

# Report: Hybrid vigor in response to Eimeria in the HMHZ

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## 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 HMMZ

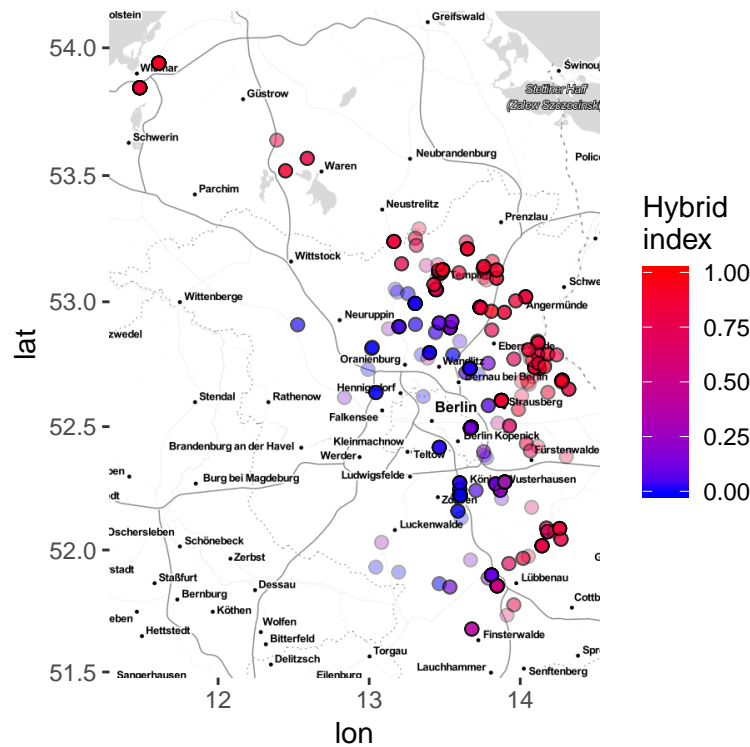


Figure 1: Map of the mice with OPG, PCR or qPCR status, caught in the Brandenburg-MVP transect in 2015, 2016 and 2017. Each point corresponds to one location, a less pronounced transparency indicating more animals sampled at this location. Hybrid index is represented by a gradient from blue (M.m.d) to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

- 666 mice were captured over three years, from 157 farms
- From these mice:
- 495 mice had Eimeria detected by feces flotation,
- 664 mice had Eimeria detected by colon content PCR (cf paper Victor),
- 182 mice had Eimeria detected by qPCR on intestinal tissues
- On average, 4.11 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)

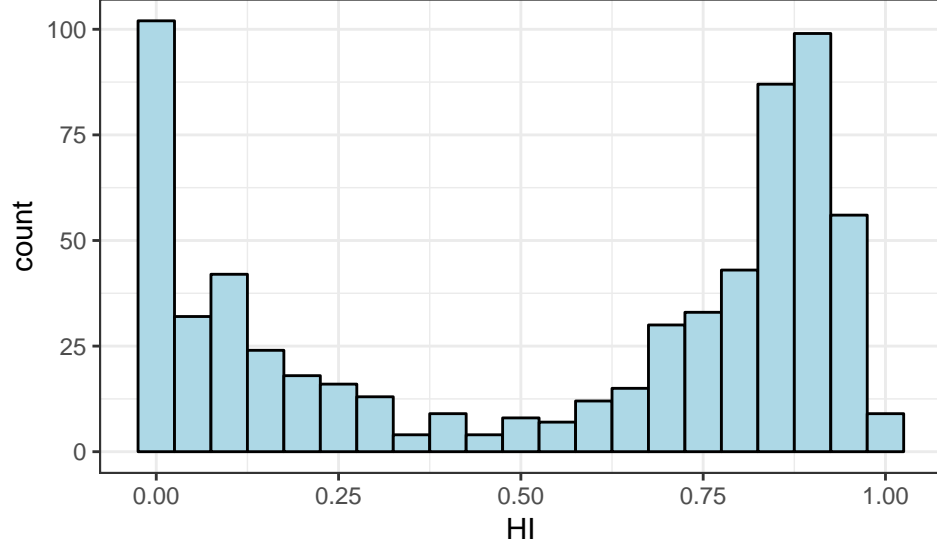


Figure 2: Number of animals caught along the hybrid index

## Comparison of prevalences based on detection method

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

	2014	2015	2016	2017
FALSE	1	94.00	126.00	166.00
TRUE	0	11.00	25.00	72.00
prevalence(%)	0	10.48	16.56	30.25

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	54.00	112.0	146.00	225.00
positive	23.00	13.0	21.00	70.00
prevalence(%)	29.87	10.4	12.57	23.73

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

	2014	2015	2016	2017
negative	0	0	129.00	8.00
positive	0	0	31.00	14.00
prevalence(%)	NaN	NaN	19.38	63.64

Table 4: Prevalence of Eimeria per year, based on all detections methods. 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	112.00	0
positive	23	18	49.00	96
prevalence(%)	100	100	30.43	100

## 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)

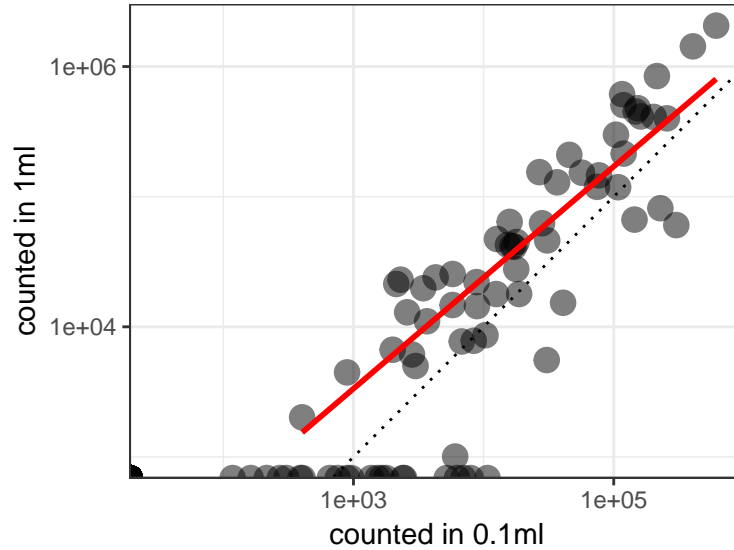


Figure 3: Comparison of OPG depending on dilution level. Red line represents linear relationship between both axis, dotted line represents the function  $y = x$

## Comparison oocysts flotation, PCR, qPCR

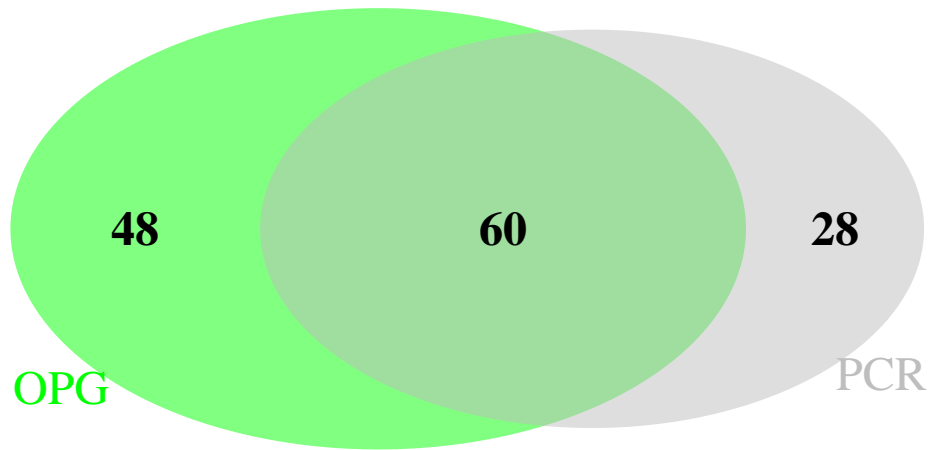


Figure 4: Comparison of detection: PCR vs flotation

## (polygon[GRID.polygon.198], polygon[GRID.polygon.199], polygon[GRID.polygon.200], polygon[GRID.polygon.201])

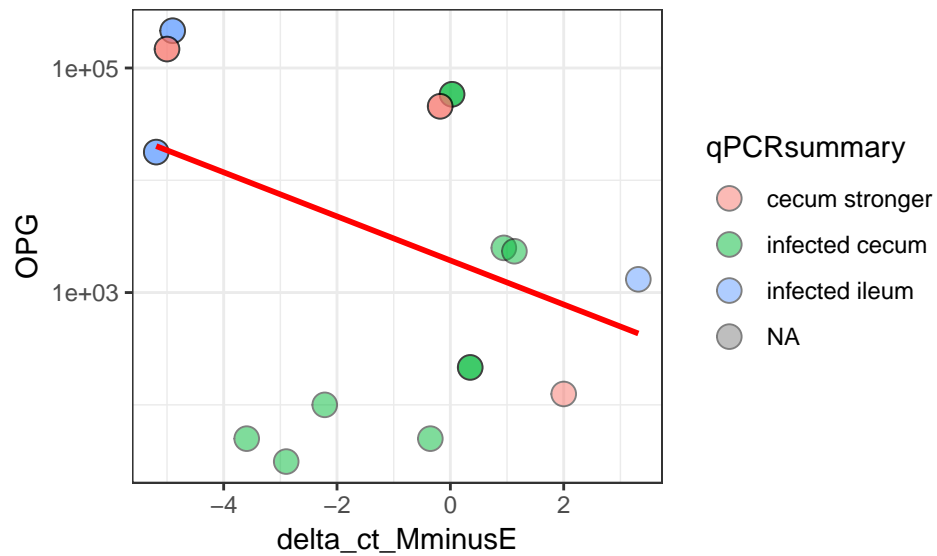


Figure 5: Comparison of positive values of OPG and qPCR for year 2016

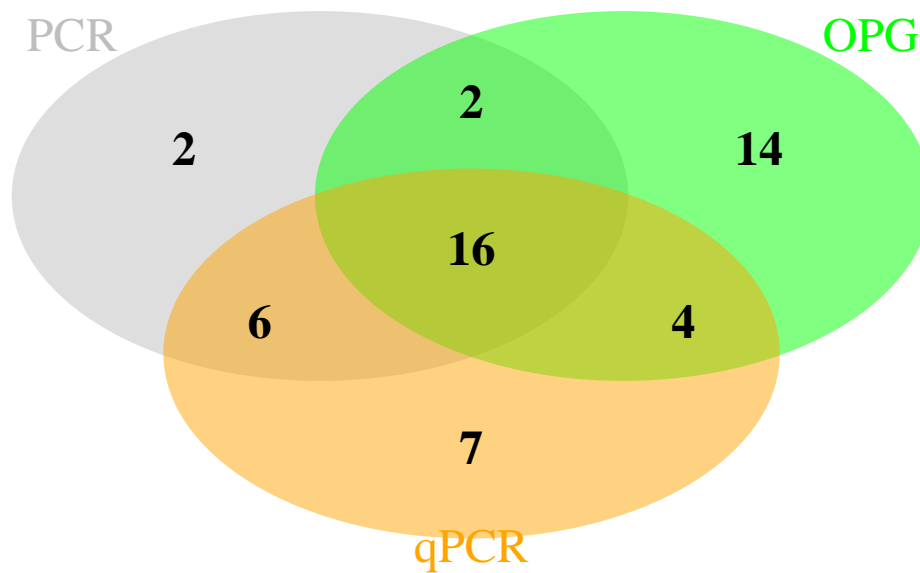


Figure 6: Comparison of detection: PCR vs flotation vs qPCR

```
## (polygon[GRID.polygon.288], polygon[GRID.polygon.289], polygon[GRID.polygon.290], polygon[GRID.polygon.291])
```

## Testing hybrid vigor along HMMZ

### Oocyst shedding proxy

First approximation:

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

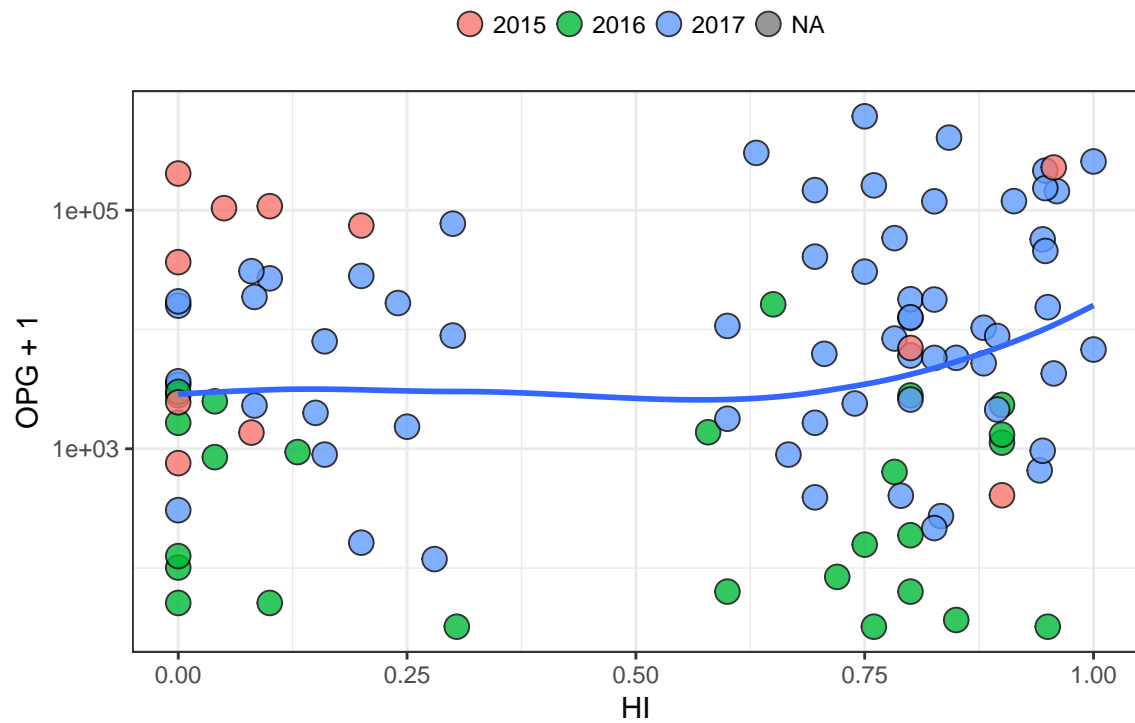


Figure 7: OPG along HI, colored per year. Blue line represent a smooth function (method = loess)

Statistical model (dvp...)

**qPCR proxy**

tbc

**BCI proxy**

First approximation:

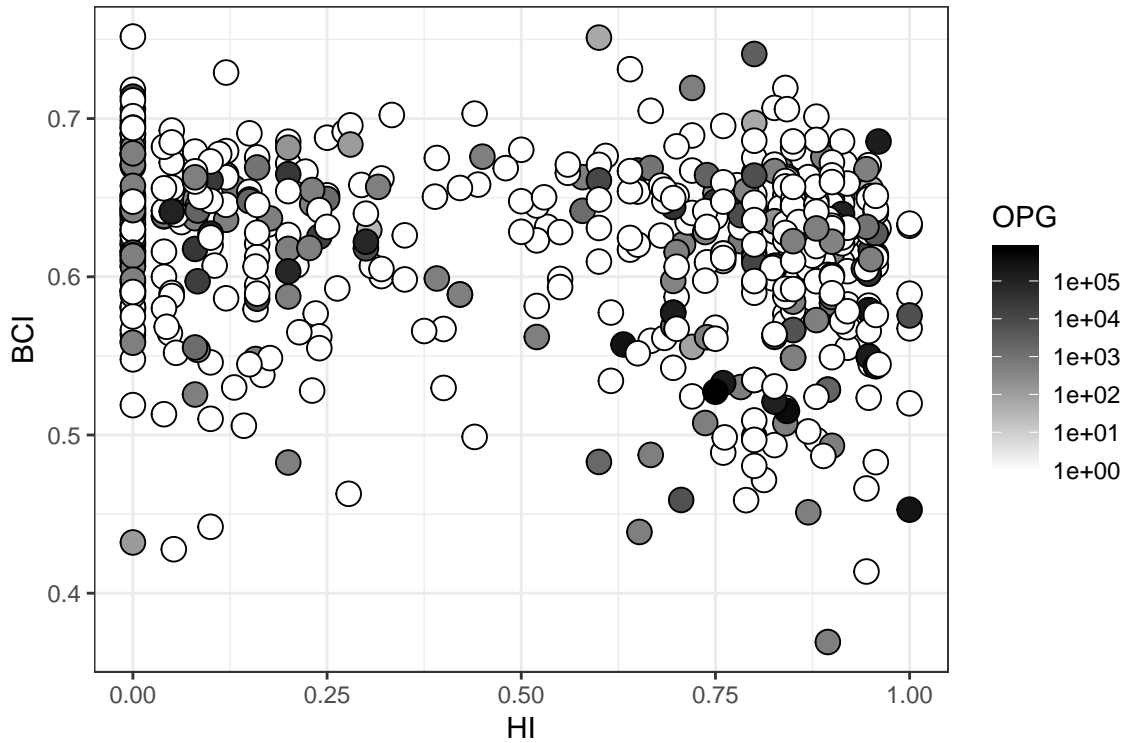


Figure 8: BCI along HI, colored per level of OPG

## Bonus part: genotyping of mice case/control

- 108 out of 493 are positive for flotation and have an hybrid index.
- 45 out of 182 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  $\sim 400 \pm 70$  infectés SNPchip.
- $H_0$ : no differences are observed
- Separate  $<0.5$  and  $>0.5$  to see the species effect
- timing : WHEN (for my thesis?)