



Cattle Molecular Markers and Parentage Testing

Organised by a Standing Committee: YES

Meeting information

Date: 27 July 2021

Time: 9 – 11:55 AM (US Central Standard Time)

Number of participants: ~120

Chair

Name: Jiansheng Qiu

Affiliation: Neogen Genomics

Contact email: jqiu@neogen.com

Agenda

Cattle Molecular Markers and Parentage Testing Workshop (orals)

Chair(s): Jiansheng Qiu, Neogen

Location: Live 1

Date & Time: Tuesday, July 27, 9:00 AM - 12:00 PM

9:00 AM Welcoming remarks.

9:05 AM Cattle STR/SNP Comparison Test 2020-2021.

9:10 AM Presentation by Duty Lab.
Emiliano Lasagna.

9:25 AM Presentation of STR results.

	Emiliano Lasagna.
9:40 AM	Presentation of SNP results. Jiansheng Qiu.
9:55 AM	Evaluation of the results by the chair. Jiansheng Qiu.
10:10 AM	Next Comparison Test (2022-2023).
10:30 AM	Break.
10:40 AM	85477 Impact of Genomic Breed Composition on Production Traits in Crossbred Dairy Cattle. M. Jaafar ^{*1} , B. Heins ² , C. Dechow ³ , and H. Huson ¹ , ¹ <i>Cornell University, Ithaca, NY, USA</i> , ² <i>University of Minnesota, Morris, MN, USA</i> , ³ <i>Penn State University, University Park, PA, USA</i> .
11:00 AM	85435 A high-throughput Applied Biosystems™ Axiom™ Bovine Genotyping array with 100,000 markers optimized for dairy evaluation. A Pirani*, D Oliver, C Bertani, and M Patil, <i>Thermo Fisher Scientific, Inc., Santa Clara, CA, USA</i> .
11:20 AM	85415 Investigating the accuracy of imputing variants on chromosome X in admixed dairy cattle using the ARS-UCD1.2 assembly of the bovine genome. Y. Wang ^{*1,2} , K. Tiplady ^{1,2} , T. J. J. Johnson ² , C. Harland ² , M. Keehan ^{1,2} , T. J. Lopdell ² , R. G. Sherlock ² , A. Wallace ² , B. Harris ² , M. D. Littlejohn ² , R. Spelman ² , D. Garrick ¹ , and C. Couldrey ² , ¹ <i>AL Rae Centre for Genetics and Breeding, School of Agriculture, Massey University, Hamilton, Waikato, New Zealand</i> , ² <i>Research and Development, Livestock Improvement Corporation, Hamilton, Waikato, New Zealand</i> .
11:40 AM	Election of committee.
11:50 AM	Any other business.

Summary of the meeting

General Information from the Duty Lab:

- 22 DNA samples (2 reference and 20 unknowns) were included
- The DNA samples were extracted and purified from whole blood from 11 breeds
- The reference DNA genotypes were confirmed by three labs prior to send the results to all participants
- Samples were distributed in 1.5 ml tubes and delivered by express couriers
- Each micro-tube contained 30 µl with a 50 ng/µl concentration
- 108 labs from 38 countries requested samples, 107 labs received samples, and 92 labs reported results

- Efforts should be planned in order to reduce the gap between the number of applicant labs requesting for samples and the number of labs submitting the results.

STR CT:

Overall performance of 12 STRs was very good with accuracy ranging from 97.3% to 99.8%:

Marker	Count of Genotypes	Genotype errors	Error rate	Marker accuracy (%)
BM1818	1817	4	0.2206	99.78
BM1824	1837	25	1.3797	98.64
BM2113	1834	32	1.7758	98.26
ETH003	1837	23	1.2679	98.75
ETH010	1835	32	1.7748	98.26
ETH225	1837	60	3.3765	96.73
INRA023	1837	23	1.2679	98.75
SPS115	1837	10	0.5473	99.46
TGLA053	1835	26	1.4373	98.58
TGLA122	1837	35	1.9423	98.09
TGLA126	1828	45	2.5238	97.54
TGLA227	1816	49	2.7731	97.30

A few labs had difficulties in detecting allele 115 for ETH3 and allele 121 for TGLA126. A few labs still reported 160 (rather than 158) for ETH225, which was not accepted per discussion at the 2019 workshop. Labs should use the published (<https://strbase.nist.gov//cattleSTRs.htm>) cattle STR alleles for references.

SNP CT:

Different from previous CTs, all 200 SNPs (rather than 100 “core” SNPs) were required for the 2020-2021 SNP CT. However, data from 5 “troubled” SNPs shown below were excluded for the rank calculations due to historical clustering issues (please refer to 2016 and 2017 CMMPT workshop reports for details).

List of 5 “Troubled” SNPs

Accreditation SNP Name (Illumina Bead Chips)	ISAG Group	Reason for Exclusion
ARS-USMARC-Parent-DQ837645-rs29015870	Core	Clustering issues*
ARS-USMARC-Parent-DQ786766-rs29012070	Core	Clustering issues*
ARS-BGFL-NGS-76191	Backup	Clustering issues*
BTA-100621-no-rs	Backup	Clustering issues*
ARS-BFGL-NGS-99210	Backup	Tri-allelic**

42 labs (compared with 37 labs in 2019, a 13% increase) submitted SNP results using multiple genotyping platforms as summarized in the table below. 36 labs (or ~86%) reported great ($\geq 95\%$ concordance) results. 6 labs (or ~14%) were ranked 3 or 4 mainly due to many missing SNPs (Note, all missing data have been treated as incorrect data).

Platform	Number
Illumina Infinium/iScan	28
Thermo Fisher Scientific (Affy/Axiom)	3
Genotype by sequencing (TFS or ILMN)	5
Fluidigm	2
Others/Not-Provided	4

Eight participants submitted comments, 3 of which were related to the confusion of TOP vs Forward call reporting. The CMMPT committee realized the issue (reporting instruction) and worked diligently with FASS, who contacted the labs and allowed them to resubmit results upon verifications. All such issues were resolved before the workshop. A lab commented discrepancy of two SNPs, which were part of the 5 “troubled” ones listed above, between Illumina and Affymetrix fixed arrays. Another lab commented the non-informativeness of ARS-USMARC-Parent-EF034087-no-rs, which was indeed the case regardless of genotyping platforms used. Continued efforts are needed to evaluate existing and new parentage SNPs as well as new genotyping platforms such as GBS (Genotyping By Sequencing).

Answers to the parentage questions were NOT included in to rank calculation. The CMMPT Committee is coordinating with ICAR DNA Working group to come up with parentage guidelines and hopefully post them in ISAG website in near future.

Elections:

Due to more applicants (some of them were nominated just a day before the workshop) than available vacancies for standing committee members, it was decided that an election after the workshop would be the most appropriate. The 1st on-line election was administered by FASS during August 3-6 and the 2nd “runoff” election (due to a tie for the fifth open committee position) was held during August 9-11. The FASS notified the chair the outcome of the election and the chair then organized a conference call to all

new members on August 13 to elect a new chair. It was very encouraging to have so many members who are willing to serve as the CMMPT standing committee members.

New Committee chair

Chair: Jiansheng Qiu (re-elected by the new committee members)
Term of service (<i>add years of first and second term of service</i>): 2 nd term (2021 – 2025)
Affiliation: Neogen Genomics
E-mail address: jqiu@neogen.com

Note: One term runs for two bi-annual conferences (i.e. four years)

New Committee members

Other committee members	First term of service (from year to year)	Email address
Marcela Martinez	2019-2023	mmartinez@sra.org.ar
Laura Nielsen	2019-2023	LauraRaagaardNielsen@eurofins.dk
Emiliano Lasagna	2021-2025	emiliano.lasagna@unipg.it
Rosina Fossati	2021-2025	fossati@genexa.com.uy
Guillermo Giovambattista	2021-2025	ggiovam@fcv.unlp.edu.ar
Yoshiyuki Miyazaki	2021-2025	y-miyazaki@liaj.or.jp
Romy Morrin-O'Donnell	<i>Ex Officio</i>	rmorrin@weatherbys.ie

COMPARISON TEST (2020-2021) YES

Duty laboratory

Contact person: Emiliano Lasagna
Affiliation: University of Perugia, Italy
E-mail address: emiliano.lasagna@unipg.it

Comments (issues rising)

<p>During the workshop, two topics were raised: 1) possibility to allow a lab to submit more than one SNP CT report (due to the use of different genotyping platforms), and 2) the inclusion of SNP genotyping platform on certificate(s). The new CMMPT committee discussed these two issues and unanimously disapproved the proposals. Instead, the committee strongly recommends the future participants to bring potential genotype conflicts of specific SNP between platforms/methodologies to the chair within one month of receiving the CT samples from the duty lab. The chair will then discuss the issue(s) with the committee members and take appropriate actions (eg. to exclude additional SNP data for rank calculations as mentioned in the SNP CT section above).</p>
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List of recommended markers with primer information

For STR, see STRBase in https://www.isag.us/committees.asp

<ul style="list-style-type: none"> For SNP, see: ISAG cattle core + additional SNP panel 2013 in https://www.isag.us/committees.asp

Duty laboratory for the next comparison test with contact details

Contact person: Emiliano Lasagna
Affiliation: Department of Agricultural, Food and Environmental Sciences, University of Perugia, Italy
E-mail address: emiliano.lasagna@unipg.it

SIGNATURES



Chair



Duty laboratory