ABSTRACT

Scrapie is a progressive neurodegenerative disorder of sheep and goats. It belongs to a class of conditions, affecting nervous system, known as transmissible spongiform encephalopathies that also include bovine spongiform encephalopathy or mad cow disease, chronic wasting disease in deer and Cruetzfeldt-Jacob disease in humans. The major characteristics of scrapie are uncoordinated gait, pruritus and wool loss etc. Biochemically, it is characterized by the presence of abnormal prion protein (PrPSc) in the nervous or lymphoid tissues. A few prion protein gene (PrP) polymorphisms are known to confer susceptibility/resistance to scrapie both in sheep and goats. A massive campaign about selective breeding to increase resistance to scrapie has led to sequencing of PrP gene's CDS hundreds of thousands times in various states of West.

The present study aimed at sequencing CDS of PrP gene in 24 sheep and 24 goats. A total of nine polymorphisms were detected in the prion protein (PRNP) gene of two goat breeds, Local Hairy and Kamori, and ten polymorphisms in two sheep breeds, Hashtnagri and Damani. Two or more than two polymorphisms were also present in the PrP of the studied animals. Polymorphism T718C was the most prevalent polymorphism in goats, while polymorphism A566T was the most prevalent polymorphism in sheep. The most prevalent allele was P^{240} (79.16%) in goats, while the most prevalent allele was L^{189} in sheep. The most prevalent genotype was s^{138} R^{143} P^{240} (25%) in goats, while the most prevalent genotype was also L^{189} (12.5%) in sheep(small alphabet letter i.e s refers to silent mutation). The polymorphisms A428G (H143R) conferring resistances to scrapie in goats, and Q171R and Q171H in sheep were detected in only eight and six animals, respectively, indicating low to moderate level of disease resistance in the studied breeds. The results of the present study warrant that further studies regarding the PrP variability in Pakistani sheep and goats should be undertaken to obtain true estimates of frequency of scrapie-associated polymorphisms, so that the risk of scrapie incidence in Pakistan could be estimated.