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GENOME-WIDE IDENTIFICATION OF SNPs AND THEIR ANNOTATION IN INDIAN GIR CATTLE

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The study was carried out in Gir cattle for identification of genome wide SNPs and then to annotate the identified high-quality SNPs to the milk production traits. A total of 99,517 SNPs were identified with respect to the Bos indicus reference genome. Upon annotation of SNPs identified with respect to Bos indicus reference genome, 984 SNPs were found to be associated with 175 candidate genes having to do with milk production traits, notably Acetyl-CoA carboxylase β -gene, which affects milk composition traits by regulation of fatty acid oxidation in the mitochondria; Growth hormone receptor gene which have role in milk yield and its composition traits; LEP gene, involved in energy partitioning and metabolism, were among others. This study provides the first analysis of ddRAD sequences to discover SNPs in Indian Gir cattle breed, aligned to reference genome. The variants mined in this study can be incorporated in existing SNP chips and thus, play an important role in understanding the genetic structure of our cattle to design appropriate breed improvement programmes.

Key words: ddRAD, Gir breed, Milk production traits, SNPs, Zebu cattle.

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ПОВНОГЕНОМНА ІДЕНТИФІКАЦІЯ ОДНОНУКЛЕОТИДНИХ ПОЛІМОРФІЗМІВ І ЇХ МАРКУВАННЯ В ІНДІЙСЬКІЙ ПОРODІ ХУДОБИ ГІР

Індійську породу великої рогатої худоби Гір було використано у дослідженні, проведеному з метою ідентифікації повногеномних однонуклеотидних поліморфізмів (SNP) та подальшого маркування ідентифікованих високоякісних SNP за ознаками молочної продуктивності. Загалом було ідентифіковано 99 517 SNP стосовно референтного геному *Bos indicus*. Після маркування SNP, ідентифікованих стосовно референтного геному *Bos indicus*, було виявлено, що 984 SNP асоціюються з 175 генами-кандидатами, пов'язаними з ознаками молочної продуктивності, особливо з β -геном ацетил-СоА карбоксилази, що впливає на характеристики складу молока шляхом регуляції окислення жирних кислот у мітохондріях; геном рецептора гормону росту, який відіграє свою роль у надоях молока та характеристиках його складу; геном LEP, залученим до розщеплення енергії і метаболізму, та іншими. У цьому дослідженні вперше проведено аналіз послідовностей ddRAD для виявлення SNP у породі Гір індійської великої рогатої худоби, вирівняних з референтним геномом. Варіанти, розглянуті у цьому дослідженні, можна інкорпорувати в наявні чіпи SNP і, таким чином, вони відіграватимуть важливу роль у розумінні генетичної структури нашої худоби для створення відповідних програм покращення породи.

Ключові слова: ddRAD, порода Гір, характеристики молочної продуктивності, однонуклеотидні поліморфізми (SNP), зебу.

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