Optimum polygenic effect in genomic evaluation

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Background

Are the SNPs on the middle density chips (50K) capable of capturing the genetic variance (LD/LE) in its entirety?

Preliminary results from 2010 comparing 1%, 10%, 20% for PRO → 10%

Aims

What is the optimum polygenic effect?

What is the optimum ”discounting factor”?

Phenotype

Full data

Mace result: April 2013

Reduced data

Data cut-off: Apr-December 2009

National EBV: 152 country-trait combination

Truncated MACE

Genomic evaluation

11 polygenic levels

SNP	99	90	80	70	60	50	40	30	20	10	1
Polygenic	1	10	20	30	40	50	60	70	80	90	99

Validation

GEBV-test

For all country-trait-polygenic level combinations

Standard setting: EDCr = 0, EDC=20, 2003-2006

Non-standard settings:

EDC = 25, 50

Sliding time window

Some numbers

33 MACE runs (full data, 175 country-traits)

33 Truncated MACE runs (reduced data, 152 country-traits)

3344 GBLUP runs (152 x 11 x 2)

26687 validation tests

Size of the reference population

TRAIT	REDUCED	FULL
ang	1761	2340
hco	1919	2853
mce	2758	3735
int	2043	3927
scs	4056	5551
fat	4265	5638
mil	4265	5638
pro	4265	5638

Selection criteria

Polygenic level

(Pass)

High R^2

$b_1 \approx 1.0$

$b_0 \approx 0.0$

(Pass)

Selection criteria

Discounting factor

Gain in REL (Model I R^2 – Model II R^2)

Gain in REL (GBLUP REL – MACE REL)

Gain in REL (GBLUP REL full data – GBLUP REL reduced data)

Optimum polygenic level

		Optimum level of SNP variance								
		R2		B1		B0		Pass GEBV test		
TRT	COU									
1	1	40	90	1	1	30	30	-	-	
1	2	99	99	1	1	10	10	1	99	B1 >>>1
1	3	20	70	99	99	1	1	1	99	B1 >> 1

Discounting factor

Reliability			DIFF
Gain			REL FULL
VAL	GBLUP		REL REDU
13	24		3
8	18		3
4	22		3

Conclusion

Trait group	SNP variance	Discount factor
Calv	60	70
conf	70	75-85
fert	60	70
long	60	70
prod	80	80
uder	60	75
work	70	80

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