

IMPLEMENTATION OF GENOMIC INFORMATION IN SELECTION OF BOARS ON SKATOLE AND ANDROSTENONE CONCENTRATIONS

Lukić, Boris

Source / Izvornik: **Poljoprivreda, 2015, 21, 78 - 80**

Journal article, Published version

Rad u časopisu, Objavljena verzija rada (izdavačev PDF)

<https://doi.org/10.18047/poljo.21.2.14>

Permanent link / Trajna poveznica: <https://um.nsk.hr/um:nbn:hr:151:388662>

Rights / Prava: [In copyright](#) / [Zaštićeno autorskim pravom.](#)

Download date / Datum preuzimanja: **2024-11-06**



Sveučilište Josipa Jurja
Strossmayera u Osijeku

**Fakultet
agrobiotehničkih
znanosti Osijek**

Repository / Repozitorij:

[Repository of the Faculty of Agrobiotechnical
Sciences Osijek - Repository of the Faculty of
Agrobiotechnical Sciences Osijek](#)



Implementation of genomic information in selection of boars on skatole and androstenone concentrations

Primjena genomskih informacija u selekciji nerasta na koncentracije skatola i androstenona

Lukić, B.

Poljoprivreda/Agriculture

ISSN: 1848-8080 (Online)

ISSN: 1330-7142 (Print)

DOI: <http://dx.doi.org/10.18047/poljo.21.2.14>



Poljoprivredni fakultet u Osijeku, Poljoprivredni institut Osijek

Faculty of Agriculture in Osijek, Agricultural Institute Osijek

ISSN 1330-7142

UDK: 636.082.2:636.4

DOI: 10.18047/poljo.21.2.14

IMPLEMENTATION OF GENOMIC INFORMATION IN SELECTION OF BOARS ON SKATOLE AND ANDROSTENONE CONCENTRATIONS

Boris Lukić, M. Eng. Agr. ⁽¹⁾

Doctoral thesis ⁽²⁾

Genomic predictors offer an opportunity to overcome the limitations of classical selection against boar taint, and this study evaluated different approaches to obtain such predictors. Samples from 941 pigs were included in a design which was dominated by 421 sib pairs, each pair having an animal with a high and a low skatole concentration ($\geq 0.3 \mu\text{g/g}$). All samples were measured for skatole and androstenone and genotyped using the Illumina SNP 60K porcine Illumina beadchip. The accuracy of predicting phenotypes was assessed by cross-validation using six different genomic evaluation methods, GBLUP and five Bayesian methods. The range of accuracies obtained by different prediction methods was narrow for androstenone, between 0.29 (Bayes Lasso) and 0.31 (Bayes B), and wide for skatole, between 0.21 (GBLUP) and 0.26 (Bayes SSVS). Relative accuracies corrected for h^2 , were 0.54-0.56 and 0.75-0.94 for androstenone and skatole, respectively. The whole genome evaluation methods gave greater accuracy than using QTL alone (one SNP for androstenone and one SNP for skatole). Also, the dominance genetic variation was ignored in national evaluations, so we estimated the dominance genetic variance for androstenone and skatole using SNP information. For androstenone, GBLUP with dominance effects included captured substantial ratio of the dominance genetic variances (13%) in total variation. For skatole, more dominance genetic variance was captured by regional chromosomal heritability approach, particularly on chromosome 9, where the proportion of chromosomal dominance genetic variance in total dominance variance was 96%. The results demonstrate that GBLUP for androstenone is the simplest genomic technology to implement and one of the most accurate methods while more specialised models may be preferable for skatole. Dominance genetic effects included could provide additional source

(1) Josip Juraj Strossmayer University of Osijek, Faculty of Agriculture in Osijek / Sveučilište Josipa Jurja Strossmayera u Osijeku, Poljoprivredni fakultet u Osijeku, Kralja Petra Svačića 1d, Osijek (blukic@pfos.hr)

(2) Doctoral thesis was defended at Josip Juraj Strossmayer University of Osijek, Faculty of Agriculture in Osijek on 8th May 2015 tutored by Prof. Dr. Goran Kušec / Disertacija je obranjena na Sveučilištu Josipa Jurja Strossmayera, Poljoprivrednom fakultetu u Osijeku 8. svibnja 2015. godine pod mentorstvom prof. dr. sc. Gorana Kušeca

of genetic variation for both traits, therefore, it is worthwhile considering in genomic evaluations.

Key-words: boar taint, skatole, androstenone, genomic selection, GBLUP, Bayes, dominance, regional heritability

Ključne riječi: nerastovsko svojstvo, skatol, androstenon, genomski selekcija, GBLUP, Bayes, dominantnost, regionalni heritabilitet

PRIMJENA GENOMSKIH INFORMACIJA U SELEKCIJI NERASTA NA KONCENTRACIJE SKATOLA I ANDROSTENONA

Disertacija

Genomski markeri, odnosno prediktori, pružaju nove mogućnosti u prevladavanju dosadašnjih ograničenja klasične selekcije protiv nerastovskoga svojstva. Stoga je cilj ovog istraživanja istražiti mogućnosti njihove primjene. U istraživanje je uključen 941 nerast, od kojih je 421 uparenih srodnika po ocu i majci, od kojih svaki nerast s visokom razinom skatola ima brata s niskom razinom skatola u masnome tkivu (≥ 0.3 ug/g). Svim su uzorcima, osim razine skatola, utvrđene i razine androstenona. Životinje su genotipizirane, koristeći Illumina SNP60K porcine beadchip. Analiza unakrsne provjere izvršena je s ciljem uspoređivanja točnosti procjene GBLUP metode i pet Bayes metoda, na osnovi regresije u procjenjivanju nepromatanih fenotipskih svojstava. Raspon ostvarenih točnosti, koristeći različite metode procjena, bio je uzak za androstenon, između 0,29 (Bayes Lasso) i 0,31 (Bayes B), te širi za skatol, između 0,21 (GBLUP) i 0,26 (Bayes SSVS). Relativne točnosti, korigirane s prosječnim h^2 , iznosile su 0,54-0,56 za androstenon i 0,75-0,94 za skatol. S obzirom na to da se učinci dominantnosti u ukupnoj genetskoj varijabilnosti uglavnom nisu promatrali u nacionalnim uzgojnim programima evaluacije, dodatni je pristup korišten za procjenu dominantne genetske varijance za androstenon i skatol. Za androstenon, GBLUP s uključenim dominantnim učincima u modelu, procijenio je značajne omjere dominantnih genetskih varijanci (13%) u ukupnoj varijabilnosti. U slučaju skatola, procijenjena dominantna genetska varijanca bila je viša pristupom regionalnoga heritabiliteta, i to najviše na kromosomu 9, gdje je udio kromosomske regionalne dominantne varijance u ukupnoj dominantnoj varijanci iznosio 96%. Dobiveni rezultati pokazuju da je GBLUP najjednostavnija metoda genomske procjene za androstenon, ujedno je lako provediva te jedna od najtočnijih metoda. U slučaju skatola, potrebno je kreirati prilagođene modele koji mogu postići značajno bolje rezultate. Također, dominantni genetski učinci pružaju dodatne izvore genetske varijabilnosti za oba svojstva i istodobno nude novi i primjenjivi pristup u genomskim procjenama u okviru nacionalnih uzgojnih programa.