

Morphometric Parameters and Evaluation of Male Persian Fallow Deer Semen

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Abstract : Persian fallow deer (*Dama dama mesopotamica*) is belonging to the family Cervidae and is only found in a few protected areas in the northwest, north, and southwest of Iran. The aims of this study were analysis of inbreeding and morphometric parameters of semen in male Persian fallow deer to investigate the cause of reduced fertility of this endangered species in Dasht-e-Naz National Refuge, Sari, Iran. The Persian fallow deer semen was collected from four adult bucks randomly during the breeding and non-breeding season from five dehorned and horned deer's by an artificial vagina. Twelve blood samples was taken from Persian fallow deer and mitochondrial DNA was extracted, amplified, extracted, sequenced and then were considered for genetic analysis. The Persian fallow deer semen, both with normal and abnormal spermatozoa, is similar to that of domestic ruminants but very smaller and difficult to observe at the primary observation. The post-mating season collected ejaculates contained abnormal spermatozoa, debris and secretion of accessory glands in horned bucks and accessory glands secretion free of any spermatozoa in dehorned or early velvet budding bucks. Microscopic evaluation in all four bucks during the mating season showed the mean concentration of 9×10^6 spermatozoa/ml. The mean \pm SD of age, testes length and testes width was 4.60 ± 1.52 years, 3.58 ± 0.32 and 1.86 ± 0.09 cm, respectively. The results identified 1120 loci (assuming each nucleotide as locus) in which 377 were polymorphic. In conclusion, reduced fertility of male Persian fallow deer may be caused by inbreeding of the protected herd in a limited area of Dasht-e-Naz National Refuge.

Keywords : Persian fallow deer, genetic analysis, spermatozoa, reproductive characteristics

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