Careful modelling highly affects QTL detection in a broiler commercial line

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Cobb | ONE FAMILY. ONE PURPOSE.

Project

Could we improve genetic estimation accuracy considering the genetic architecture of traits?

Identification of QTL to apply genomic feature model and WGBLUP

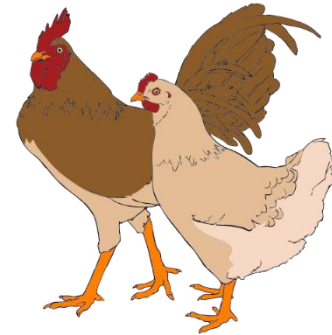Genotypes and Phenotypes from a commercial line

2 Environments :

Bio-secure	Commercial

- On-going selection
- Selective genotyping
- Body weight at 41 days or 35 days

- All population is genotyped
- Weekly from week 1 to week 5

Effects

- Generation of individuals (G)
- Generation of dams (SG)
- Hatch of individuals (H)
- Hatch of dams (DH)
- Dam age (DAGE)
- Individual additive genetic effect (a)
- Maternal additive genetic effect (m)
- Maternal permanent environmental effect (pem)
- Sexes
- Ages

Each of these effects were tested such as all the interactions

For each traits the model giving the less bias and more accurate breeding value was determined

Model

A trait = 1 age of measurement and one sexe

Where $V(a) = A.\sigma_a^2$ and $V(m) = A.\sigma_m^2$

Bio-secure : 1 model

$y = \mu + SGGDH + DAGE + a + pem + e$

Commercial : 2 models

$y = \mu + GH + SGDH + DAGE + a + pem + m + e$

Week 1 to Week 3

$y = \mu + GH + SG + DAGE + a + pem + e$

Week 4 to Week 5

Model - GWAS

A trait = 1 age of measurement and one sexe

Bio-secure : 1 model

Where $V(a) = A.\sigma_a^2$ and $V(m) = A.\sigma_m^2$

$$y = \mu + SGGDH + DAGE + b.snp + a + pem + e$$

14 QTL identified among the population spread on 10 chromosomes

Commercial : 2 models

$$y = \mu + GH + SGDH + DAGE + b.snp + a + pem + m + e$$ Week 1 to Week 3

$$y = \mu + GH + SG + DAGE + b.snp + a + pem + e$$

Week 4 to Week 5

34 QTL identified among the population spread on 14 chromosomes

GWAS – Bio-secure

Group	Chr	Lbp	Rbp	Trait
1	1	46067552	46544521	BS41m
2	1	137228683	139289663	BS41m,BS41f
3	2	20966346	20966346	BS35f
4	3	59272512	61357569	BS41f
5	5	30554456	30901355	BS41m
6	6	4503981	4503981	BS41m
7	6	17486982	18966702	BS41m
8	7	3684647	3684647	BS35m
9	7	16995973	16995973	BS41f
10	7	20952457	21016986	BS41f
11	9	11214014	13103886	BS41f
12	13	6768675	7605519	BS41f
13	20	12960493	13279648	BS41m
14	27	3625011	3853042	BS41f

Only one QTL identical for two traits.
No QTL common to BS41 and BS35.
4 QTL have been already reported in the QTLdb for BW

QTL	Chr	Lbp	Rbp	Trait
1	1	42409520	44780169	CBW5m,CBW4f
2	1	88265123	88265123	CBW4f,CBW5f
3	1	125898906	125898906	CBW1f
4	1	154586289	154586289	CBW3f
5	2	63056973	63056973	CBW5m
6	2	90619921	90619921	CBW3m
7	2	98781961	102789571	CBW5m,CBW4f,CBW5f
8	2	116084901	116777472	CBW1m,CBW2m,CBW3m,CBW4m,CBW5m
9	3	15911257	15911257	CBW4f
10	3	75971111	76203776	CBW3f,CBW5f
11	3	78745441	79953182	CBW3m,CBW4m,CBW5m,CBW5f
12	4	28765793	29513476	CBW1m
13	4	33753562	36283256	CBW1m,CBW2f,CBW4f,CBW5f
14	4	40586245	40586245	CBW5f
15	4	49039885	49044189	CBW4f,CBW5f
16	4	61611774	61611774	CBW5f
17	4	66284039	66987453	CBW1m,CBW2m,CBW3m,CBW1f,CBW2f,CBW3f,CBW4f

| QTL	Chr	Lbp	Rbp	Trait
18	5	23762044	23775734	CBW4m,CBW5m
19	6	10097366	11347856	CBW2m
20	6	15348991	23417558	CBW1m,CBW2m,CBW3m,CBW4m,CBW5m,CBW6m,CBW1f,CBW2f,CBW3f
21	6	26252710	26252710	CBW4f
22	6	29747642	29747642	CBW4f
23	7	21504977	21504977	CBW4f
24	7	30140661	30140661	CBW3m
25	8	20282701	20282701	CBW1f
26	9	4827224	12207043	CBW4m,CBW5m
27	10	3053466	3127139	CBW2f
28	10	4828216	5449237	CBW1f,CBW2f,CBW3f
29	11	8298366	8298366	CBW3m
30	23	4194942	4194942	CBW5f
31	23	5007642	5772929	CBW5f
32	24	119925	2707652	CBW1m,CBW2m,CBW3m,CBW4m,CBW1f,CBW2f,CBW3f,CBW4f,CBW5f
33	24	3595848	3595848	CBW2m,CBW3m
34	26	2297688	2297688	CBW4f

QTL in common between traits were found

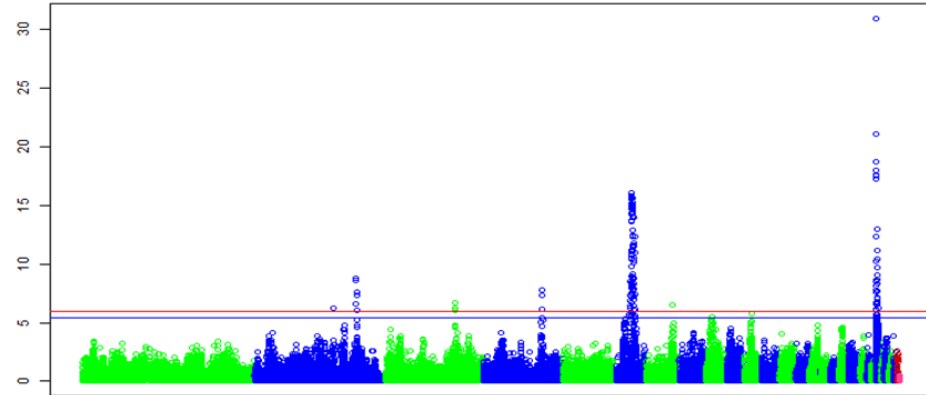Some seems to be sex specific (ex QTL8)

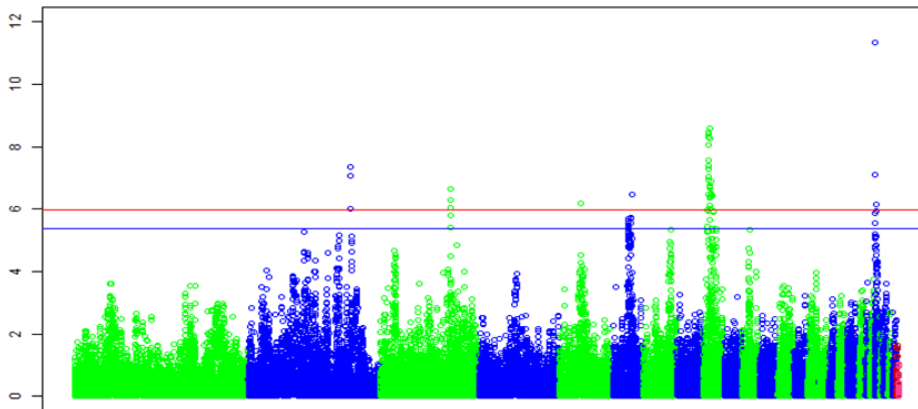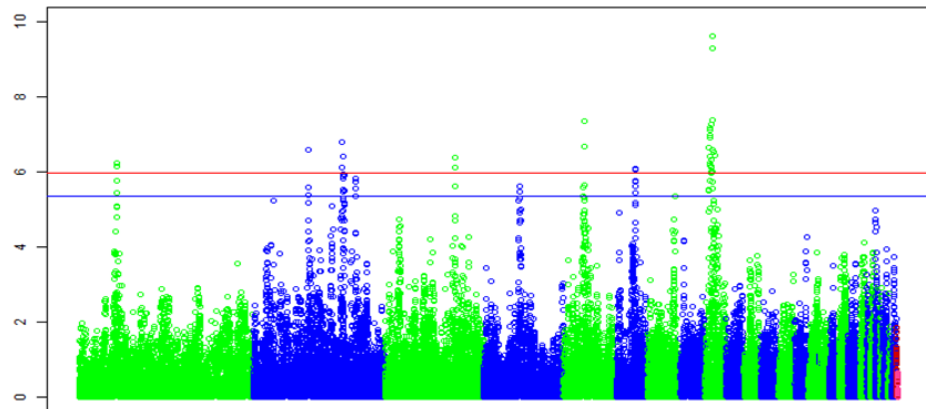Some seems to be age specific (ex QTL7)

GWAS – Commercial
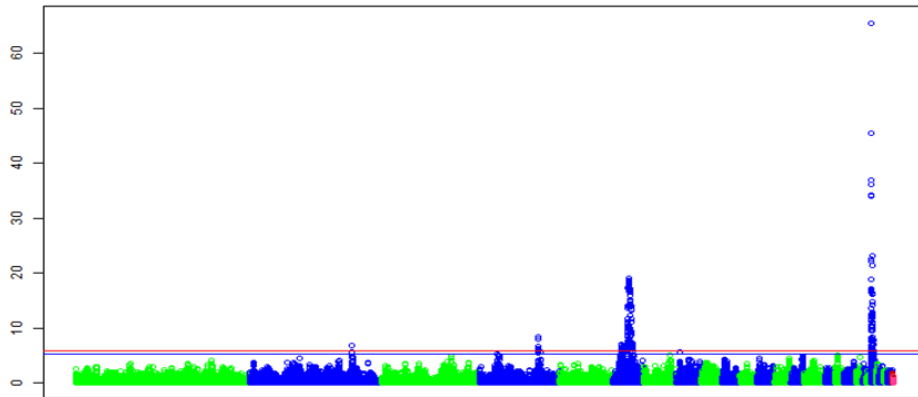
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Week 1 to Week 3

$$y = \mu + GH + SG + DAGE + b.snp + a + pem + e$$

Week 4 to Week 5

Maternal effect

So, we have QTL….

….but what if we change a bit the model

▶ The maternal effect : m

- Add to the model for week4 and week5

    No change => m was not significant in the model

- Remove from the model for week1 to week3

    W3   No change => m was barely significant

    W2   No change => m was significant

    W1   Some change => m was significant

    Variance explained by pem increased

Fixed effects

So, we have QTL….

….but what if we change a bit the model

► The maternal effect: No impact on W4-W5, small impact on W1

► The pem + m: Impact is bigger (Ex CBW1f : -3 QTL)

Fixed effects

So, we have QTL….

….but what if we change a bit the model

► The maternal effect: No impact on W4-W5, small impact on W1

► The pem + m: Impact is bigger (Ex CBW1f : -3 QTL)

► Fixed effects:

$GH + SGDH + DAGE$ => $G + H + SG + DH + DAGE$

$-SGDH - GH$

- No change in term of QTL

- SNP effect is different

Conclusions

▶ Differences observed between W4/5 and W2/3 were probably due to the genetic architecture of traits

▶ Except the random effects, effects included in the model did not have a huge effect on QTL detection

▶ But it has an impact on QTL effect

    ↳ Could influence WGBLUP?

▶ Combining sexes or ages was having more influence on QTL detection

▶ But what is the "true" QTL

    ↳ Look at the variance explained by QTL vs variance explained by remaining SNP
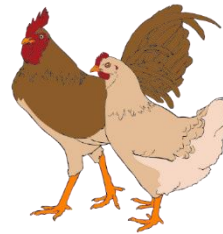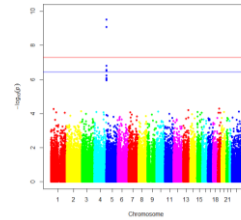
Acknowledgments

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Poultry team

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