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SURVEYING SELECTION SIGNATURES IN MURRAH BUFFALO USING GENOME-WIDE SNP DATA

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The population of in-milk buffaloes climbed by 4.3 % in 2012–2019, as compared to the decline of 28.9 % in 2007–2012, suggesting a trend reversal towards buffalo rearing due to consumer preferences and policy interventions. Moreover, Murrah buffaloes have quadrupled in the same period from 11.7 million to 47.06 million headcounts, constituting about 42.8 % of the total buffaloes. Analysis of selection signatures reveals important details about how the genomic environments of contemporary livestock have been altered by both natural and artificial selective pressures. In the present study to delineate signals of positive selection, a total of 246 million (98.08 %) clean ddRAD-seq reads were mapped to Bubalus bubalis reference genome assembly. CLR approach was used to detect selected regions and a total of 289 selection signatures were found in Murrah genome. The outlier fraction containing 289 sites, bracketed by a 10 kb window, 5 kb up- and down- stream were declared as the putative selection signatures. A total of 106 genes and 22 loci were traced in 179 selective sweep regions in Murrah buffalo. The information mined in this study will aid in future polymorphism studies of economic traits in buffaloes.

Key words: *selection; CLR; murrah; ddRAD-seq; genome.*

ДОСЛІДЖЕННЯ ХАРАКТЕРНИХ СЕЛЕКЦІЙНИХ ОЗНАК БУЙВОЛІВ ПОРОДИ МУРРА З ВИКОРИСТАННЯМ ДАНИХ SNP ПО ВСЬОМУ ГЕНОМУ

У 2012–2019 рр. популяція дійних буйволиць зросла на 4,3 % порівняно зі спадом на 28,9 % у 2007–2012, що дозволяє припустити зміну тенденції щодо розведення буйволів внаслідок преференцій споживачів та втручань у політику. Крім того, поголів'я буйволів породи Мурра за той же період зросло в чотири рази – з 11,7 млн до 47,06 млн голів, що становить близько 42,8 % від загального поголів'я буйволів. Аналіз селекційних ознак розкриває важливі деталі того, як геномне середовище сучасної худоби було змінено під природним і штучним селективним тиском. У цьому дослідженні для визначення сигналів позитивного добору було зіставлено 246 мільйонів (98,08 %) чистих ddRAD-секвенів на референтну збірку генома *Bubalus bubalis.* Для виявлення відібраних ділянок було використано підхід CLR, і в цілому в геномі Мурра було знайдено 289 селекційних ознак. Фракція викидів, що містить 289 ділянок, розділених вікном розміром 10 кб, по 5 кб вгору і вниз, була визначена як передбачувані селекційні ознаки. Загалом було відстежено 106 генів і 22 локуси в 179 регіонах селективного розгортання буйволів Мурра. Інформація, отримана в цьому дослідженні, буде корисною для майбутніх досліджень поліморфізму економічно цінних ознак буйволів.

Ключові слова: селекція, CLR, Мурра, ddRAD-секвени, геном.

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