

## عنوان مقاله:

Comparative Analysis of Differential Exon Usage between the Breeds of Sheep and Goats Using RNA-Seq Data

## محل انتشار:

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## خلاصه مقاله:

Alternative splicing, alternative transcript start site, and alternative transcript polyadenylation site are the main factors resulting in diversity of the transcripts of a gene. The main objectives of this study were to analyze the alternation process in breeds of sheep and goat, and to identify its role in differentiation of breeds of a species. RNA-seq data were prepared from ovarian tissue of two breeds of Shal and Sangsari sheep and two breeds of Tibetan and Jintang black goats. Reads were aligned to the reference genome and significant genes with respect to differential exon usage were identified. The statistical comparison revealed that 8,104 genes were significantly different in exon usage between the sheep breeds and 173 genes differed between the goat breeds. Out of the 121,861 studied exons, only 22.7% were preserved during future generations between the breeds, of which 99.3% did not display any alternatives. The high protection was probably due to the lack of involvement of the exons in alternative process. The genes with differential exon usage in goat had a higher percentage of alternatives than those in sheep. The interracial analysis showed that alternative splicing was the most influential type of alternatives in the breeds of sheep and goats. It seems that the conservation process of the exons is related to the contribution of these exons in alternative process in both sheep and goat breeds. The significant PI3K-Akt and alternative splicing pathways play a role in cell growth, development of ovaries, and mRNAs splicing.

## کلمات کلیدی:

.Alternative splicing, Interethnic analysis, Ovarian tissue, Transcription

## لینک ثابت مقاله در پایگاه سیویلیکا:

<https://civilica.com/doc/1815341>

