

<ポスター発表 I>

(説明 5 分 / 人、10:00~11:30)

演題番号 I-01-04

座長: 福井えみ子先生 (宇都宮大学) 10:00 ~

I-01

兵庫黒毛和種集団を用いた 17 番染色体における脂肪交雑 QTL の探索

○伊藤ひかり (神戸大院農)、足立亮仁 (神戸大院農)、川口英岐 (神戸大院農)、万年英之 (神戸大院農)、笹崎晋史 (神戸大院農)

I-02

*PMEL* p.L18del は代謝関連遺伝子群の発現変動を起こし肉質等級に影響する

○山下泰斗 (東海大農)、橋本峻 (東海大農)、大山泰生 (東海大農)、木村聡志 (東海大院農)、神鷹孝至 (東海大フェニックスカレッジ熊本オフィス)、久保和弘 (東海大フェニックスカレッジ熊本オフィス)、稲永敏明 (東海大農)、樫村敦 (東海大農)、松本大和 (東海大農)

I-03

黒毛和種牛における肉量および肉質の指標としての血中マイクロ RNA の探索

○稲垣翔太 (京大院農)、足立裕哉 (京大院農)、Kevin Otieno Amolo (京大院農)、楊曾 (京大院農)、横井伯英 (京大院農)

I-04

**Investigation of genetic variants related to growth and reproductive traits in Vietnamese native buffalo**

○**Nguyen Thanh Thuy**<sup>1,2</sup>, Yuji Imai<sup>3</sup>, Tsuyoshi Koide<sup>3</sup> and Takehito Tsuji<sup>1</sup>

<sup>1</sup>Graduate School of Environmental and Life Science, Okayama University, Japan

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<sup>3</sup>Mouse Genomics Resource Laboratory, National Institute of Genetics

演題番号 I-05-08

座長: 横井伯英先生 (京都大学) 10:25 ~

I-05

黒毛和種雌牛集団における受胎に関わる DNA マーカーの探索

○大郷すみれ (宇都宮大院地域創生科学)、永井友香理 (栃木県畜産酪農研究センター)、岡本優 (栃木県畜産酪農研究センター)、松本浩道 (宇都宮大農)、福井えみ子 (宇都宮大農)

## Investigation of genetic variants related to growth and reproductive traits in Vietnamese native buffalo

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[Background] Water buffaloes play a crucial role in the rural economies of numerous developing nations by supplying draught power, meat, and milk. There has been a rising demand for buffalo meat worldwide, including Vietnam. Nevertheless, buffalo breeding encounters challenges because of their low reproductive efficiency and poor meat production. Therefore, our study aims to discover candidate variants associated with growth and reproductive traits in Vietnamese buffaloes. [Materials and Methods] Genomic DNA was extracted from the hair follicles of Vietnamese buffaloes. Twenty-nine SNPs associated with growth and reproductive traits in cattle and buffalo were genotyped in 24 Vietnamese buffaloes using a Nanopore sequencer. Whole-genome sequencing (WGS) was conducted with the DNA pool of ten buffaloes. The frequency of a variant in *MTNR1A*, identified by WGS, was analyzed in 76 buffaloes by Sanger sequencing. Knock-in mice (KI)

were generated by CRISPR-Cas9 genome editing in the wild-derived mouse strain MSM/Ms. [Results and discussions] In the first study, a favorable allele (g.14939017C>T) in *GH*, known to improve carcass weight, was found in 0.08% of the buffaloes, and six other favorable alleles were fixed in the buffalo population. From the WGS data, 6,990 variants within 25 candidate genes were revealed. Notably, a novel nonsense variant in *MTNR1A* may have a high impact on improved reproduction, being confirmed in 0.03% of buffaloes. To elucidate the impact of this variant, KI mice carrying the *MTNR1A* variant were successfully generated. To date, both male and female KI mice have shown fertility, indicating the utility of this model for this study. Our findings suggest that the variants in *GH* and *MTNR1A* may enhance beneficial traits in Vietnamese buffalo.