



IRISH CATTLE BREEDING FEDERATION

Breeding for Tuberculosis and Liver Fluke Resistance



Siobhán Ring

ICBF & Sheep Ireland
Genetics Conference 2018

Wednesday & Thursday
5th & 6th December
Hodson Bay Hotel,
Athlone

Sheep Ireland
www.sheep.ie

ICBF.com

"Sustainable Farming –
Progress through Genetics"



Department of
**Agriculture,
Food and the Marine**
An Roinn
**Talmhaíochta,
Bia agus Mara**



#ISGC18

Industry Concerns Prompt Research



"...My Beef HealthCheck report says 2 out of the cattle I slaughtered had livers damaged by fluke ... are they a bad breed?"

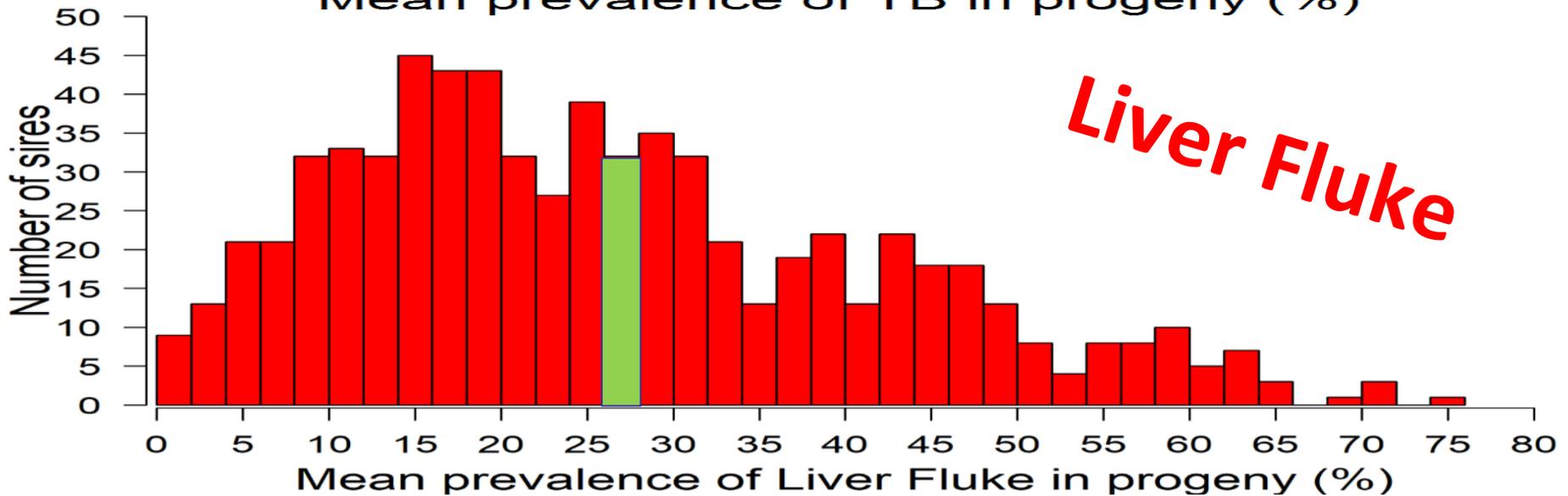
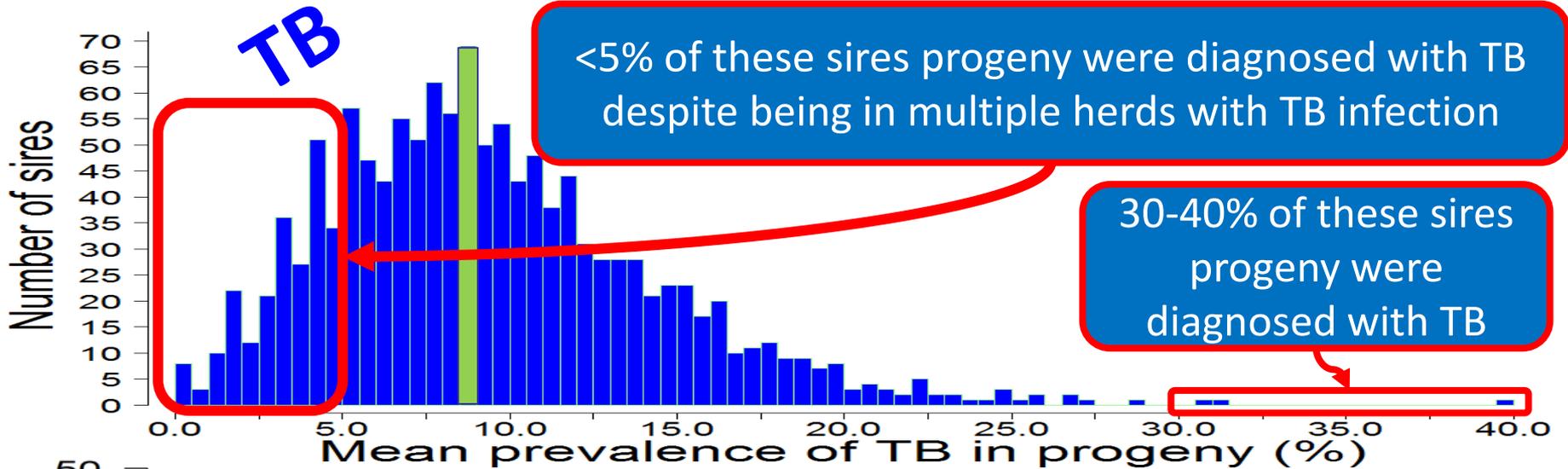
"...why is it only a few cattle in herds get TB? ... are some cattle more attracted to wildlife carrying M.bovis?"



Maybe genetics is responsible for some of the on-farm variability in resistance to TB & fluke??



Observing Genetic Variation



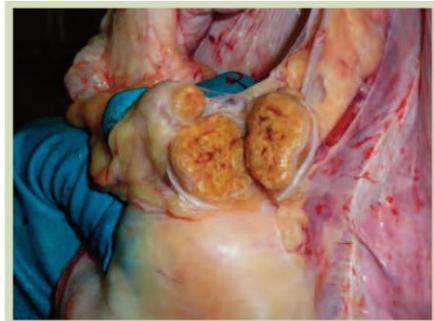
Sourcing Data



TB



Liver Fluke



*SICTT, lesion, & confirmed lab TB
(~1m records since 2000)*



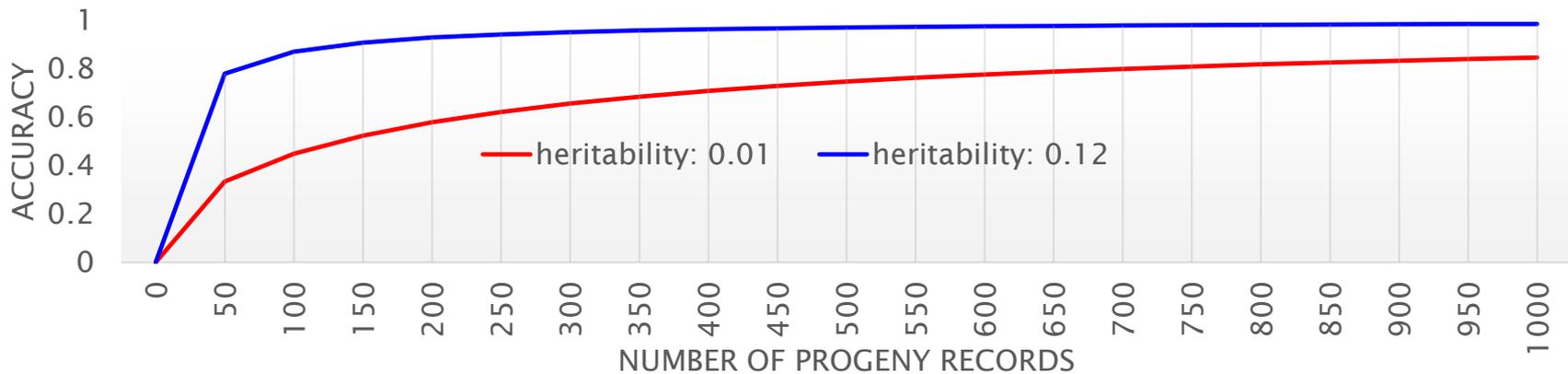
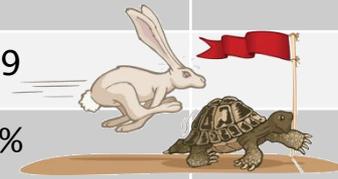
*Damage & live fluke
(~300k records since 2012)*

Quantifying Genetic Variation



Maybe genetics is responsible for some of the on-farm variability in resistance to TB & fluke!

	TB	Liver Fluke
Heritability	12%	1%
Genetic SD	0.09	0.04
Potential prevalence reduction per year	1.9%	0.09%



Validating Predicted Performance

Herds A, B, C: Health & Pedigree known

Herds D, E, F: Only pedigree known

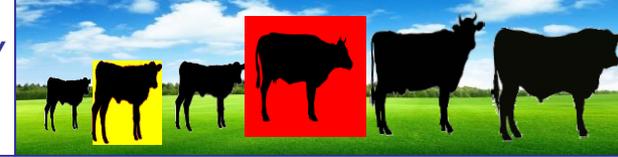
How well can breeding value predict performance when only pedigree known?

2.5% unit (TB) and 6% (Fluke) unit higher prevalence in worst EBV group compared to the best EBV group

Herd D



Herd E



Herd F



1541284360	3	0	-0.12682E-01
1541377739	5	0	-0.12682E-01
108377794	6	0	0.69870E-02
70371223	4	0	-0.78839E-02
70371292	2	0	0.22666E-01
70371352	2	0	-0.19077E-01
70371559	1	0	-0.15002E-01
70372039	1	0	-0.16737E-01
72867024	1	0	-0.89423E-02
72867084	0	1	0.80600E-01
72867165	0	1	-0.11736E-01
72867171	0	1	0.27391E-01
72867189	1	0	-0.15190E-01
72867279	1	0	0.33715E-02
72867345	0	1	-0.14097E-01
72867432	1	0	0.14733E-01
74996948	1	0	0.80968E-02
75527908	1	0	-0.18284E-01
75649645	1	0	-0.33901E-01
75649648	2	0	-0.34840E-01
76766574	1	0	-0.13491E-01

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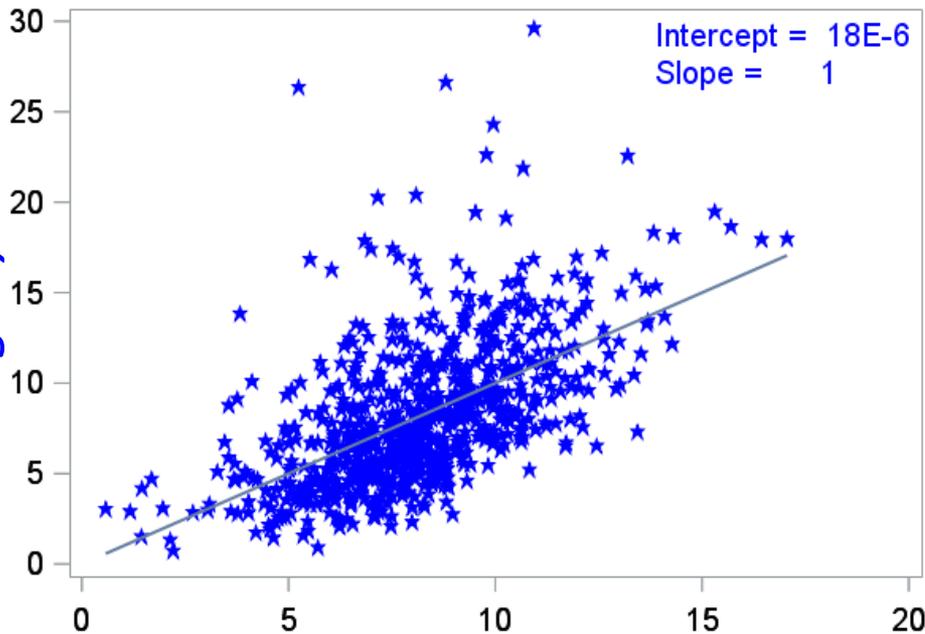
EBV calculated for all animals

Presentation of Breeding Values

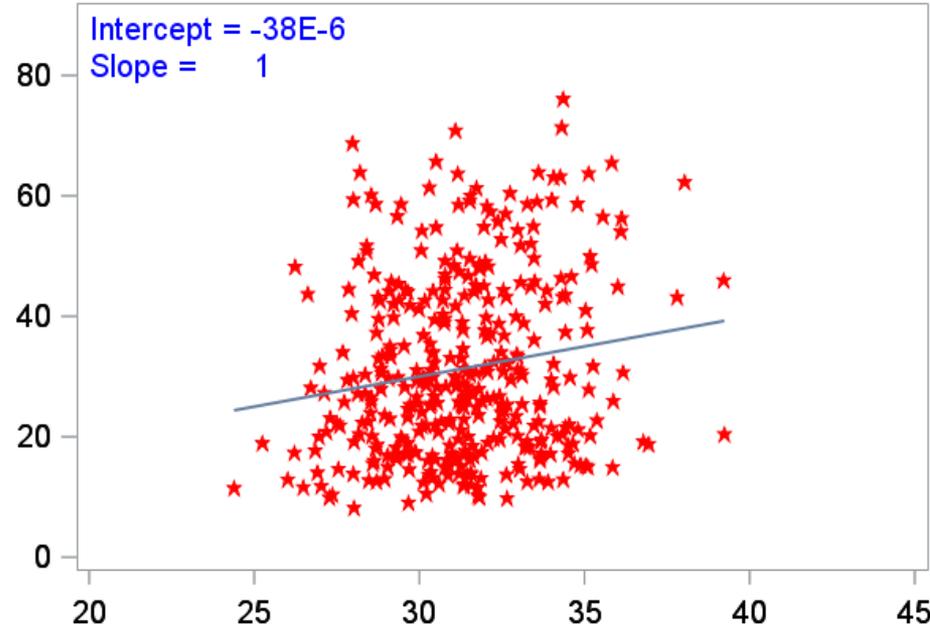
(predicted % prevalence among animal's progeny)

Observed Progeny Prevalence (%)

TB



Fluke

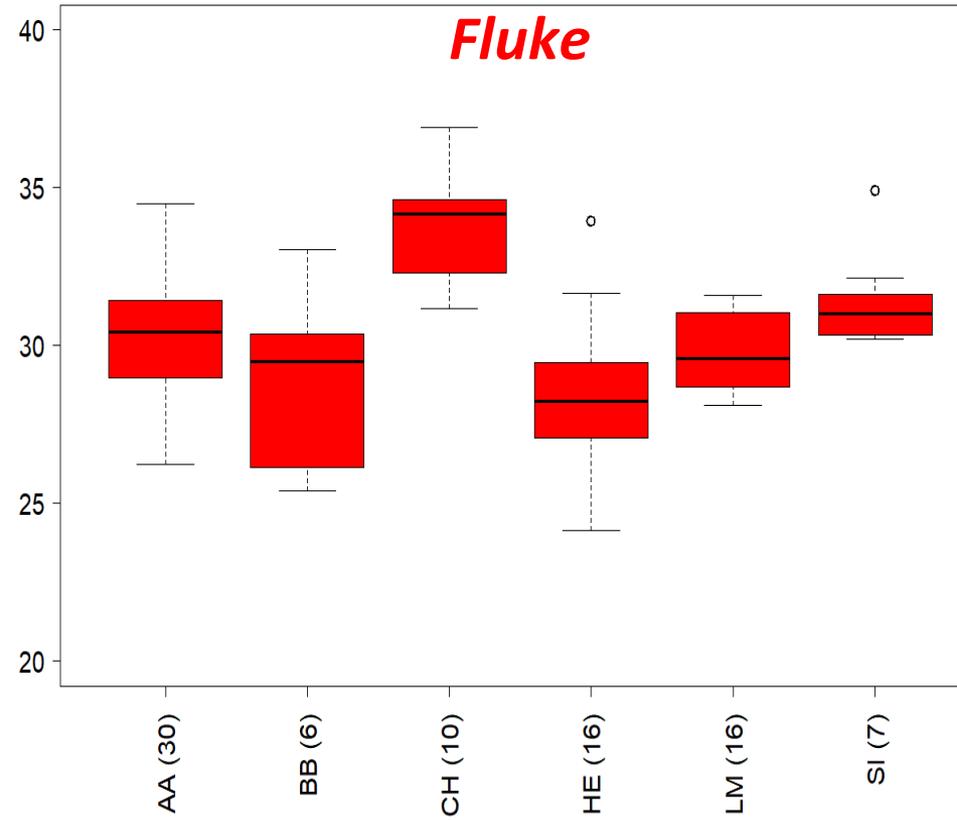
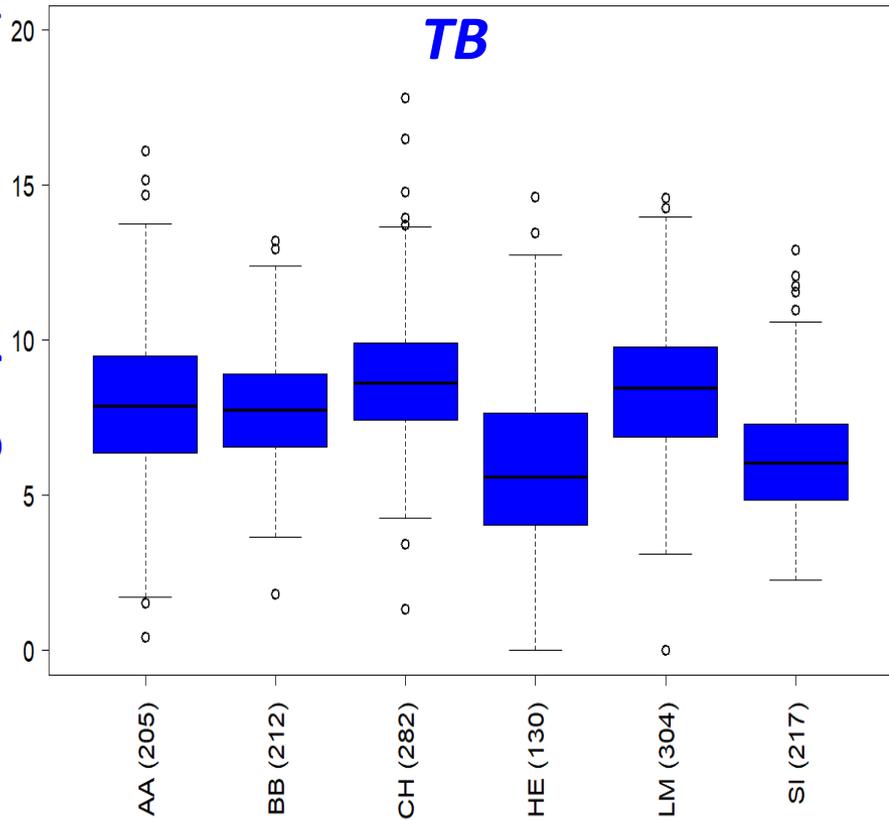


Predicted Progeny Prevalence (%)

Breed Differences

(AI sires born ≥ 2000 , reliability $\geq 40\%$)

Predicted Progeny Prevalence (%)



Considerations for Using Breeding Values

- Screen-out worst males & females

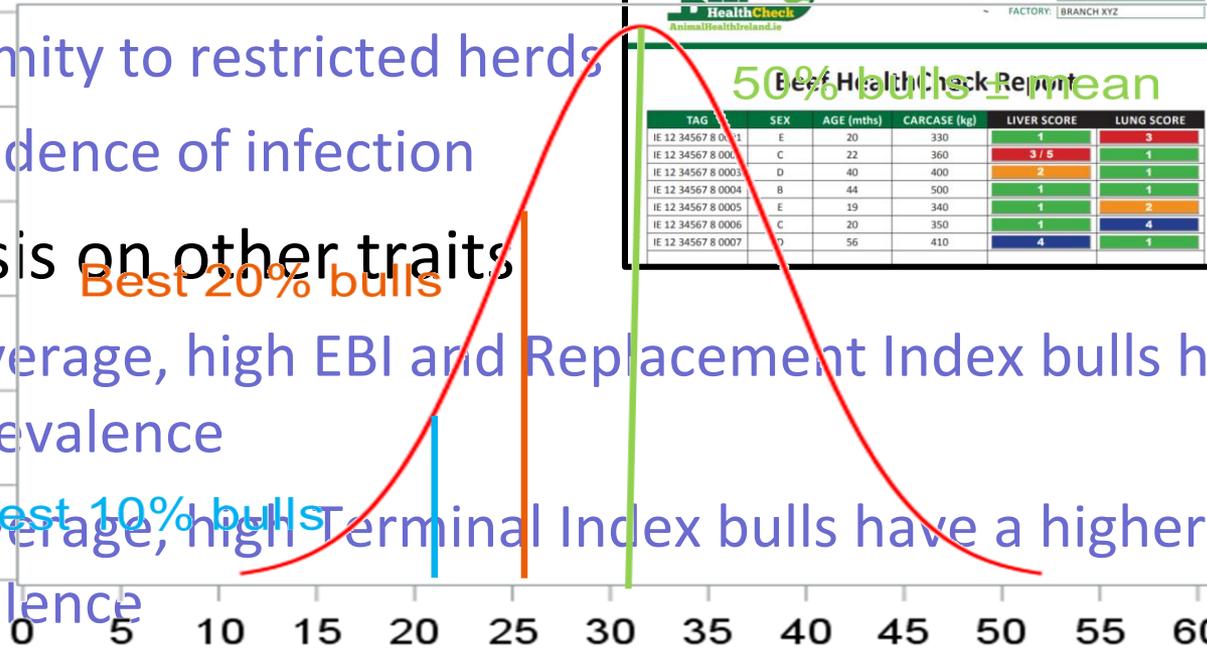
- Cut-off for 'worst' may vary

- Risk of infection

- Proximity to restricted herds
 - Precedence of infection

- Emphasis on other traits

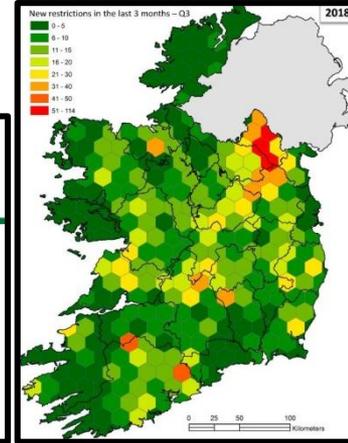
- On average, high EBI and Replacement Index bulls have a lower TB prevalence
 - On average, high Terminal Index bulls have a higher TB prevalence



DEEP HealthCheck Report

SUPPLIER: A. FARMER
 HERD NO: A123456
 DATE OF SLAUGHTER: 01/01/2016
 FACTORY: BRANCH XYZ

TAG	SEX	AGE (mths)	CARCASE (kg)	LIVER SCORE	LUNG SCORE
IE 12 34567 8 0001	E	20	330	1	3
IE 12 34567 8 0002	C	22	360	3 / 5	1
IE 12 34567 8 0003	D	40	400	2	1
IE 12 34567 8 0004	B	44	500	1	1
IE 12 34567 8 0005	E	19	340	1	2
IE 12 34567 8 0006	C	20	350	1	4
IE 12 34567 8 0007	D	56	410	4	1



Change per +€10 Index	TB (%)	Fluke (%)
EBI	-0.026	-0.022
Replacement	-0.031	-0.012
Terminal	+0.029	+0.006

Publications

Under-review



RESEARCH ARTICLE

Open Access

GWAS for endo-parasite phenotypes using imputed whole-genome sequence data in dairy and beef cattle

Journal of ANIMAL SCIENCE

Genetic parameters for both a liver damage phenotype caused by *Fasciola hepatica* and antibody response to *Fasciola hepatica* phenotype in dairy and beef cattle

A. J. Twomey, R. G. Sayers, R. I. Carroll, N. Byrne, E. O' Brien, M. L. Doherty, J. C. McClure, D. A. Graham, D. P. Berry ✉

Journal of ANIMAL SCIENCE

Genetic correlations between endo-parasite phenotypes and economically important traits in dairy and beef cattle

Alan J Twomey, Rebecca I Carroll, Michael L Doherty, Noel Byrne, David A Graham, Riona G Sayers, Astrid Blom, Donagh P Berry ✉

Journal of ANIMAL SCIENCE

Little genetic variability in resilience among cattle exists for a range of performance traits across herds in Ireland differing in *Fasciola hepatica* prevalence

Alan J Twomey, David A Graham, Michael L Doherty, Astrid Blom, Donagh P Berry ✉

Published by the
American Society of Animal Science
Since 1910



J. Dairy Sci. 93:5413–5422
doi:10.3168/jds.2009-2925

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Genetic correlations between measures of *Mycobacterium bovis* infection and economically important traits in Irish Holstein-Friesian dairy cows

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†Centre for Veterinary Epidemiology and Risk Analysis, School of Agriculture, Food Science and Veterinary Medicine, University College Dublin,

Richardson et al. *Genetics Selection Evolution* 2014, **46**:77
http://www.gsejournal.org/content/46/1/77



RESEARCH

Open Access

Variance components for susceptibility to *Mycobacterium bovis* infection in dairy and beef cattle

Richardson et al. *Genet Sel Evol* (2016) 48:19
DOI 10.1186/s12711-016-0197-x



RESEARCH ARTICLE

Open Access



A genome-wide association study for genetic susceptibility to *Mycobacterium bovis* infection in dairy cattle identifies a susceptibility QTL on chromosome 23

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Je



Under-review

Analysis of Imputed Whole Genome Sequence Data in Multiple Breeds Reveal Novel Single-Nucleotide Polymorphisms on BTA 15 and BTA 23 Associated with Bovine Tuberculosis Infection

S.C. Ring, D. C. Purfield, M. Good, P. Breslin, E. Ryan, A. Blom, R. D. Evans, M. L. Doherty, D. G. Bradley, D. P. Berry

Take Home Message

- Considerable exploitable genetic variation
 - As much variation within breed as across breed
- Planned TB & Fluke EBV roll-out
 - Test proofs for AI sires Jan'19
 - Stand-alone traits
- Likely varying herd emphasis
 - Risk of infection
 - Emphasis on other traits (complimentary to EBI & Repl. Index)





Our Farmer & Government Representation



Our AI & Milk Recording Organisations



Our Herdbooks



Acknowledging Our Members