Report: Hybrid vigor in response to Eimeria in the HMHZ

Alice

22 June 2018

Contents

To be fixed before all

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

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, SK_3174

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

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
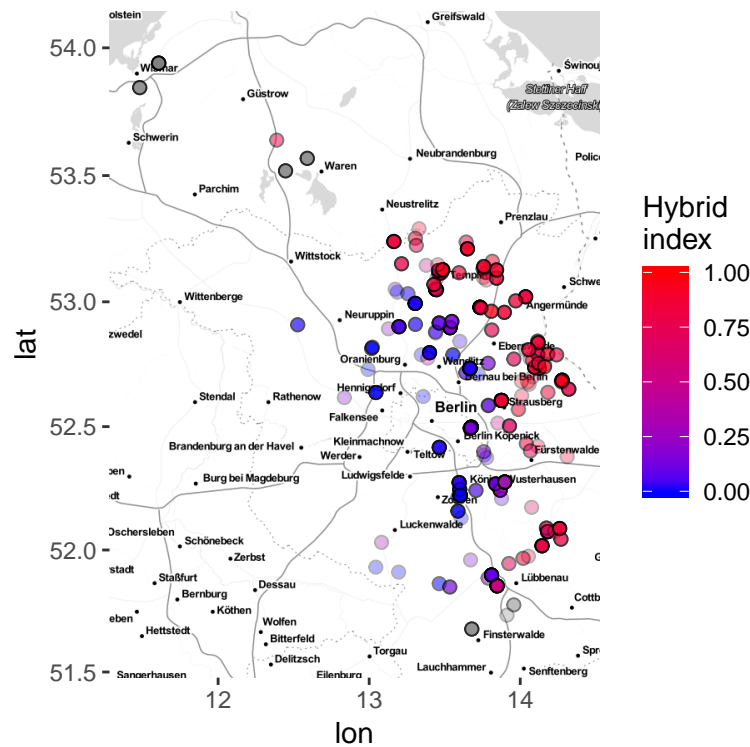
General informations on HMHZ

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)

- 630 mice were captured over three years, from 156 farms

- From these mice:

- 485 mice had Eimeria detected by feces flotation,

- 628 mice had Eimeria detected by colon content PCR (cf paper Victor),

- 160 mice had Eimeria detected by qPCR on intestinal tissues

- On average, 4.04 mice were caught per farm (95% CI 0.35)

- **Hybrid indexes** were calculated as ratio of M.m.d/M.m.m alleles (between 4 and 14, on average 13 loci)
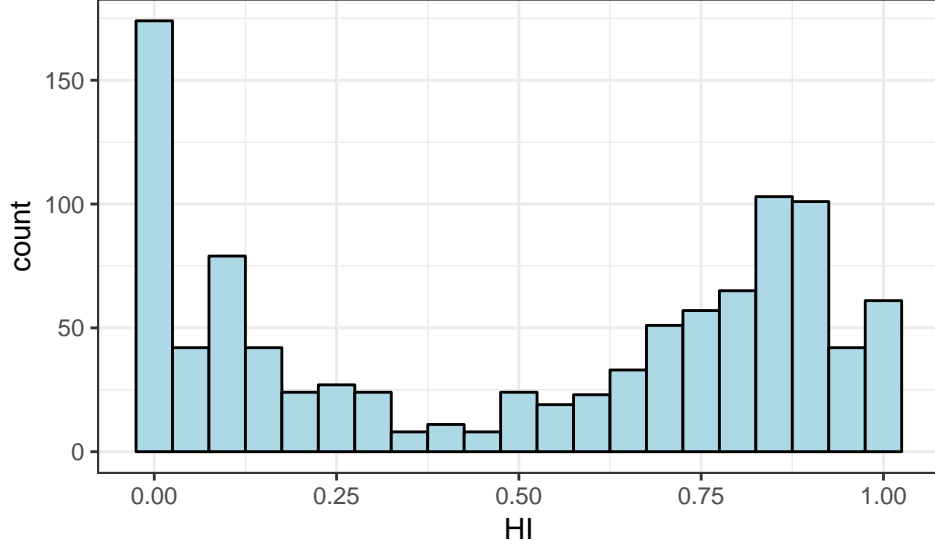
Figure 2: Number of animals caught along the hybrid index

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	126	167.00
TRUE	0	10.0	24	66.00
prevalence(%)	NaN	9.8	16	28.33

Table 2: Prevalence of Eimeria per year, based on PCR detection and oocysts flotation. A mouse was considered infected by Eimeria if it had a positive oocyst count in its feces, or if one of the 3 markers (COI, 18S or ORF470) gave a sequence

	2014	2015	2016	2017
negative	53.00	110.00	146.00	201.00
positive	23.00	12.00	20.00	63.00
prevalence(%)	30.26	9.84	12.05	23.86

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

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

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.

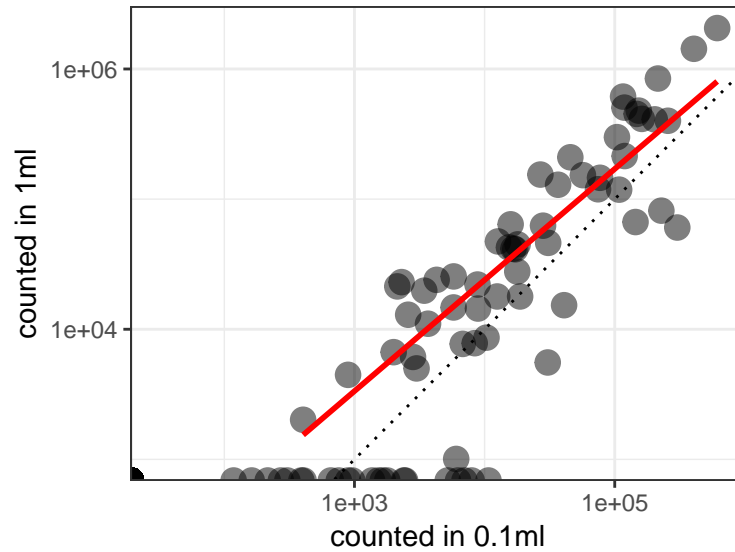*https://www.r-bloggers.com/correlation-and-linear-regression/ (for Lorenzo)*

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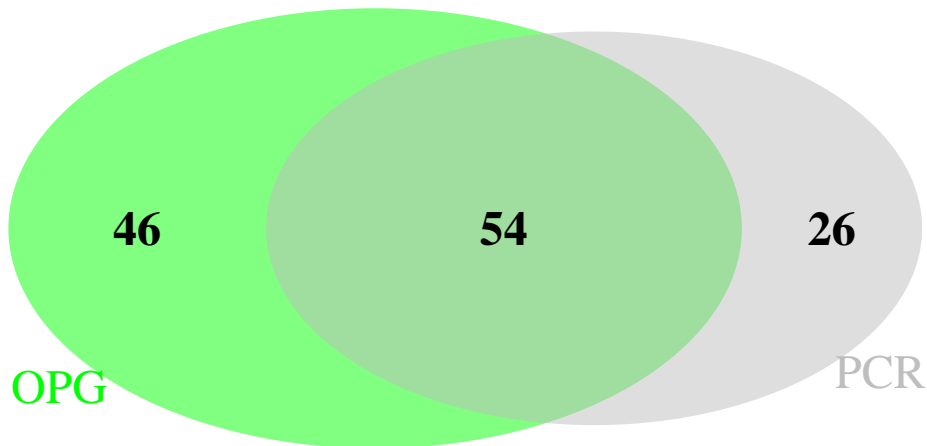
Comparison oocysts flotation, PCR, qPCR

Figure 4: Comparison of detection: PCR vs flotation

(polygon[GRID.polygon.186], polygon[GRID.polygon.187], polygon[GRID.polygon.188], polygon[GRID.polyg
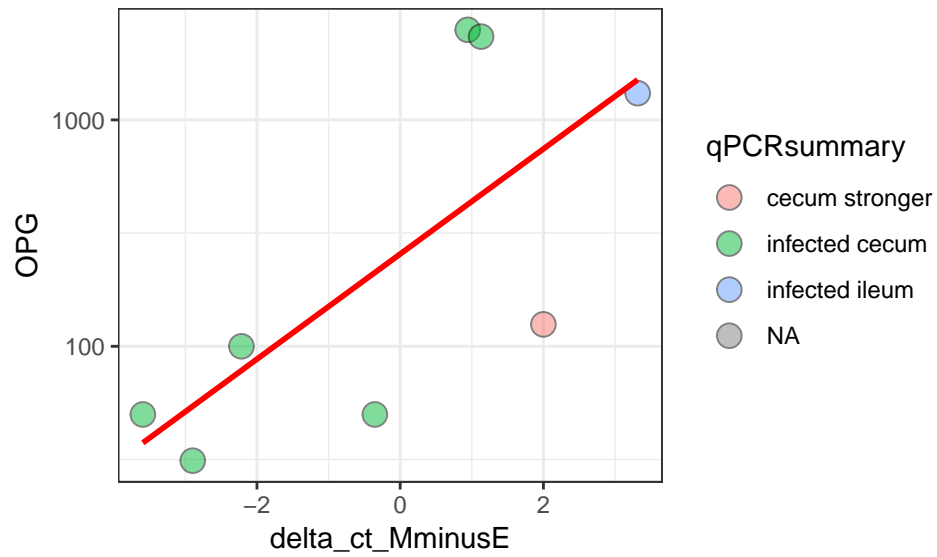
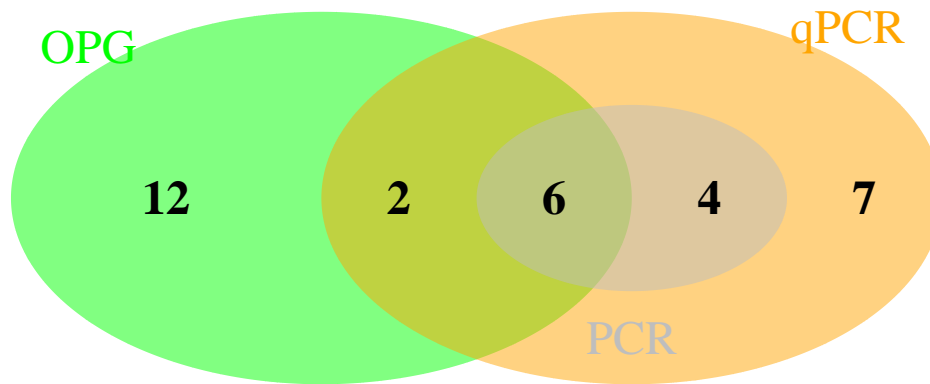Figure 5: Comparison of positive values of OPG and qPCR for year 2016

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

```
## (polygon[GRID.polygon.276], polygon[GRID.polygon.277], polygon[GRID.polygon.278], polygon[GRID.polyg
```

Testing hybrid vigor along HMHZ

Oocyst shedding proxy

First approximation:

```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```
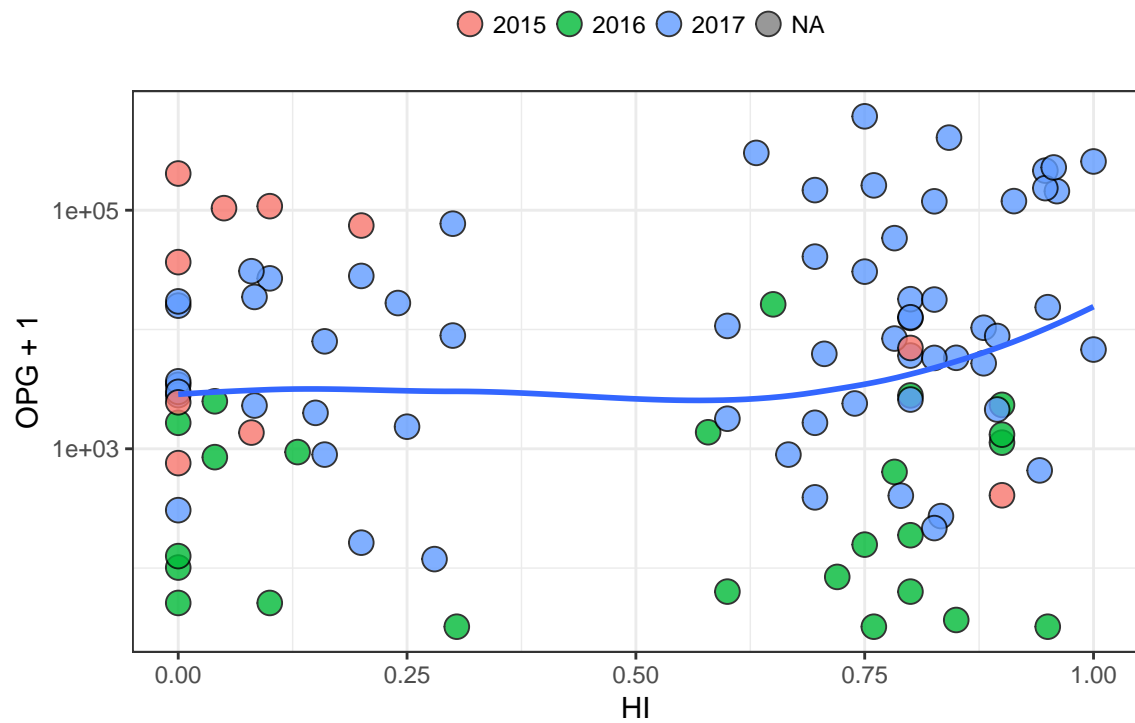
Figure 7: OPG along HI, colored per year. Blue line represent a smooth function (method = loess)

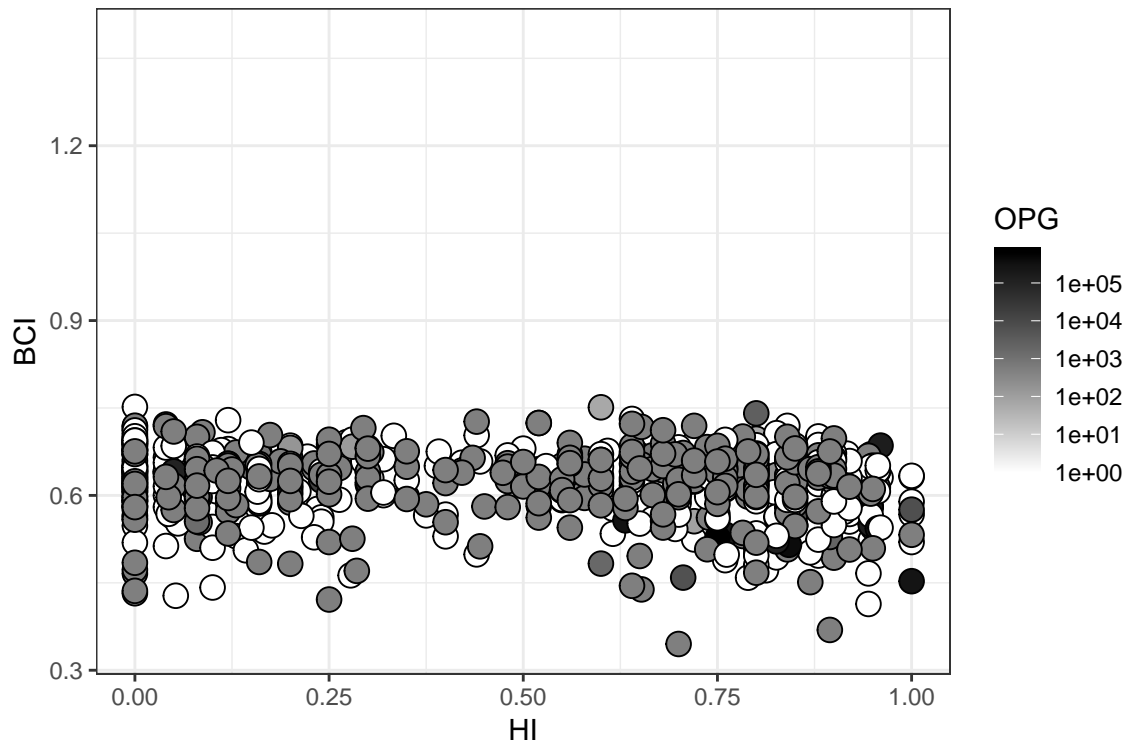Statistical model (dvp. . .)

qPCR proxy

tbc

BCI proxy

First approximation:

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