Report: Hybrid vigor in response to Eimeria in the HMHZ

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Contents

General informations on HMHZ

- 485 mice were captured over three years and had fecal samples processed, from 146 farms.
- From these mice, *(tbc : N had colon content and intestinal tissues collected for PCR and qPCR detection)*
- 3.79 mice were caught on average by farm (95% ci : 0.36)
- **Hybrid indexes** were calculated as ratio of M.m.d/M.m.m alleles (between 4 and 14, on average 13 loci)

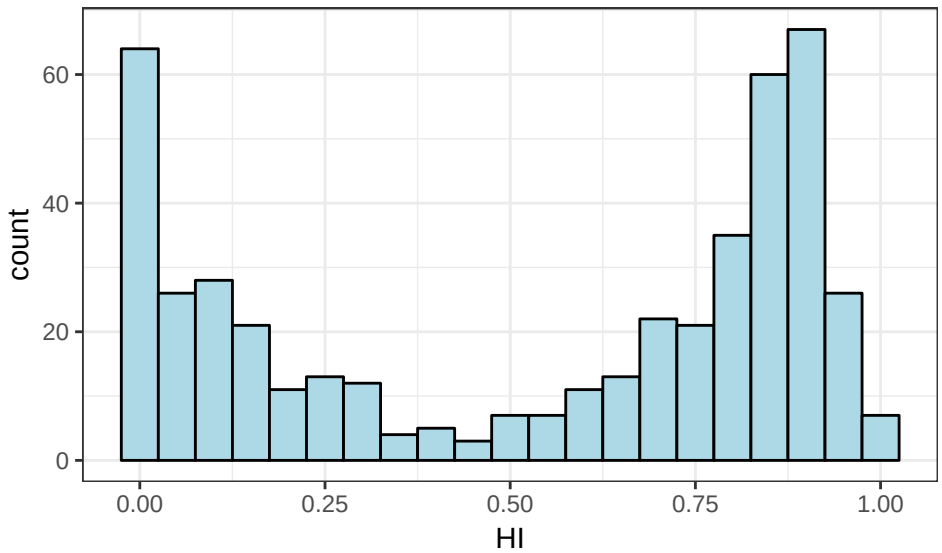

Figure 1: Number of animals caught along the hybrid index

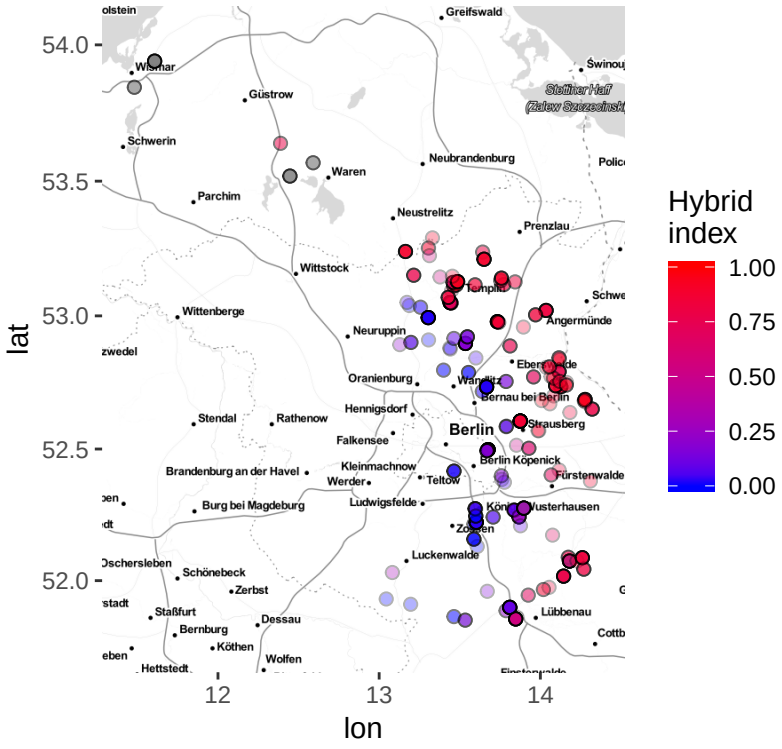

Figure 2: Samples map. Each point correspond to one location, a less pronounced transparency indicating more animals sampled at this location. Hybrid index is represented by a gradient from blue (M.m.d) to red (M.m.m)

The average *Eimeria* prevalence per farm based on oocysts flotation is 15.22. We observed, based on this technique, a variation between years (Table 1).

Table 1: Prevalence of Eimeria based on OPG per year

	2015	2016	2017
FALSE	92.0	126	167.00
TRUE	10.0	24	66.00
prevalence(%)	9.8	16	28.33

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)

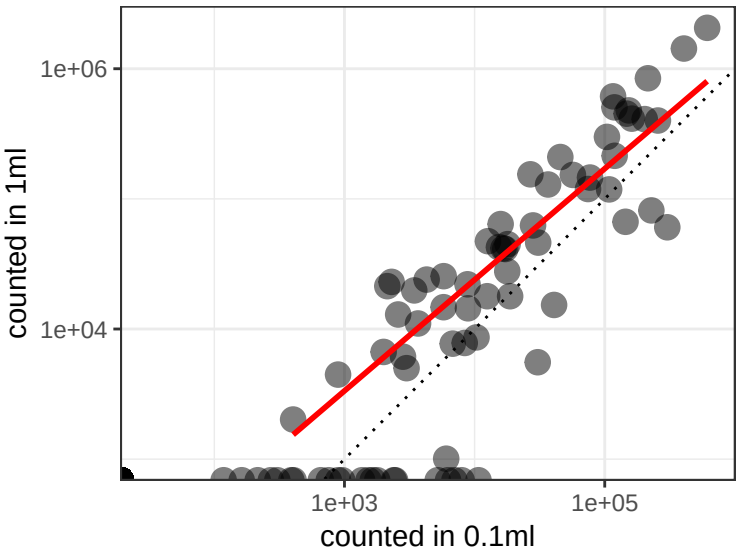

Figure 3: Comparison of OPG depending on dilution level. Red line represents linear relationship between both axis, dotted line represents

Missing data (to complete with Victor)

Some mice do not have an hybrid index yet: SK_3174, AA_0411, AA_0412, AA_0489, AA_0490, AA_0491, 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_0511, AA_0512, AA_0513, AA_0514, AA_0515

PCR

```
getPrevalenceTable(table(myData$Ap5_PCR, myData$year))
```

```
##                2015 2016  2017
## negative          0    0 33.00
## positive          0    0  8.00
## prevalence(%)   NaN  NaN 19.51
```

```
getPrevalenceTable(table(myData$PCR.positive, myData$year))
```

```
##                2015 2016 2017
## FALSE             0    0 36.0
## TRUE              0    0  5.0
## prevalence(%)   NaN  NaN 12.2
```

qPCR

```
getPrevalenceTable(table(myData$qPCRstatus, myData$year))
```

```
##                2015   2016 2017
## negative          0 125.00    0
## positive          0  19.00    0
## prevalence(%)   NaN  13.19  NaN
```

Comparison oocysts flotation, PCR, qPCR

```
#getPrevalenceTable(table(myData$qPCRstatus, myData$year))
```

Testing hybrid vigor along HMHZ

Oocyst shedding proxy

First approximation:

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

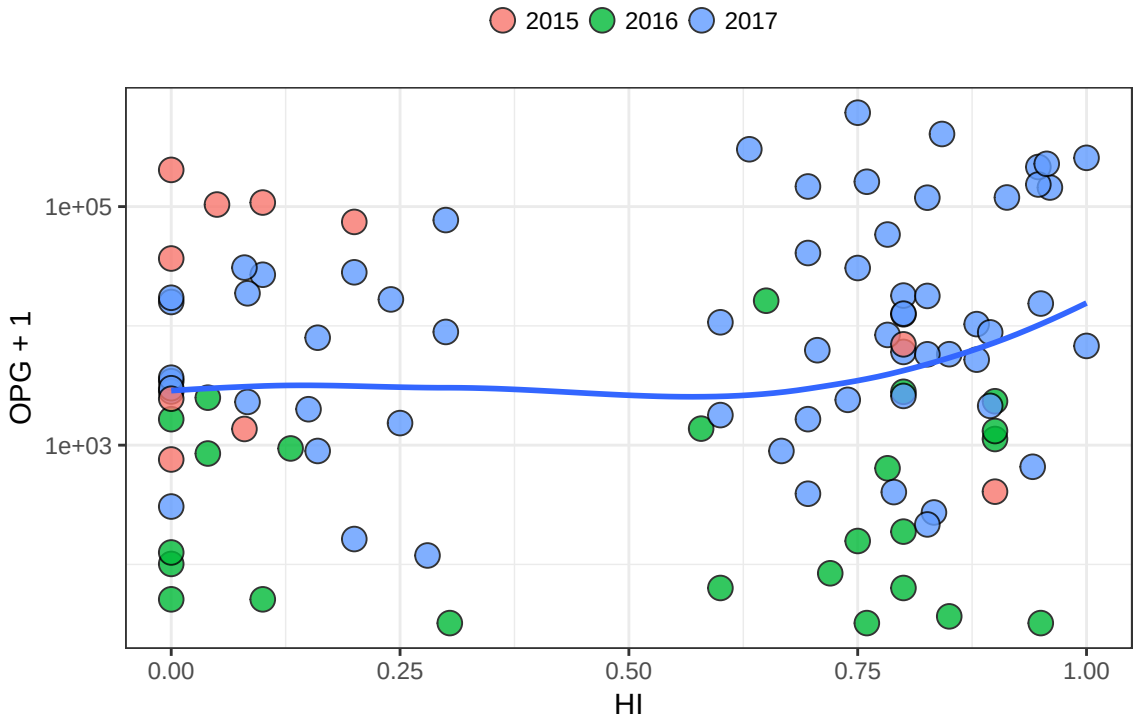

Figure 4: OPG along HI, colored per year. Blue line represent a smooth function (method = loess)

Statistical model (dvp...)

qPCR proxy

tbc

BCI proxy

First approximation:

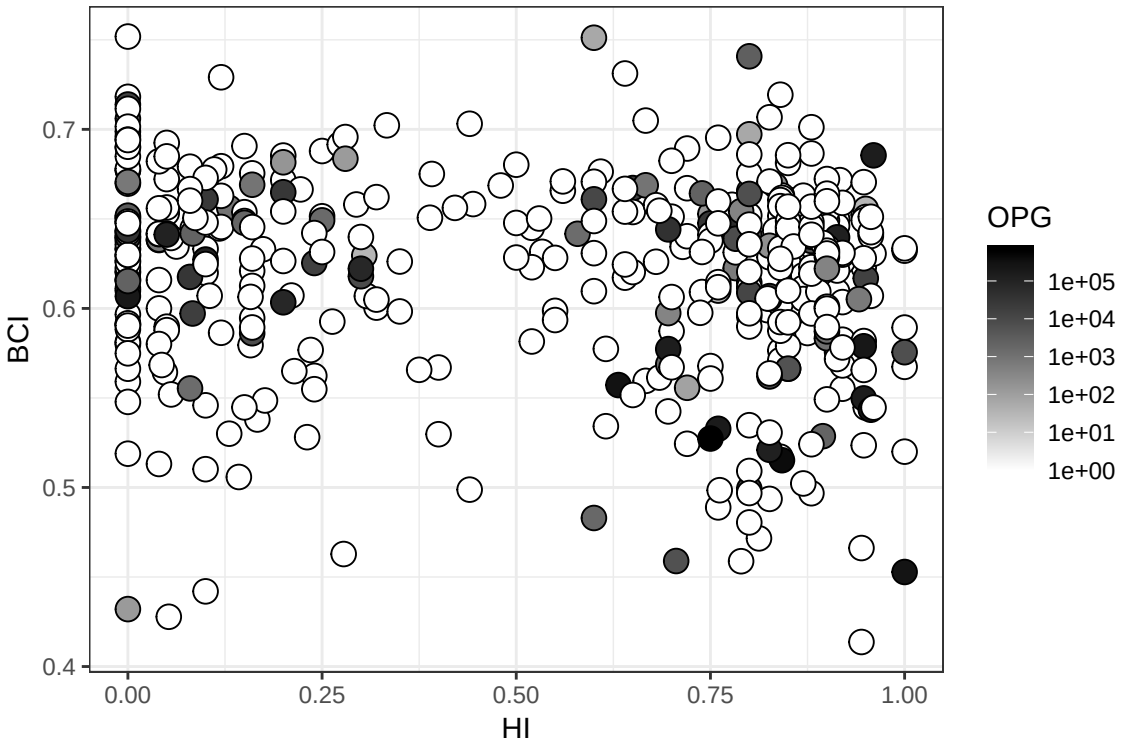

Figure 5: BCI along HI, colored per level of OPG