0.36 (116)	≥9	14.15^c±0.19 (203)	30.69^c±0.28 (174)

Mean with different superscript differs significantly ($p<0.05$).

Table 3. Effect of generation and sex on all the measured phenotypic traits F_0 and F_1 inbred generation mice

Effect Generation	BW (g) Mean±SE (N)	LSB Mean±SE (N)	WW (g) Mean±SE (N)	LSW Mean±SE (N)	ABW (g) Mean±SE (N)	Effect Sex	WW (g) Mean±SE (N)	ABW (g) Mean±SE (N)
F_0	1.68^a±0.01	9.46^a±0.08	13.39^b±0.15	7.99^a±0.07	33.34^a±0.30	Male	13.76^a±0.21 (341)	35.26^a±0.41 (194)
	(918)	(918)	(641)	(731)	(357)	Female	12.96^b±0.20 (300)	31.06^b±0.39 (163)
F_1	1.62^b±0.01	8.71^b±0.10	16.45^a±0.16	7.89^a±0.09	32.07^b±0.21	Male	16.87^a±0.24 (261)	34.52^a±0.24 (220)
	(707)	(708)	(521)	(584)	(444)	Female	16.04^b±0.23 (260)	29.66^b±0.26 (224)

Mean with different superscript differs significantly ($p<0.05$); (N) indicates sample size.

significantly higher ($p<0.05$) than LSW (6–8) and LSW (≥9) groups in both the generations of mice (Table 2). Generally, body weight of rodents at weaning is inversely related to size of litter. Therefore, as litter size is increased body weight of offspring is decreased at postnatal days, 4, 7, 14, 21 in both sexes of mice (Tanaka 2004). Our results were in agreement with the findings of (Epstein 1978) which justified that when there is less litter size, less number of pups are available for nursing and gives a good environment as a result pups are healthier.

Effect of generation on all the measured phenotypic traits: Inbreeding frequently affects traits associated with reproductive ability and physiological efficiency in livestock species and laboratory animals, resulting in a reduction in the mean phenotypic value of certain traits (Frankham *et al.* 2002). The extent and practical consequences of inbreeding differ as they depend on the trait, the genetic make-up of the species or populations within the species, and on how these inbreeding effects interact with the environment (Hedrick and Kalinowski 2000).

In the currently studied population, the BW of F_0 population (1.68±0.01) was significantly higher ($p<0.05$) than the F_1 inbred population (1.62±0.01) which showed slight reduction in the birth weight in the F_1 inbred (Table 3). The mean ABW of F_1 inbred population (32.07±0.21) was significantly lower ($p<0.05$) than the mean ABW of F_0 population (33.34±0.30). White (1972) observed that increasing inbreeding rates were found to cause linear depression of postnatal maternal performance and significantly depressed the birth weight and weight at 12, 21, 42 and 56 days in the litter. Therefore, it is expected that increasing levels of inbreeding might be a cause of depression in body weight performances. The WW of the F_1 inbred (16.45±0.16) was significantly higher ($p<0.05$) in comparison to the F_0 generation (13.39±0.15). In present study effect of inbreeding on WW was not observed. It might be associated with the fact that reduction in LSB of inbred mice, which leads to an improved environment for the young and hence a cancellation of the genetic effect on WW due to inbreeding in mice (Roberts 1960). Beilharz (1982) and Bünger and Hill (1999) have documented a negative effect of inbreeding on body weight of mice but McCarthy (1967) and Holt *et al.* (2004) did not find it.

Holt *et al.* (2004) noticed that inbreeding has a reducing effect on the average litter size. They reported that litter size reduced by 0.09 pups per 1% increasing in inbreeding coefficient. In the present study, LSB in F_0 (9.46±0.08) population was significantly higher ($p<0.05$) than the F_1 inbred (8.71±0.10) (Table 3). There was a reduction of approximately one litter size in the F_1 generation due to inbreeding. No significant difference was noticed in LSW in F_0 (7.99±0.07) and F_1 inbred (7.89±0.09) population, thus the trait was not much affected due to inbreeding.

Effect of sex of mice on all the measured phenotypic traits: The WW of F_0 (13.76±0.21) and F_1 inbred (16.87±0.24) male mice were significantly higher ($p<0.05$) than the WW of F_0 (12.96±0.20) and F_1 inbred (16.04±0.23) female mice (Table 3). The ABW of males of F_0 (35.26±0.41) and F_1 inbred (34.52±0.24) mice was significantly higher than the ABW of females in both the generations (Table 3). As a result, males had a higher WW and ABW than females in both generations. Consequently, the findings showed that, male mice had a comparatively higher body weight than female mice and were in agreement with White (1972).

Genotypic characterization of F_0 and F_1 inbred mice: In the present study, 100 mice from each population of F_0 and F_1 inbred generation were genotyped by PCR-microsatellite analysis technique for 10 loci. All genotyped loci were polymorphic and a total of 34 alleles were detected across the 10 loci in both the generation mice. Numbers of alleles, PIC, heterozygosity, allelic diversity and F_{IS} statistics of all studied microsatellite loci in F_0 and F_1 inbred population are shown in Table 4. The representative images of gel electrophoresis of a microsatellite (D2Mit61) locus in 4% ultra-high-resolution agarose gel of the both generations are shown in Fig. 1 and Fig. 2, respectively.

The total number of alleles per locus ranged from 3 (D2Mit61, D3Mit55, D8Mit14, D9Mit27, D10Mit180, D11Mit167) to 4 (D1Mit15, D2Mit51, D5Mit18, D7Mit323) in F_0 and F_1 inbred population, with a mean value of 3.4 indicating polymorphism in all 10 loci. The effective number of alleles varied from 2.145 (D3Mit55) to 3.724 (D2Mit51) and from 2.02 (D3Mit55) to 3.542 (D1Mit15), with an average of 2.935 and 2.733 in F_0 and F_1 inbred population, respectively (Table 4). The observed heterozygosity (H_o) and expected heterozygosity (H_e) values in the F_0 population ranged from 0.300 (D8Mit14)

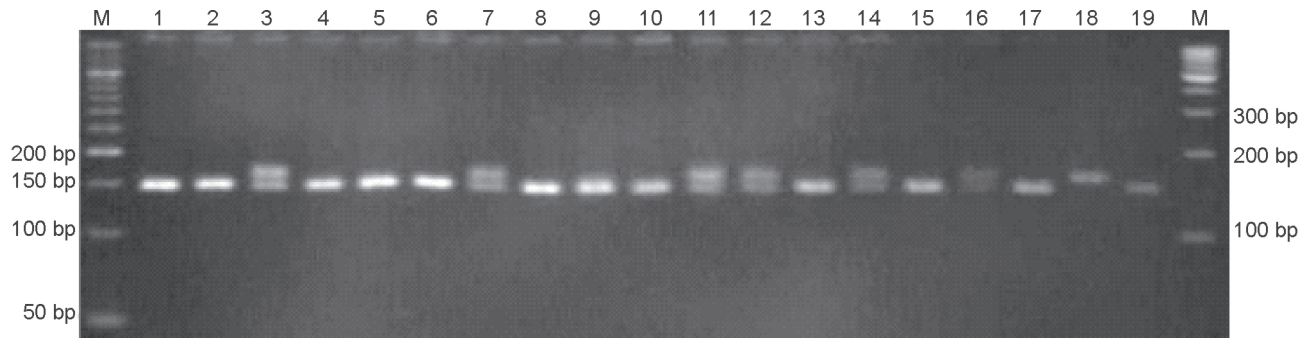

Fig. 1. PCR-microsatellite allele profile of D2Mit61 locus in Swiss albino mice of F_0 generation (4% ultra-high-resolution agarose gel). Lane M1, 50 bp marker; Lane M2, 100 bp marker; Lanes 1–19, Resolved PCR products (Animal no. 1 to 19).

Table 4. Observed number of alleles (N_a), the effective number of alleles (N_e), polymorphic information content (PIC), observed heterozygosity (H_0), expected heterozygosity (H_e), allelic diversity and F_{IS} statistics of all studied microsatellite loci in F_0 and F_1 inbred population

Locus	N_a	F_0						P value	F_1						P value
		Ne	H_0	H_e	PIC	Allelic diversity	F_{IS}		N_e	H_0	H_e	PIC	Allelic diversity	F_{IS}	
D1Mit15	4	3.615	0.45	0.727	0.674	0.723	0.378	<.0001	3.542	0.52	0.721	0.668	0.718	0.275	<.0001
D2Mit51	4	3.724	0.58	0.735	0.682	0.732	0.207	<.0001	2.892	0.21	0.658	0.588	0.654	0.679	<.0001
D2Mit61	3	2.611	0.35	0.62	0.548	0.617	0.433	<.0001	2.102	0.3	0.527	0.468	0.524	0.428	<.0001
D3Mit55	3	2.145	0.39	0.537	0.477	0.534	0.269	<.0001	2.02	0.45	0.507	0.447	0.505	0.109	0.0273
D5Mit18	4	2.86	0.57	0.654	0.604	0.65	0.216	<.0001	3.152	0.51	0.686	0.626	0.683	0.253	<.0001
D7Mit323	4	3.046	0.53	0.675	0.614	0.672	0.211	<.0001	2.827	0.48	0.65	0.595	0.646	0.257	<.0001
D8Mit14	3	2.701	0.3	0.633	0.554	0.63	0.524	<.0001	2.764	0.31	0.641	0.566	0.638	0.514	<.0001
D9Mit27	3	2.812	0.58	0.645	0.571	0.644	0.999	0.1777	2.746	0.35	0.639	0.558	0.636	0.45	<.0001
D10Mit180	3	2.859	0.56	0.654	0.576	0.65	0.139	0.1603	2.97	0.44	0.667	0.589	0.663	0.337	<.0001
D11Mit167	3	2.981	0.35	0.668	0.591	0.665	0.473	<.0001	2.316	0.33	0.571	0.501	0.568	0.419	<.0001
Mean	3.4	2.935	0.46	0.654	0.589	0.651	0.294		2.733	0.39	0.627	0.56	0.623	0.372	

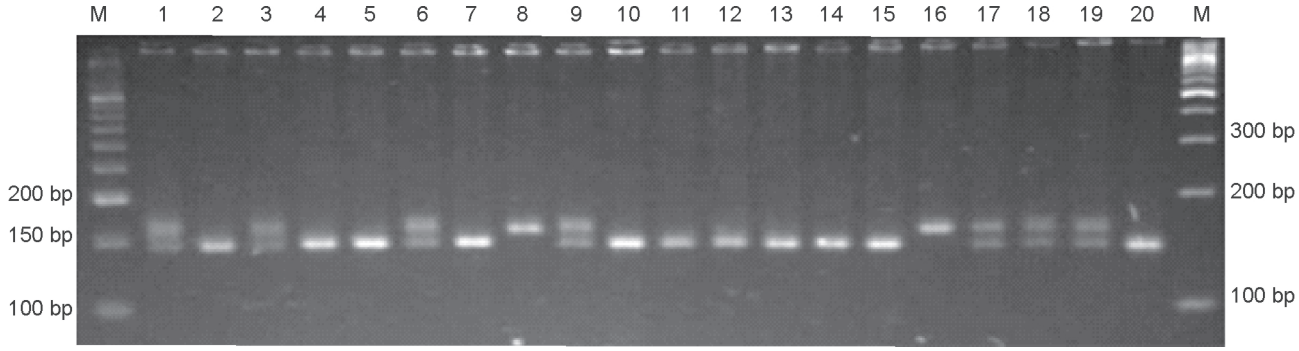

Fig. 2. PCR-microsatellite allele profile of D2Mit61 locus in Swiss albino mice of F_1 inbred generation (4% ultra-high-resolution agarose gel). Lane M1, 50 bp marker; Lane M2, 100 bp marker; Lanes 1–20, Resolved PCR products (Animal no. 1 to 20).

to 0.580 (D2Mit51) and 0.537 (D3Mit55) to 0.735 (D2Mit51), respectively (Table 4). In F_1 inbred populations, these values (H_o and H_e) ranged from 0.210 (D2Mit51) to 0.520 (D1Mit15) and 0.507 (D3Mit55) to 0.721 (D1Mit15), respectively (Table 4). Normally, the effective number of alleles and the average heterozygosity are used as estimators to assess genetic characteristics and diversity. Moderate to high level of heterozygosity was observed for all studied loci in both the population. The results implied that there is abundant genetic variation in population of Swiss albino mice under present study. Slight reduction of heterozygosity (0.07) was observed in the F_1 inbred population. Such findings were comparable with Yu and Peng (2002) who observed that effective number of alleles and expected heterozygosity ranged from 3.17 to 8.50 and from 0.35 to 0.83, respectively for six microsatellite loci polymorphism study in house mice in Taiwan. Shang *et al.* (2009) also studied the two Chinese Kunming mice population and observed that the mean number of alleles and mean of expected heterozygosity for each studied locus was 5.933 and 0.572, respectively.

The ranges of PIC value in F_0 (0.477 to 0.682) and F_1 inbred (0.447 to 0.668) population for various microsatellite loci revealed that population under investigation was of high diversity maintaining a multiple allele in both the population. PIC values for all loci were moderate to highly informative in the studied population. While the mean PIC value reported by Purohit *et al.* (2015) was 0.395 for 14 different microsatellite markers.

Estimation of inbreeding coefficient using microsatellite markers: The F_{IS} measures the reduction of an individual's heterozygosity due to non-random mating within the population. The value of F_{IS} which is significantly lower or higher or than zero shows, outbreeding or inbreeding, respectively. In current study, estimates of the F_{IS} (inbreeding coefficient) ranged from 0.139 (D10Mit180) to 0.999 (D9Mit27) and from 0.109 (D3Mit55) to 0.679 (D2Mit51), respectively for F_0 and F_1 inbred populations (Table 4). The highest F_{IS} was observed for the microsatellite locus D9Mit27 (0.999) and D2Mit51 (0.679) in F_0 and F_1 inbred populations, respectively (Table 4). The mean marker-based F_{IS} was 0.294 and 0.372 in F_0 and F_1 inbred populations, respectively. Eight microsatellite loci (D1Mit15, D2Mit51, D2Mit61, D3Mit55, D5Mit18, D7Mit323, D8Mit14 and D11Mit167) and all 10 loci showed significant deviations ($p<0.05$) from HWE in F_0 and F_1 inbred population, respectively. Shang *et al.* (2009) observed that F_{ST} per locus varied from 0.013 (D2Mit30) to 0.569 (D7Mit281) and the average F_{ST} of all loci was 0.143. This F_{IS} of the current study was comparable to that

of 0.122 reported for house mice of Taiwan (Yu and Peng 2002) and 0.287 reported for Chinese Kunming mice (Shang *et al.* 2009). Thus with 29.4% F_{IS} in the F_0 population of the present study indicating that the population were more related than expected under random mating. There was increase of 7.8% inbreeding in the F_1 inbred population in comparison to F_0 population as full sib mating was practiced to produce the F_1 inbred population. In the current population, only two loci (D9Mit27 and D10Mit180) in F_0 population were in HWE ($p>0.05$) indicating random mating at these marker loci. In the global HWE deviation experiment, the deviations from the expected value may be due to a number of reasons like, population subdivision due to genetic drift, artificial selection, migration, inbreeding, excess of heterozygous individuals than homozygous individuals, and high microsatellite mutation rate and artificial selection in a breed (Aminafshar *et al.* 2008,Vajed Ebrahimi *et al.* 2017). This study reports the molecular genetic profiles of F_0 outbred and the F_1 inbred strain of Swiss albino mice by means of 10 microsatellite analysis. The study also shows the usefulness of microsatellite markers in estimation of inbreeding in the population. However, it is advisable to use genome wide microsatellite genotyping for accurate measurement and reliable estimation of population genetic parameters and inbreeding coefficient.

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REFERENCES

Aminafshar M, Amirinia C and Torshizi R V. 2008. Genetic diversity in buffalo population of guilan using microsatellite markers. *Journal of Animal and Veterinary Advances* **7**: 1499–1502.

Amos W, Worthington Wilmer J, Fullard K, Burg T M, Croxall J P, Bloch D and Coulson T. 2001. The influence of parental relatedness on reproductive success. *Proceedings of the Royal Society of London. Series B: Biological Sciences* **268**(1480): 2021–27.

Arends D, Hesse D and Brockmann G A. 2018. Invited review: Genetic and genomic mouse models for livestock research. *Archives Animal Breeding* **61**(1): 87–98.

Beck J A, Lloyd S, Hafezparast M, Lennon-Pierce M, Eppig J T, Festing M F and Fisher E M. 2000. Genealogies of mouse inbred strains. *Nature Genetics* **24**(1): 23–25.

Beilharz R G. 1982. The effect of inbreeding on reproduction in mice. *Animal Science* **34**(1): 49–54.

Bünger L and Hill W G. 1999. Inbred lines of mice derived from long-term divergent selection on fat content and body weight. *Mammalian Genome* **10**(6): 645–48.

Casellas J. 2011. Inbred mouse strains and genetic stability: A review. *Animal* **5**(1): 1–7.

Danneman P J, Suckow M A and Brayton C. 2012. *The Laboratory Mouse*. CRC Press.

Das A K, Kumar S, Rahim A and Kokate L S. 2016. Association study between microsatellite genotypes and layer performances in Rhode Island Red chicken. *Indian Journal of Animal Sciences* **86**(9):1021–24.

Epstein H T. 1978. The effect of litter size on weight gain in mice. *Journal of Nutrition* **108**(1): 120–23.

Frankham R, Briscoe D A and Ballou J D. 2002. *Introduction to Conservation Genetics*. Cambridge University Press.

Gulcher J. 2012. Microsatellite markers for linkage and association studies. *Cold Spring Harbor Protocols* **2012**(4).

Hedrick P W and Kalinowski S T. 2000. Inbreeding depression in conservation biology. *Annual Review of Ecology and Systematics* **31**(1): 139–62.

Holt M, Nicholas F W, James J W, Moran C and Martin I C. 2004. Development of a highly fecund inbred strain of mice. *Mammalian Genome* **15**(12): 951–09.

Keller L F and Waller D M. 2002. Inbreeding effects in wild populations. *Trends in Ecology and Evolution* **17**(5): 230–41.

McCarthy J C. 1967. The effects of inbreeding on the components of litter size in mice. *Genetical Research* **10**(1): 73–80.

Naghavian S, Hasani S, Ahani Azari M, Khan Ahmadi A R, Saghi D A and Mami Zade N. 2016. Estimation of inbreeding coefficients using pedigree and microsatellite markers and its effects on economic traits of Shirvan Kordi sheep. *Iranian Journal of Applied Animal Science* **6**(1): 133–41.

Papa R and Gepts P. 2003. Asymmetry of gene flow and differential geographical structure of molecular diversity in wild and domesticated common bean (*Phaseolus vulgaris* L.) from Mesoamerica. *Theoretical and Applied Genetics* **106**(2): 239–50.

Purohit N, Kumar M, Srivastav A K and Purohit D C. 2015. Evaluation of genetic relationship within and between mice strains using microsatellite markers. *Research in Biotechnology* **6**(6).

Roberts R C. 1960. The effects on litter size of crossing lines of mice inbred without selection. *Genetics Research* **1**(2): 239–52.

Selvaggi M, Dario C, Peretti V, Ciotola F, Carnicella D and Dario M. 2010. Inbreeding depression in Leccese sheep. *Small Ruminant Research* **89**(1): 42–46.

Shang H, Wei H, Yue B, Xu P and Huang H. 2009. Microsatellite analysis in two populations of Kunming mice. *Laboratory Animals* **43**(1): 34–40.

Tanaka T. 2004. The relationships between litter size, offspring weight, and behavioral development in laboratory mice *Mus musculus*. *Mammal Study* **29**(2): 147–53.

Vajed Ebrahimi M T, Mohammadabadi M and Esmailizadeh A. 2017. Using microsatellite markers to analyze genetic diversity in 14 sheep types in Iran. *Archives Animal Breeding* **60**(3): 183–89.

de Vicente M C, Guzman F A, Engels J and Rao V A. 2006. Genetic characterization and its use in decision-making for the conservation of crop germplasm. *The role of biotechnology in exploring and protecting agricultural genetic resources* (Eds) John R and Andrea S. pp 129–138. FAO, Rome.

White J M. 1972. Inbreeding effects upon growth and maternal ability in laboratory mice. *Genetics* **70**(2): 307–17.

Yeh F C, Boyle T and Yang R C. 1999. PopGene: Microsoft Window-based freeware for population genetic analysis, version 1.31'.

Yu H T, Peng Y H. 2002. Population differentiation and gene flow revealed by microsatellite DNA markers in the house mouse (*Mus musculus castaneus*) in Taiwan. *Zoological Science* **19**(4): 475–84.