## Apr 4, 2017

# **AJCA Genomic Evaluation Report**

### **45K GENOTYPE**

Apr 4, 201

FEMALE: SUN VALLEY REGENCY FLIRT JEUSA000119872772 JH1F JH2F

Sire: TJF VISIONARY REGENCY JEUSA000067248196 JH1F JH2F 14JE662

Dam: SUN VALLEY RENEGADE FLIRT JEUSA000118243449

**5** O

Owner: SUN VALLEY FARM 10389 MEDA LOOP RD CLOVERDALE, OR 97112

| 6 | P-level Q |   | Inbreeding Percents |  |  |  |  |
|---|-----------|---|---------------------|--|--|--|--|
| U | P9        |   | Genomic: 6.5%       |  |  |  |  |
|   | BBR       |   | Pedigree: 6.9%      |  |  |  |  |
| 7 | 100       | G | enomic Future: 8 2% |  |  |  |  |

Tattoo: S4142

4 n: 9/3/2016

Jersey Haplotype 1 (JH1) and Jersey Haplotype 2 (JH2) are associated with embryo loss. Official status is listed as F for Free, C for Carrier. Breed Base Representation: CDCB policy is to report BBR values of 94 or greater for one breed as 100. BBRs below 94 are reported as calculated. BBR is reported once, unless animal is re-genotyped with a higher density chip.

Adjustments are applied by CDCB to Traditional Evaluations for yield traits (third column from right) to correct for bias in female genetic evaluations. The Adjusted Evaluations are provided for index and yield traits. The impact of genomic information can be assessed by comparing Genomic Evaluation with the Adjusted Evaluation (column labeled Genomic Impact).

|                    |                   | A          | D IN       | DEX     | U                | <u> </u> | Г           |  |
|--------------------|-------------------|------------|------------|---------|------------------|----------|-------------|--|
| 9                  |                   | Genomic    | Adjusted   | Genomic | Traditional Eval | Genomic  | Traditional |  |
|                    | Trait             | Evaluation | Evaluation | Impact  | 4/2017           | REL %    | REL %       |  |
|                    | JPI               | 124        | 99         | 25      | 101              | 66       | 21          |  |
|                    | Net Merit (\$)    | 405        | 297        | 108     |                  |          |             |  |
|                    | Cheese Merit (\$) | 437        | 330        | 107     |                  |          |             |  |
|                    | Fluid Merit (\$)  | 328        | 219        | 109     |                  |          |             |  |
| Grazing Merit (\$) |                   | 328        |            |         |                  |          |             |  |
|                    | VIELD             |            |            |         |                  |          |             |  |

|   | TILLD        |                       |                        |                   |                            |                  |                      |  |  |
|---|--------------|-----------------------|------------------------|-------------------|----------------------------|------------------|----------------------|--|--|
| 0 | Trait        | Genomic<br>Evaluation | Adjusted<br>Evaluation | Genomic<br>Impact | Traditional Eval<br>4/2017 | Genomic<br>REL % | Traditional<br>REL % |  |  |
|   | IIait        | Lvaluation            | Lvaluation             | Impact            | 4/201/                     | KLL 70           | RLL 70               |  |  |
|   | Milk (lb)    | 500                   | 104                    | 396               | 104                        | 70               | 23                   |  |  |
|   | Fat (lb)     | 50                    | 36                     | 14                | 36                         | 70               | 23                   |  |  |
|   | Fat (%)      | 0.13                  | 0.15                   | -0.02             |                            | 70               | 23                   |  |  |
|   | Protein (lb) | 36                    | 22                     | 14                | 23                         | 71               | 24                   |  |  |
|   | Protein (%)  | 0.09                  | 0.09                   | 0.00              |                            | 71               | 24                   |  |  |

Note: Genomic and Traditional Evaluations for Health, Fitness and Type traits are expressed on similar scales. No adjustments have been applied. A comparison of the Genomic Evaluation with the April 2017 Traditional Eval indicates the Genomic Impact.

| A HEALTH : FITNESS          |            |                  |         |         |             |  |  |
|-----------------------------|------------|------------------|---------|---------|-------------|--|--|
|                             | Genomic    | Traditional Eval | Genomic | Genomic | Traditional |  |  |
| Trait                       | Evaluation | 4/2017           | Impact  | REL %   | REL %       |  |  |
| Daughter pregnancy rate (%) | -1.7       | 0.1              | -1.8    | 57      | 18          |  |  |
| Cow conception rate (%)     | 0.1        |                  |         | 55      |             |  |  |
| Heifer conception rate (%)  | 2.5        |                  |         | 41      |             |  |  |
| Productive life (mo)        | 3.8        | 2.5              | 1.3     | 61      | 18          |  |  |
| Somatic cell score          | 3.02       | 2.93             | -0.09   | 68      | 20          |  |  |
| TVDF                        |            |                  |         |         |             |  |  |

| ТҮРЕ                  |                       |                            |                   |                  |                      |  |  |
|-----------------------|-----------------------|----------------------------|-------------------|------------------|----------------------|--|--|
| Trait                 | Genomic<br>Evaluation | Traditional Eval<br>4/2017 | Genomic<br>Impact | Genomic<br>REL % | Traditional<br>REL % |  |  |
| Final score (PTAT)    | 1.00                  | 0.50                       | 0.50              | 72               | 22                   |  |  |
| Stature               | 0.20                  | -0.50                      | 0.70              |                  |                      |  |  |
| Strength              | -0.10                 | -0.30                      | 0.20              |                  |                      |  |  |
| Dairy form            | 0.50                  | -0.10                      | 0.60              |                  |                      |  |  |
| Rump angle            | -0.10                 | -0.30                      | 0.20              |                  |                      |  |  |
| Rump width            | 0.10                  | -0.10                      | 0.20              |                  |                      |  |  |
| Rear legs (side view) | -0.20                 | -0.30                      | 0.10              |                  |                      |  |  |
| Foot angle            | 0.60                  | 0.50                       | 0.10              |                  |                      |  |  |
| Fore udder attachment | 1.30                  | 1.40                       | -0.10             |                  |                      |  |  |
| Rear udder height     | 1.70                  | 0.90                       | 0.80              |                  |                      |  |  |
| Rear udder width      | 0.40                  | 0.83                       | -0.43             |                  |                      |  |  |
| Udder cleft           | 0.20                  | -0.20                      | 0.40              |                  |                      |  |  |
| Udder depth           | 1.00                  | 1.40                       | -0.40             | 75               | 25                   |  |  |
| Front teat placement  | -0.30                 | 0.20                       | -0.50             |                  |                      |  |  |
| Teat length           | 0.30                  | -0.50                      | 0.80              |                  |                      |  |  |
| Jersey Udder Index    | 12.55                 | 13.00                      | -0.45             |                  |                      |  |  |

## How to Read the AJCA Genomic Evaluation Report

- 1. Issue Date. Date this genomic evaluation was issued.
- **2. Genotype Chip Version.** Source of genomic information will be identified by density of chip.
- 3. Identification. This block includes sex of the animal, AJCA registration name and registration number, date of birth and permanent identification of the animal, labeled by form (either tattoo or AJCA-approved eartag). Listed in separate lines below are (1) name of sire, registration number, status for JH1 and JH2 and NAAB number (if applicable); and (2) name of dam, registration number and JH1 and JH2 status.
- **4. JH1 and JH2 Status.** Jersey Haplotype 1 (JH1) and Jersey Haplotype 2 (JH2) impact fertility and are associated with decreased conception rate. Official designation of status is based on 6K or higher density genotype. F designates status Free, C designates status Carrier.
- **5. Owner.** Name and mailing address of the Recorded Owner, as indicated on the records of the AJCA.
- **6. P-Level.** The P-level is a percentile ranking of the JPI displayed as P0 through P9. To interpret, insert the P-level in the blank in this sentence: "This heifer/bull has a higher JPI than \_0 percent of the registered Jersey heifers (bulls) born in the same year."
- 7. Breed Base Representation. Measure of similarity to the Jersey breed reference group. CDCB reports BBR values of 94 or greater for one breed as 100. BBRs below 94 are reported as calculated. Value determined and reported once, unless regenotyped with a higher density chip.
- **8. Inbreeding Percents.** Three distinctly different estimates of inbreeding are provided.
  - Genomic Inbreeding: A direct measure of homozygosity (or genes in common) based on the observed DNA. Values may be positive indicating degree of inbreeding, or negative indicating heterosis. The zero point is the average relationship to the Jersey population as it existed in 1960.
  - Pedigree Inbreeding: An estimate of the percent of genes in common based on pedigree information. This estimate remains static across time unless the pedigree is modified. Genomic Future: Estimate of inbreeding of future offspring, based on the percentage of SNPs in common with the genotyped Jersey population. This may change over time as the basis for comparison, the genotyped population, changes.
- for combined genetic merit for production, type and fitness traits based on different sets and weighting of traits.

  Jersey Performance Index™ (2017 update) is a breed-specific index that includes PTA protein, 30%; PTA fat, 15%; CFP Milk, 8%; Functional Trait Index (incorporating Jersey Udder Index™, Body Weight Composite, and mobility), 20%; Productive Life, 6%; Livability, 4%; Somatic Cell Score, 6%; Daughter Pregnancy Rate, 7%; and Cow Conception Rate and Heifer Conception Rate, 2% each.
  - USDA Net Merit, Cheese Merit, Fluid Merit and Grazing Merit indexes estimate expected lifetime profit for these economic scenarios compared to breed base cows born in 2010. These traits are described in AIP Research Report NM\$6 (2-17) at http://aipl.arsusda.gov/reference/nmcalc-2017.htm.
- **10. Yield.** This section lists the animal's Predicted Transmitting Ability (PTA) for pounds milk, pounds fat and fat percentage, and pounds protein and protein percentage.

- 11. Health and Fitness. Includes evaluations for: Daughter Pregnancy Rate, a genetic evaluation of fertility, with 1% DPR equal to four (4) fewer days open. Cow Conception Rate, lactating cow's ability to conceive defined as percentage of inseminated cows that become pregnant at each service. A CCR of 1 implies that daughters of this animal are 1% more likely to become pregnant during that lactation than daughters of an animal with an evaluation of 0. Heifer Conception Rate, maiden heifer's ability to conceive defined as percentage of inseminated heifers that become pregnant at each service. An HCR of 1 implies that daughters of this animal are 1% more likely to become pregnant as a heifer than daughters of an animal with an evaluation of 0. Productive Life, a multi-trait genetic evaluation of longevity in the herd before removal by voluntary culling, involuntary culling, or death.
  - *Somatic Cell Score,* an indicator trait for mastitis resistance based on direct measure of somatic cells in milk samples.
- 12. Type. Includes genetic evaluations for PTA Final Score (PTAT), 14 linear type traits, and Jersey Udder Index™ (JUI). The trait Rear Udder Width is not genomically evaluated. It is a calculated value based on the genetic relationship of Rear Udder Width with the genomic evaluation of Rear Udder Height.

Jersey Udder Index<sup>™</sup> is the contribution of udder traits expressed as total points to Jersey Performance Index<sup>™</sup>.  $JUI = [(2.4 \times FU) + (1.8 \times RUH) + (0.1 \times RUW) + (4.7 \times UD) + (1.9 \times UC) + (0.9 \times TP) + (-0.9 \times TL)]$ 

#### **Information Presented in Columns**

- A. Genomic Evaluation. Prediction of what will be transmitted to the next generation based on pedigree, performance and genomic information from the genotype (SNPs observed in the DNA). For Index and Yield traits, genomic information is combined with the Adjusted Evaluation (*B*, see below) to produce the Genomic Evaluation (*A*). For Health and Fitness and Type traits, genomic information is combined with the Traditional Evaluation (*D*, see below) to produce the Genomic Evaluation.
- **B.** Adjusted Evaluation. Adjustments are applied by USDA-CDCB to Traditional Evaluations for yield traits (*E, see below*) to correct for bias in female genetic evaluations. The result is the Adjusted Evaluation.
- **C. Genomic Impact.** For Index and Yield traits, Genomic Impact is a comparison of Genomic (A) and Adjusted (B) evaluations. For Health and Fitness and Type traits, the Genomic Impact is a comparison of Genomic (A) and Traditional (E) evaluations.
- **D.** Traditional Eval (evaluation date). This is the Traditional Genetic Evaluation based only on pedigree and performance information. Date of evaluation release is included.
- E. Genomic REL%. Genomic Reliability is a measure of accuracy associated with the Genomic Evaluation (column A). A comparison with the Traditional REL% (F, below) provides an assessment of the relative increase in accuracy of the prediction by adding genomic information to the evaluations.
- F. Traditional REL%. Traditional Reliability is a measure of accuracy associated with the Traditional genetic evaluation

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