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**Microsatellite markers linked to fecundity gene revealed genetic variation and strong association with litter size in indigenous sheep**

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# Table S1

Microsatellite primer sequences, annealing temperature (AT) of the primers used in the current study

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| S.N | Name | sequence (5' to 3') | AT | dye |
| 1 | BM1329 | F: TTGTTTAGGCAAGTCCAAAGTC | 55-60°C | 6-FAM |
|  |  | R: AACACCGCAGCTTCATCC |  |  |
| 2 | OarAE101 | F: TTCTTATAGATGCACTCAAGCTAGG | 55-60°C | NED |
|  |  | R: TAAGAAATATATTTGAAAAAACTGTATCTCCC |  |  |
| 3 | BMS2508 | F: TTTCTGGGATTACAAAATGCTC | 55-60°C | PET |
|  |  | R: TTTCTTAGGGGAGTGTTGATTC |  |  |
| 4 | TGLA54 | F: CTCAATATTTTGCAATAACATATAAGG | 55-60°C | VIC |
|  |  | R: ACGATATCATGTTAGTTTCAGGTG |  |  |
| 5 | TGLA68 | F: ATCTTACTTACCTTCTCAGAGCT | 55-60°C | PET |
|  |  | R: GGGACAAAATTTTACATATACACTT |  |  |

# Table S2

Effects of genotypes of BMS2508 BM1329 and OAR101, microsatellite markers linked to *Booroola* (FecB) mutation on litter size in indigenous sheep

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| BMS2508 genotypes | | | | | | |
|  | Variation | Sum of Squares | DF | Mean Square | F value | P value |
| Parity 1 | Between population | 52.98 | 9 | 5.89 | 96.61 | 0.00 |
| Within population | 17.49 | 287 | 0.06 |  |  |
| Total | 70.47 | 296 |  |  |  |
| Parity 2 | Between population | 29.52 | 9 | 3.28 | 27.69 | 0.00 |
| Within population | 33.99 | 287 | 0.12 |  |  |
| Total | 63.50 | 296 |  |  |  |
| BM1329 genotypes | | | | | | |
| Parity 1 | Between population | 17.64 | 5 | 3.53 | 21.416 | 0.00 |
| Within population | 38.89 | 236 | 0.17 |  |  |
| Total | 56.53 | 241 |  |  |  |
| Parity 2 | Between population | 22.88 | 5 | 4.56 | 30.47 | 0.00 |
| Within population | 35.44 | 236 | 0.15 |  |  |
| Total | 58.31 | 241 |  |  |  |
| OAR101 genotypes | | | | | | |
| Parity 1 | Between population | 121.58 | 8 | 15.19 | 339.02 | 0.00 |
| Within population | 12.78 | 285 | 0.05 |  |  |
| Total | 134.35 | 293 |  |  |  |
| Parity 2 | Between population | 87.81 | 8 | 10.98 | 96.73 | 0.00 |
| Within population | 32.34 | 285 | 0.113 |  |  |
| Total | 120.15 | 293 |  |  |  |

# Table S3

Effects of genotypes of TGLA54 and TGLA68 microsatellite markers linked to *Inverdale* (FecXI) mutation on litter size in indigenous sheep

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| TGLA54 genotypes | | | | | | |
| Parity | Variation | Sum of Squares | DF | Mean Square | F value | P value |
| 1 | Between population | 6.22 | 6 | 1.04 | 3.41 | 0.00 |
| Within population | 46.16 | 152 | 0.30 |  |  |
| Total | 52.38 | 158 |  |  |  |
| 2 | Between population | 0.79 | 6 | 0.13 | 0.78 | 0.58 |
| Within population | 37.95 | 227 | 0.17 |  |  |
| Total | 38.74 | 233 |  |  |  |
| TGLA68 genotypes | | | | | | |
| Parity 1 | Between population | 19.04 | 4 | 4.76 | 16.38 | 0.00 |
| Within population | 56.38 | 194 | 0.29 |  |  |
| Total | 75.42 | 198 |  |  |  |
| Parity 2 | Between population | 4.09 | 4 | 1.02 | 4.92 | 0.00 |
| Within population | 55.99 | 269 | 0.21 |  |  |
| Total | 60.09 | 273 |  |  |  |