

Report: Hybrid vigor in response to Eimeria in the HMHZ

Alice

26 June 2018

Contents

To be fixed before all	1
General informations on HMHZ	2
Comparison of prevalences based on detection method	3
Improving Eimeria oocysts detection	4
Comparison oocysts flotation, PCR, qPCR	5
Testing hybrid vigor along HMHZ	6
Oocyst shedding proxy	6
qPCR proxy	7
BCI proxy	7
Bonus part: genotyping of mice case/control	7

To be fixed before all

- Some information regarding latitude and longitude are missing for the following mice:

AA_0212, AA_0213, AA_0214, AA_0215, AA_0216, AA_0217, AA_0218, AA_0219, AA_0220, AA_0221,
AA_0222, AA_0223, AA_0224, AA_0225, AA_0226, AA_0227, AA_0228, AA_0229, AA_0230, AA_0231,
AA_0232, AA_0233, AA_0234, AA_0235, AA_0236, SK_3174

- We still miss info (HI) on the following mice (ask Jarda):

AA_0161, AA_0162, AA_0163, AA_0164, AA_0165, AA_0166, AA_0167, AA_0168, AA_0169, AA_0170,
AA_0171, AA_0172, AA_0174, AA_0175, AA_0176, AA_0190, AA_0212, AA_0213, AA_0214, AA_0215,
AA_0216, AA_0217, AA_0218, AA_0219, AA_0220, AA_0221, AA_0222, AA_0223, AA_0224, AA_0225,
AA_0226, AA_0227, AA_0228, AA_0229, AA_0230, AA_0231, AA_0232, AA_0233, AA_0234, AA_0235,
AA_0236, AA_0411, AA_0412, AA_0420, AA_0464, AA_0472, AA_0473, AA_0474, AA_0475, AA_0476,
AA_0477, AA_0478, AA_0479, AA_0480, AA_0481, AA_0482, AA_0483, AA_0484, AA_0485, AA_0486,
AA_0487, AA_0488, AA_0489, AA_0490, AA_0491, AA_0492, AA_0493, AA_0494, AA_0495, AA_0496,
AA_0497, AA_0498, AA_0499, AA_0500, AA_0501, AA_0502, AA_0503, AA_0504, AA_0505, AA_0506,
AA_0507, AA_0508, AA_0511, AA_0512, AA_0513, AA_0514, AA_0515, AA_0516, AA_0517, AA_0518,
AA_0519, AA_0520, AA_0521, AA_0522, AA_0523, SK_2668, SK_2669, SK_2671, SK_2674, SK_2675,
SK_2676, SK_2677, SK_2678, SK_2681, SK_2682, SK_2684, SK_2685, SK_2687, SK_2688, SK_2690,
SK_2692, SK_2693, SK_2695, SK_2696, SK_2699, SK_2700, SK_2701, SK_2702, SK_2703, SK_2704,
SK_2705, SK_2710, SK_2713, SK_2715, SK_2724, SK_2727, SK_2729, SK_2733, SK_2734, SK_2736,
SK_2737, SK_2738, SK_2739, SK_2745, SK_2750, SK_2751, SK_2752, SK_2754, SK_2755, SK_2756,
SK_2758, SK_2759, SK_2760, SK_2761, SK_2775, SK_2778, SK_2780, SK_2782, SK_2789, SK_2792,
SK_2793, SK_2794, SK_2795, SK_2798, SK_2799, SK_2800, SK_2801, SK_2802, SK_2803, SK_2804,
SK_2805, SK_2851, SK_2852, SK_2853, SK_2854, SK_2855, SK_2856, SK_2857, SK_2858, SK_2859,
SK_2860, SK_2861, SK_2862, SK_2863, SK_2864, SK_2865, SK_2866, SK_2868, SK_2869, SK_2870,

SK_2871, SK_2873, SK_2874, SK_2875, SK_2876, SK_2877, SK_2878, SK_2879, SK_2880, SK_2881, SK_2884, SK_2885, SK_2886, SK_2887, SK_2888, SK_2889, SK_2958, SK_2959, SK_2960, SK_2961, SK_3174, SK_3333, SK_3417, SK_3461, SK_3462, SK_3463, SK_3464, SK_3465, SK_3466, SK_3467, SK_3468, SK_3469, SK_3470, SK_3471, SK_3472, SK_3473, SK_3474, SK_3475, SK_3476, SK_3477, SK_3478, SK_3894, SK_3895, SK_3896, SK_3897, SK_3898, SK_3899, SK_3900, SK_3901, SK_3902, SK_3903, SK_3904, SK_3905, SK_3906, SK_3907, SK_3908, SK_3909, SK_3910, SK_3911, SK_3912, SK_3913

General informations on HMMZ

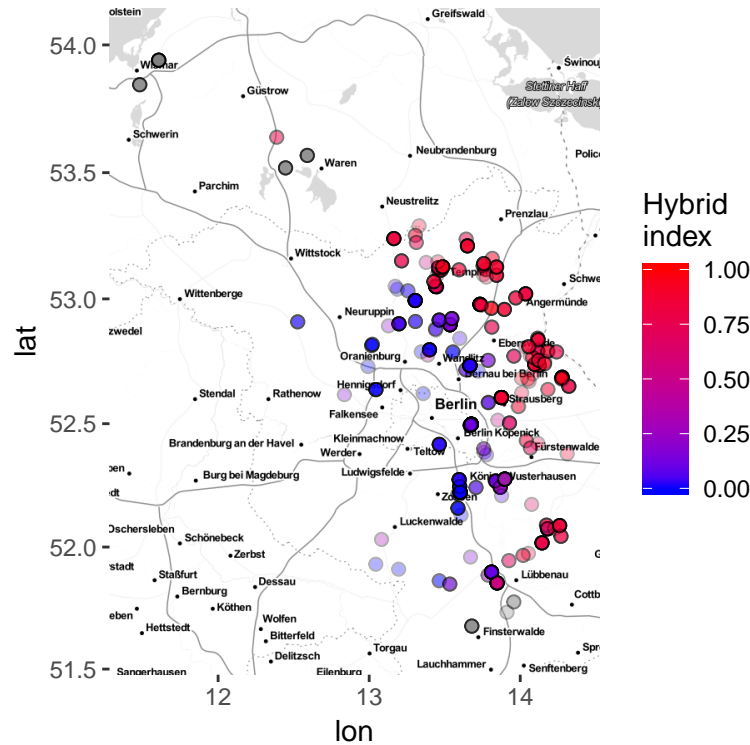


Figure 1: Map of the mice with OPG, PCR or qPCR status, caught in the Brandenburg-MVP transect in 2015, 2016 and 2017. Each point corresponds to one location, a less pronounced transparency indicating more animals sampled at this location. Hybrid index is represented by a gradient from blue (M.m.d) to red (M.m.m)

- 645 mice were captured over three years, from 156 farms
- From these mice:
- 498 mice had *Eimeria* detected by feces flotation,
- 643 mice had *Eimeria* detected by colon content PCR (cf paper Victor),
- 169 mice had *Eimeria* detected by qPCR on intestinal tissues
- On average, 4.13 mice were caught per farm (95% CI 0.37)
- **Hybrid indexes** were calculated as ratio of M.m.d/M.m.m alleles (between 4 and 14, on average 13 loci)

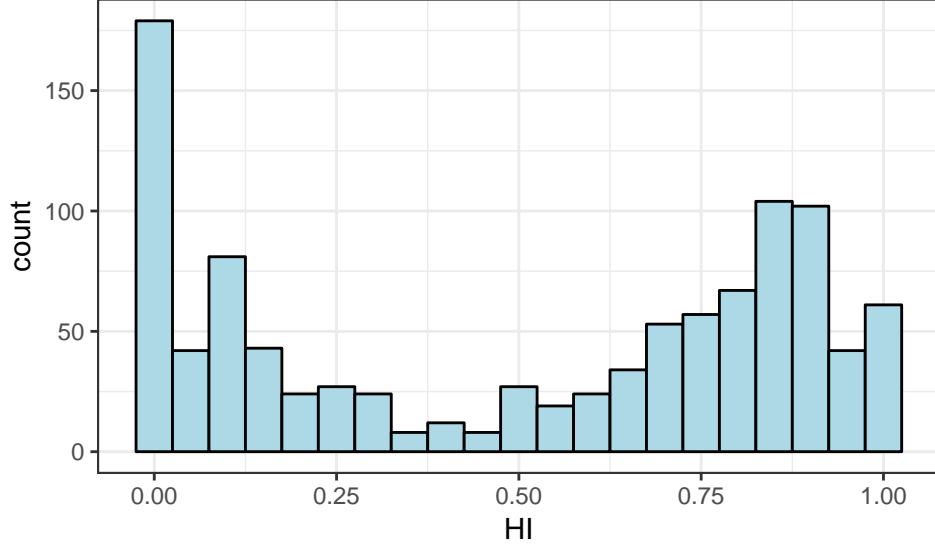


Figure 2: Number of animals caught along the hybrid index

Comparison of prevalences based on detection method

Table 1: Prevalence of Eimeria per year, based on oocyst flotation

	2014	2015	2016	2017
FALSE	0	92.0	132.00	171.00
TRUE	0	10.0	27.00	66.00
prevalence(%)	NaN	9.8	16.98	27.85

Table 2: Prevalence of Eimeria per year, based on PCR detection. A mouse was considered infected by Eimeria if one of the 3 markers (COI, 18S or ORF470) gave a sequence

	2014	2015	2016	2017
negative	53.00	111.00	156.00	205.00
positive	23.00	12.00	20.00	63.00
prevalence(%)	30.26	9.76	11.36	23.51

Table 3: Prevalence of Eimeria per year, based on qPCR

	2014	2015	2016	2017
negative	0	0	138.00	0
positive	0	0	31.00	0
prevalence(%)	NaN	NaN	18.34	NaN

Table 4: Prevalence of Eimeria per year, based on PCR detection. A mouse was considered infected by Eimeria if one of the 3 markers (COI, 18S or ORF470) gave a sequence, OR if it had a positive count of oocysts in its feces, OR if it was qPCR positive

	2014	2015	2016	2017
negative	0	0	118.00	0
positive	23	17	51.00	87
prevalence(%)	100	100	30.18	100
ERROR TO FIX THE	RE			

Improving Eimeria oocysts detection

22 new samples were detected while diluting by 0.1mL PBS instead of 1mL before counting in Neubauer chamber.

Adjusted R-squared = 0.81 represents the amount of variation in y explained by x.

<https://www.r-bloggers.com/correlation-and-linear-regression/> (for Lorenzo)

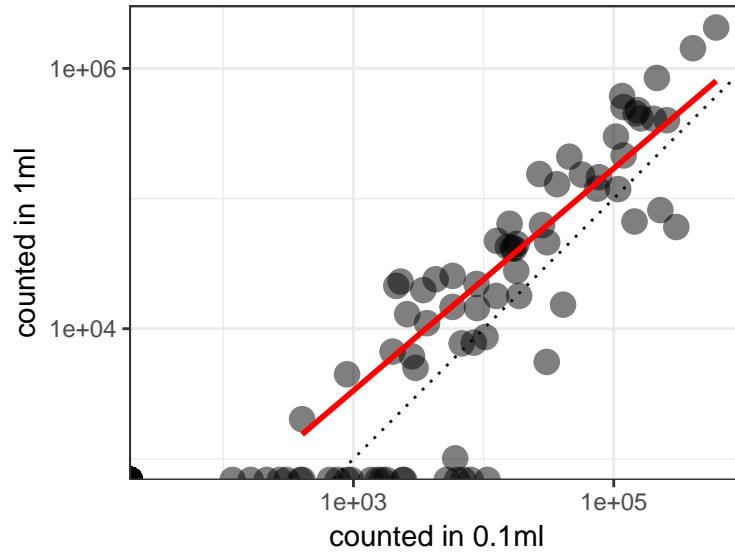


Figure 3: Comparison of OPG depending on dilution level. Red line represents linear relationship between both axis, dotted line represents the function $y = x$

Comparison oocysts flotation, PCR, qPCR

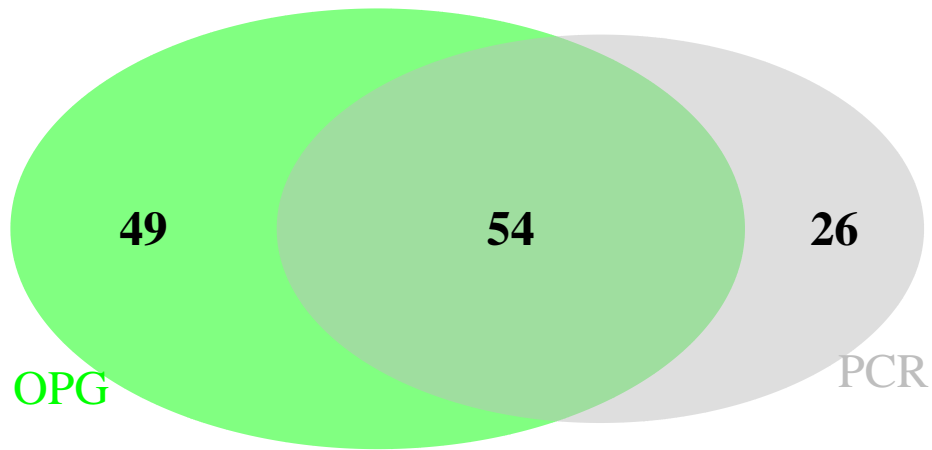


Figure 4: Comparison of detection: PCR vs flotation

(polygon[GRID.polygon.196], polygon[GRID.polygon.197], polygon[GRID.polygon.198], polygon[GRID.polygon.199])

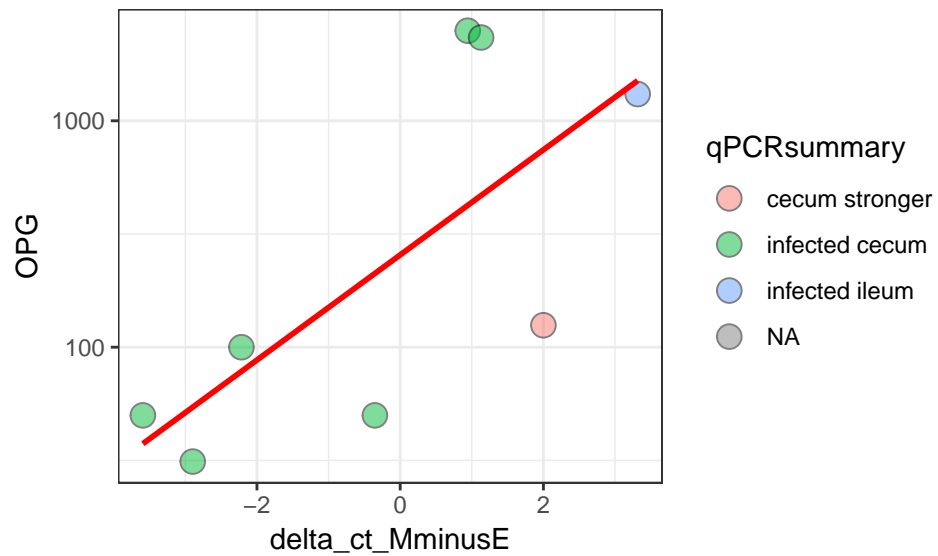


Figure 5: Comparison of positive values of OPG and qPCR for year 2016

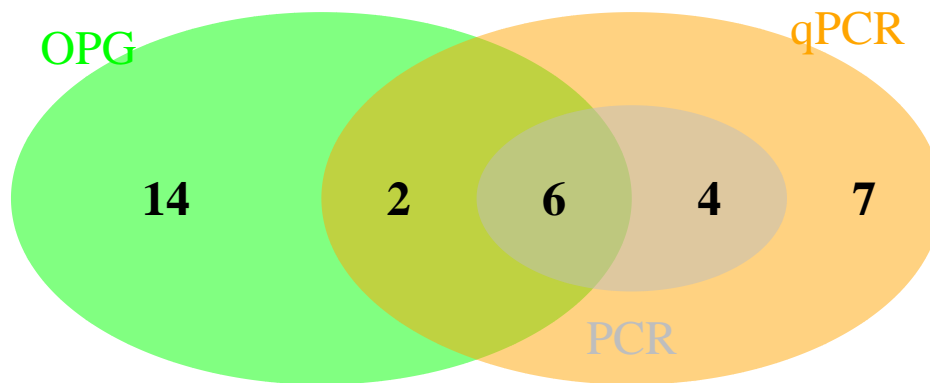


Figure 6: Comparison of detection: PCR vs flotation vs qPCR

```
## (polygon[GRID.polygon.286], polygon[GRID.polygon.287], polygon[GRID.polygon.288], polygon[GRID.polygon.289])
```

Testing hybrid vigor along HMMZ

Oocyst shedding proxy

First approximation:

```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```

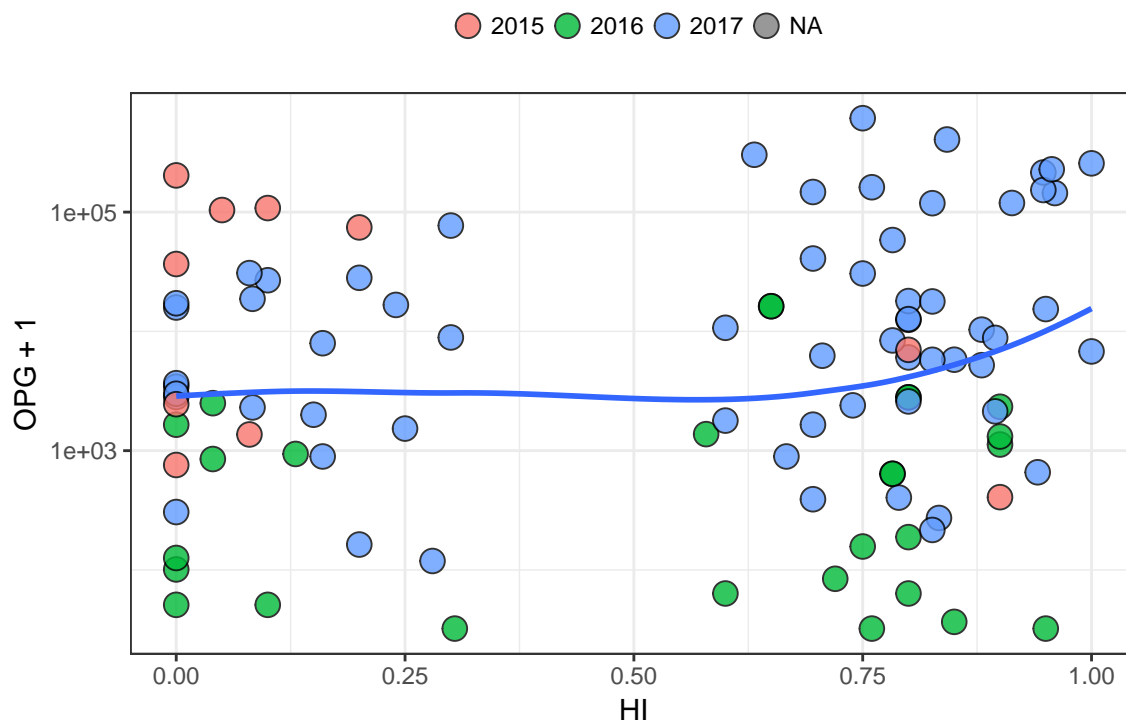


Figure 7: OPG along HI, colored per year. Blue line represent a smooth function (method = loess)

Statistical model (dvp...)

qPCR proxy

tbc

BCI proxy

First approximation:

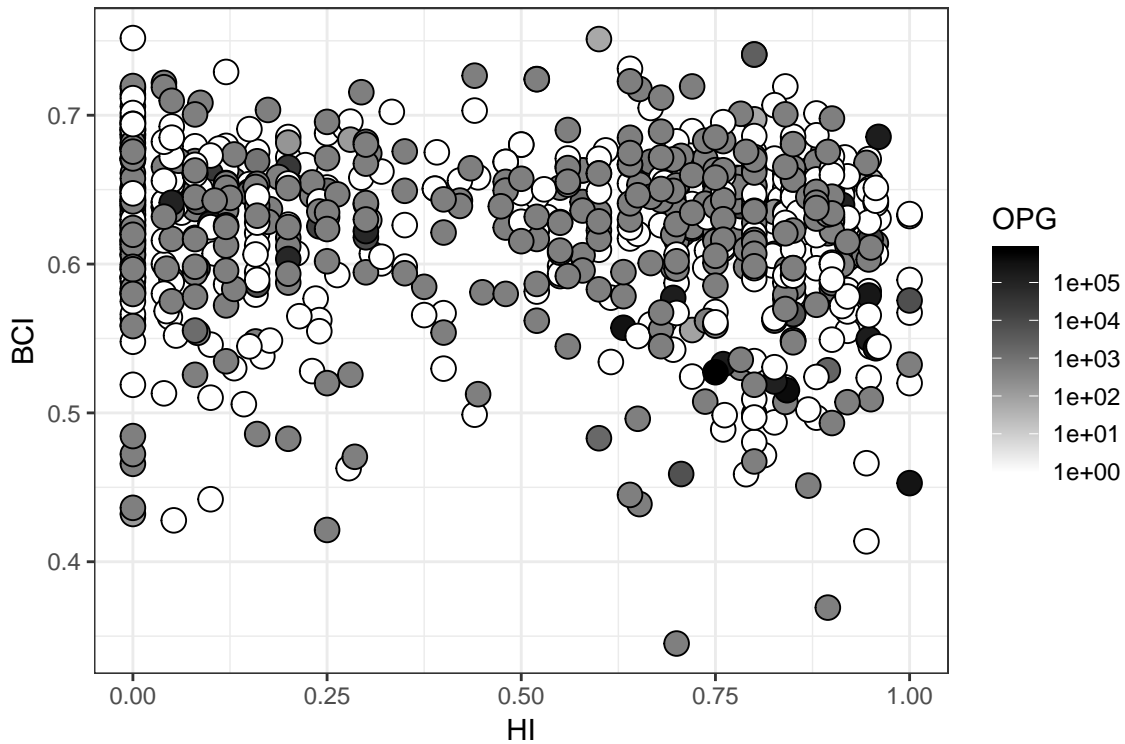


Figure 8: BCI along HI, colored per level of OPG

Bonus part: genotyping of mice case/control

Discussed with Stuart:

- Test distributions 0 or counts. Test all vs only infected (“intensity”) distribution. We should be able to fit the distribution of infected on all. Zeros are data. Stochastic move.
- Separation of the zero class. balanced design case/control ~ 400 +/- 70 infectés SNPchip.
- H0: no differences are observed
- Separate <0.5 and >0.5 to see the species effect
- timing : WHEN (for my thesis?)