Report: Hybrid vigor in response to Eimeria in the HMHZ

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Contents

To be fixed before all

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

SK_3174

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

AA_0411, AA_0412, AA_0420, 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_3174

General informations on HMHZ

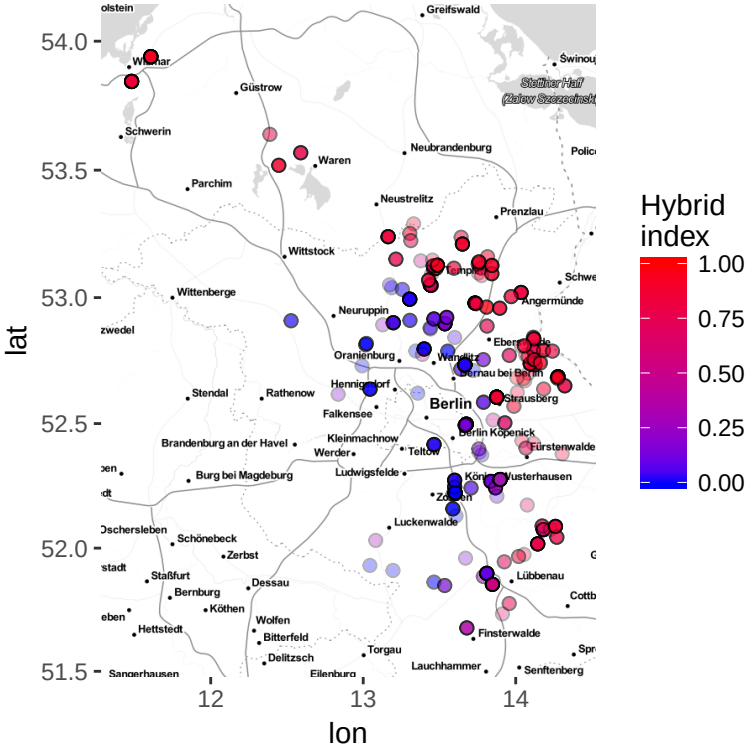

Figure 1: Map of the mice with OPG, PCR or qPCR status, caught in the Brandenburg-MVP transect in 2015, 2016 and 2017. Each point corresponds to one location, a less pronounced transparency indicating more animals sampled at this location. Hybrid index is represented by a gradient from blue (M.m.d) to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

- 656 mice were captured over three years, from 157 farms
- From these mice:
- 485 mice had Eimeria detected by feces flotation,
- 652 mice had Eimeria detected by colon content PCR (cf paper Victor),
- 397 mice had Eimeria detected by qPCR on intestinal tissues
- On average, 4.04 mice were caught per farm (95% CI 0.34)
- **Hybrid indexes** were calculated as ratio of M.m.d/M.m.m alleles (between 4 and 14, on average 13 loci)

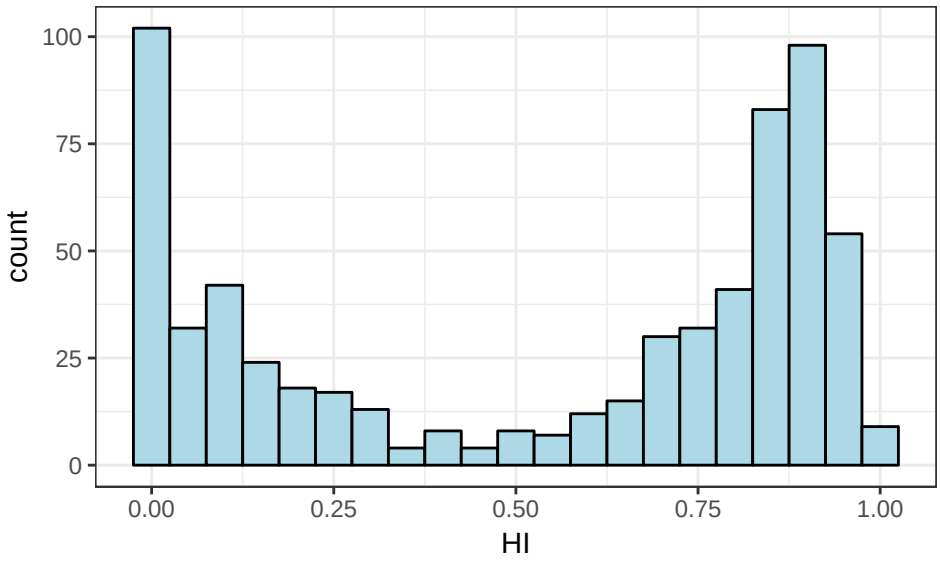

Figure 2: Number of animals caught along the hybrid index

Comparison of prevalences based on detection method

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

	2014	2015	2016	2017
FALSE	1	93.00	126.00	165.00
TRUE	0	10.00	25.00	65.00
prevalence(%)	0	9.71	16.56	28.26

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

	2014	2015	2016	2017
negative	54.00	111.00	146.00	224.00
positive	23.00	12.00	20.00	62.00
prevalence(%)	29.87	9.76	12.05	21.68

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

	2014	2015	2016	2017
negative	0	1	131.00	159.00
positive	1	0	34.00	71.00
prevalence(%)	100	0	20.61	30.87

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)

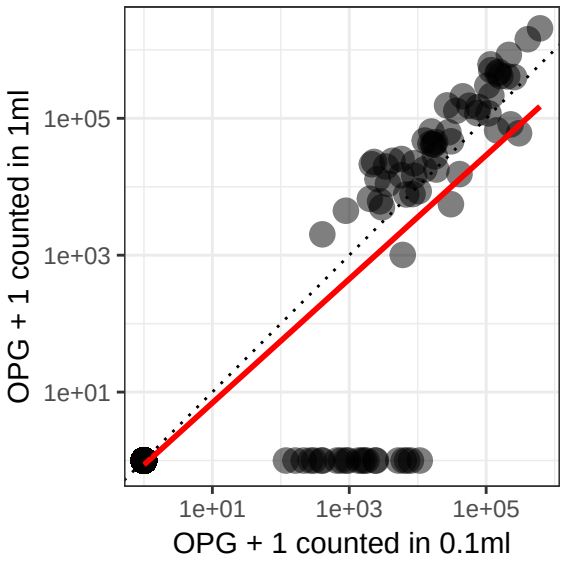

Figure 3: Comparison of OPG depending on dilution level. Red line represents linear relationship between both axis, dotted line represents the function y = x

Comparison oocysts flotation, PCR, qPCR

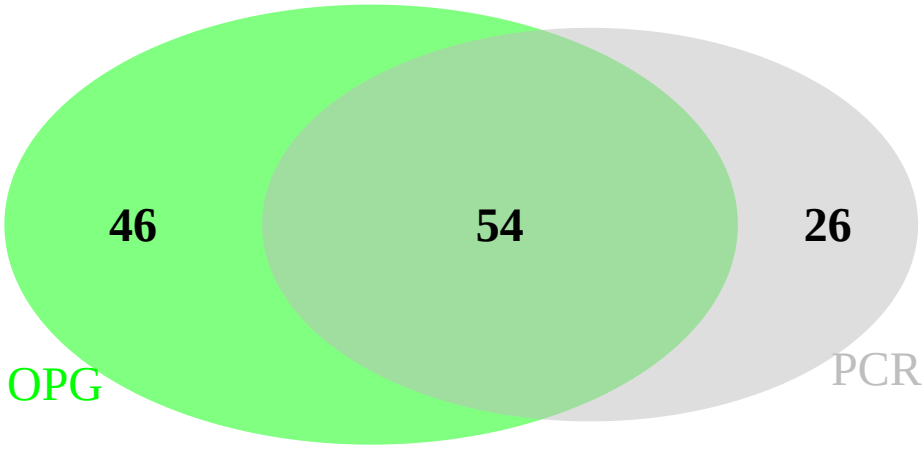

Figure 4: Comparison of detection: PCR vs flotation

```
## (polygon[GRID.polygon.192], polygon[GRID.polygon.193], polygon[GRID.polygon.194], polygon[GRID.polyg
```

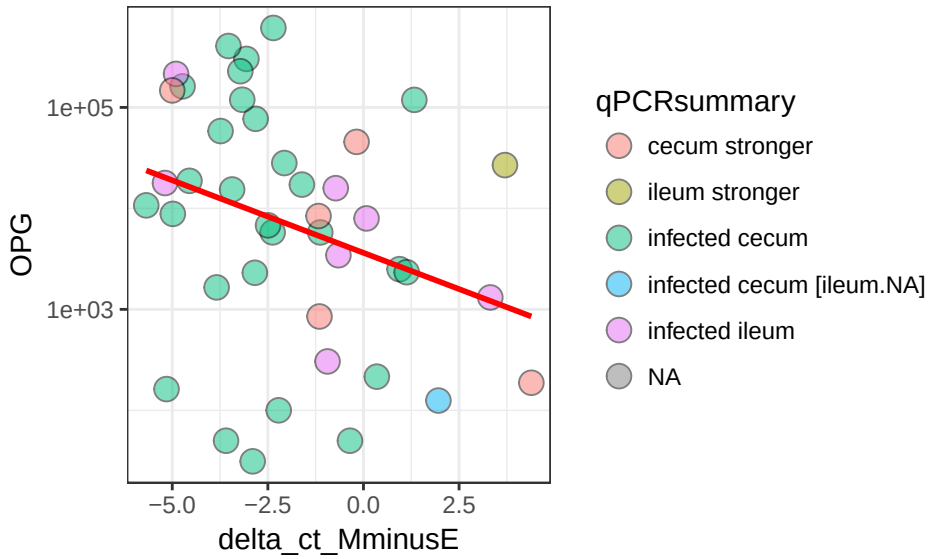

Figure 5: Comparison of positive values of OPG and qPCR for year 2016

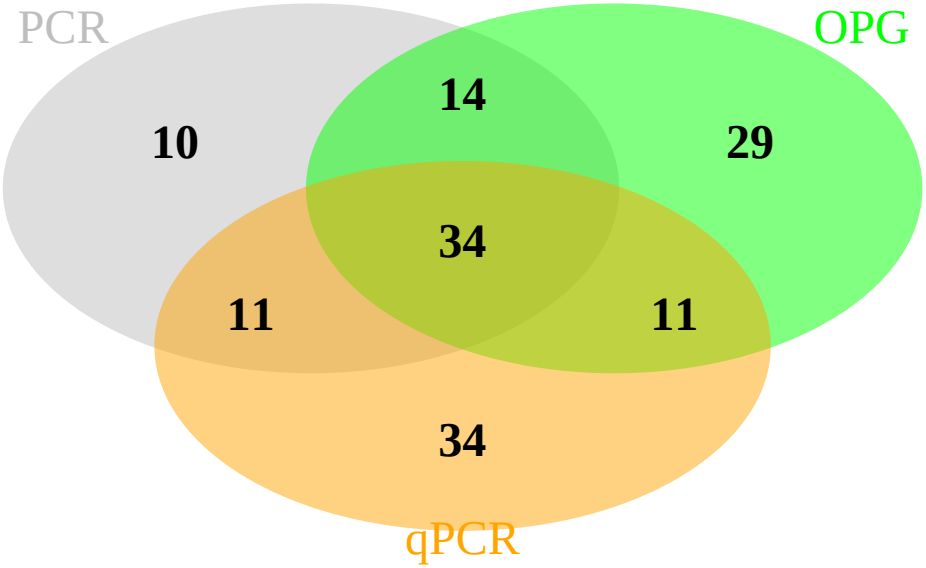

Figure 6: Comparison of detection: PCR vs flotation vs qPCŔ

```
## (polygon[GRID.polygon.281], polygon[GRID.polygon.282], polygon[GRID.polygon.283], polygon[GRID.polyg
```

Testing hybrid vigor along HMHZ

Oocyst shedding proxy

First approximation:

```
## `geom_smooth()` using method = 'loess'
```

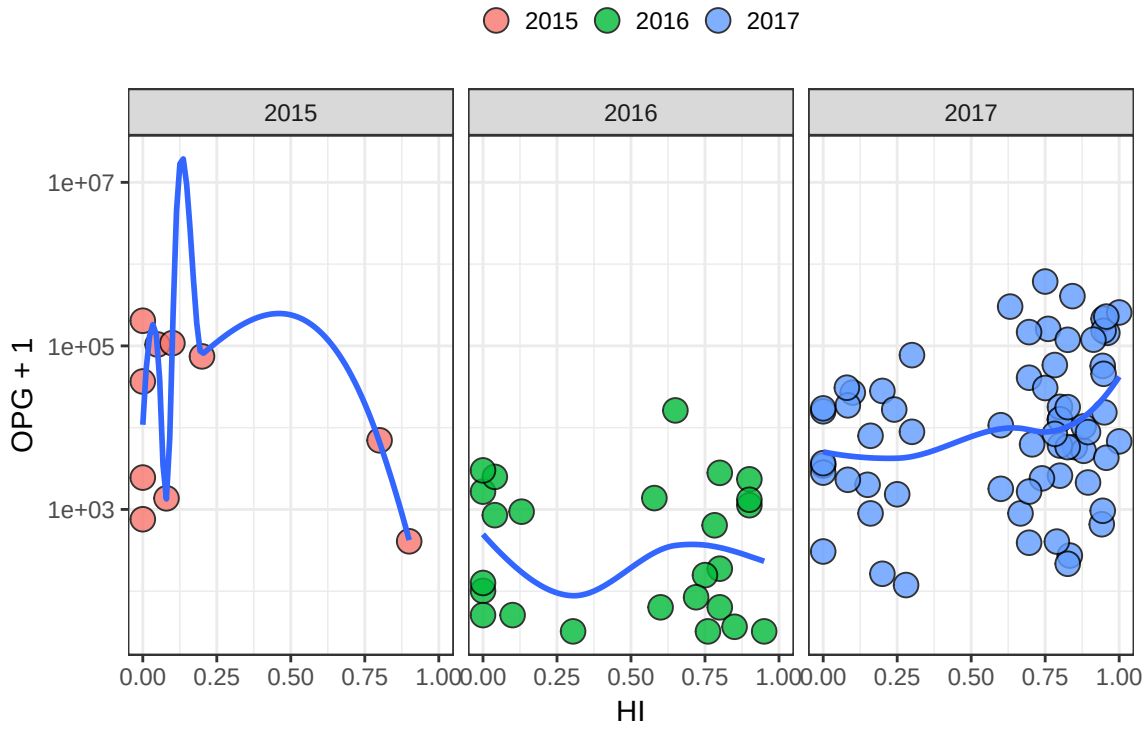

Figure 7: OPG along HI, colored per year. Blue line represent a smooth function (method = loess)

Statistical model (dvp...)

qPCR proxy

tbc

BCI proxy

First approximation:

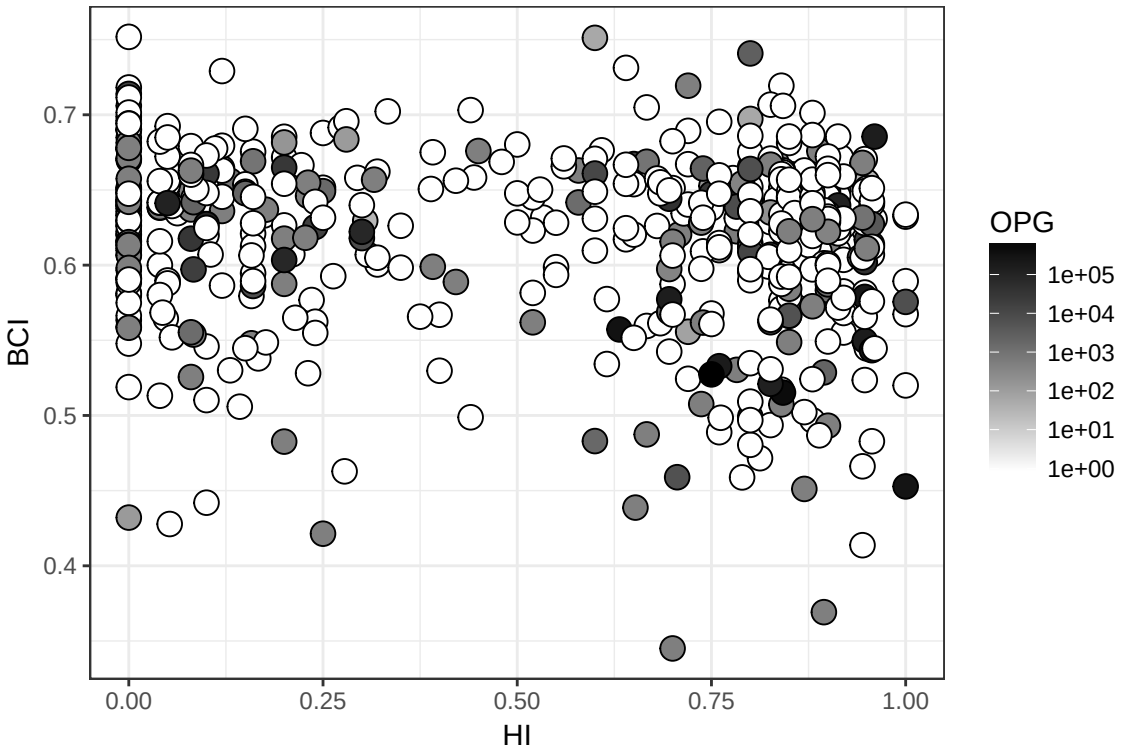

Figure 8: BCI along HI, colored per level of OPG

Bonus part: genotyping of mice case/control

- 100 out of 483 are positive for flotation and have an hybrid index.
- 106 out of 395 are positive for qPCR and have an hybrid index.

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 +/-70infectés SNPchip.
- H0: no differences are observed
- Separate <0.5 and >0.5 to see the species effect
- timing : WHEN (for my thesis?)