Report: Hybrid vigor in response to Eimeria in the HMHZ

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Contents

```r
# How many mice from which year?
miceTable <- miceTable[miceTable$Year %in% c("2015", "2016", "2017"),]
table(miceTable$Year)
```

```
##
## 2015 2016 2017
##  163  167  247
```

```r
# and for detection every method?

# qPCR
sum(table(miceTable$delta_ct_cewe_MminusE > -5 | miceTable$delta_ct_ilwe_MminusE > -5))
```

```
## [1] 364
```

```r
table(miceTable$delta_ct_cewe_MminusE > -5 | miceTable$delta_ct_ilwe_MminusE > -5)
```

```
##
## FALSE  TRUE
##   294    70
```

```r
# OPG
sum(table(miceTable$OPG > 0))
```

```
## [1] 463
```

```r
table(miceTable$OPG > 0)
```

```
##
## FALSE  TRUE
##   367    96
```

```
# species
sum(table(miceTable$eimeriaSpecies != "Negative"))
```
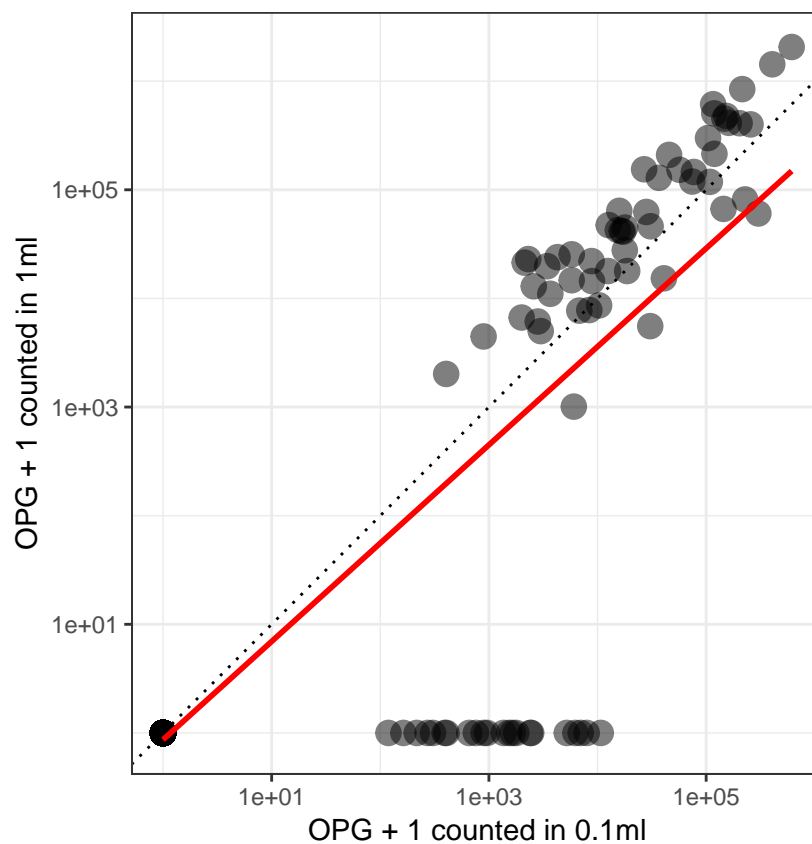
```
## [1] 560
```

```
table(miceTable$eimeriaSpecies != "Negative")
```

```
##
## FALSE  TRUE
##   459   101
```

Eimeria detection oocysts flotation

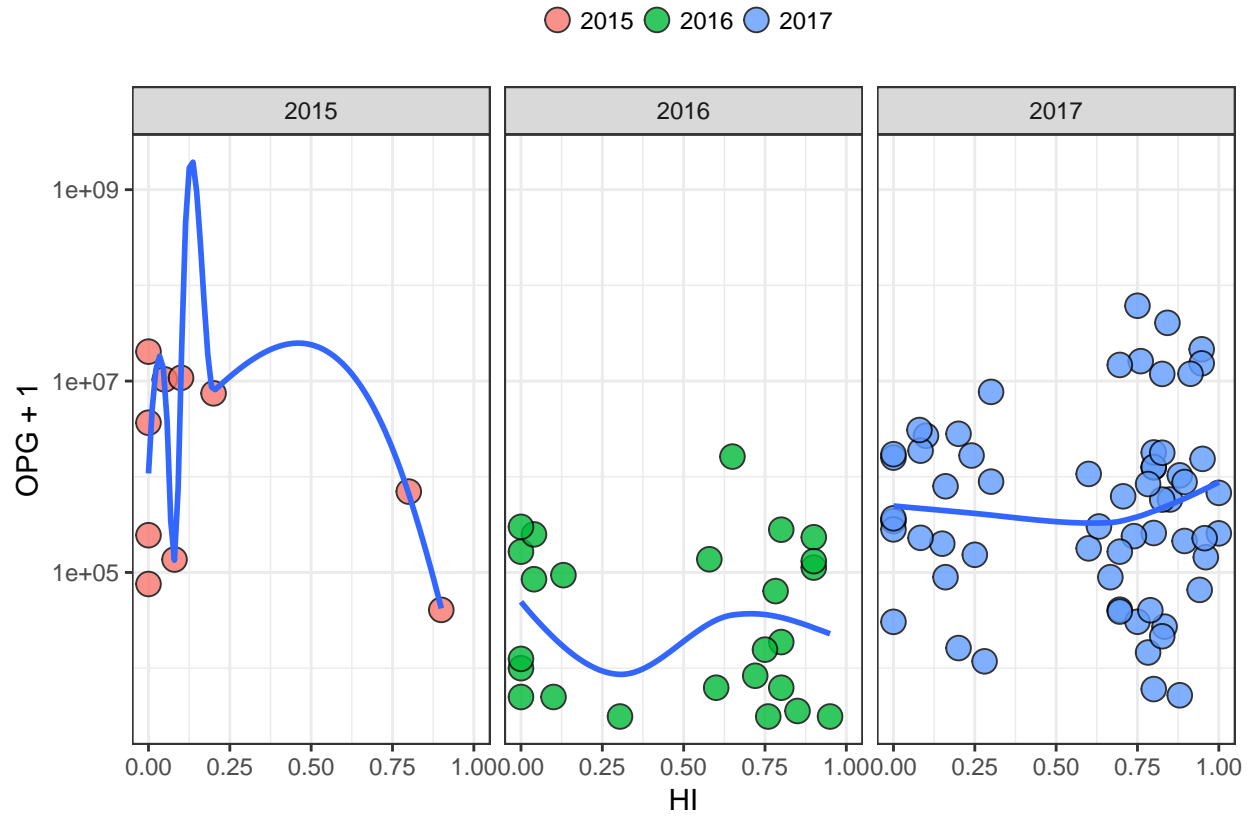### Improving Eimeria oocysts detection

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.

OPG that we keep

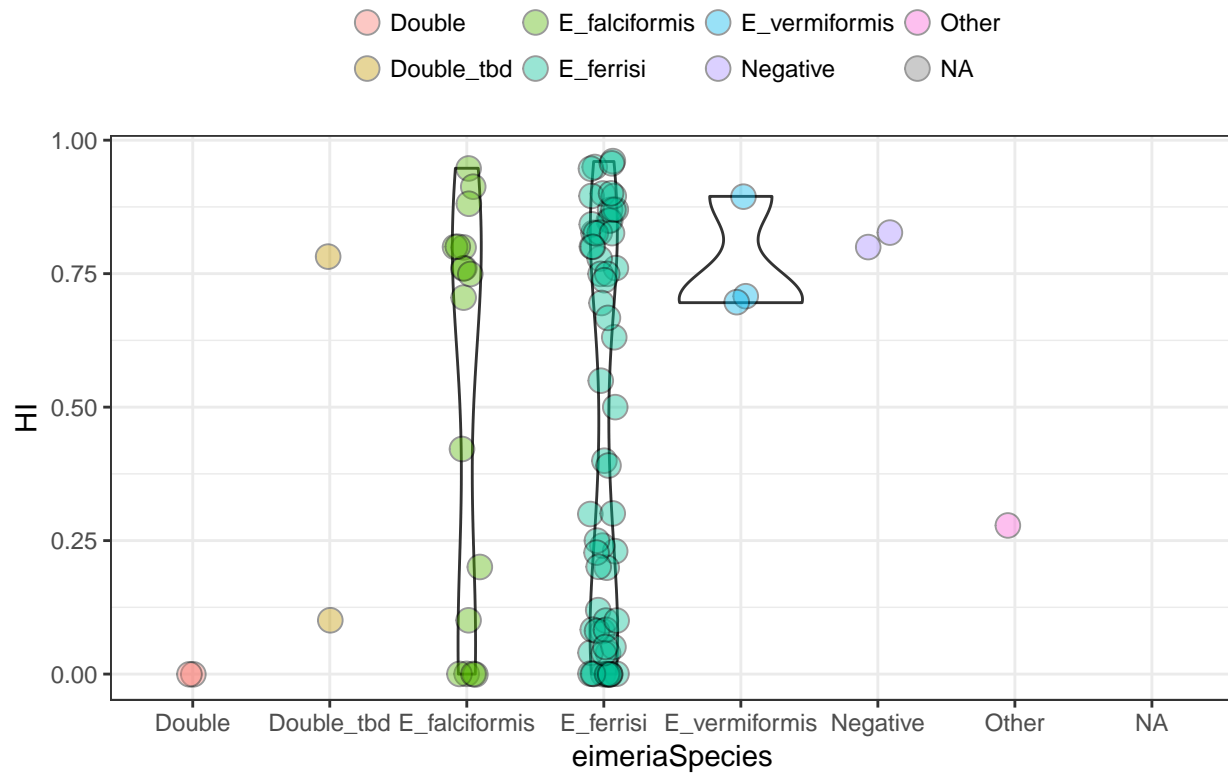Number of Mus musculus caught with OPG values: 463

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

Eimeria detection PCR

PCR positive = one of the 3 other markers than AP5 sequenced (Ap5 was used for detection only, the other markers for confirmation)
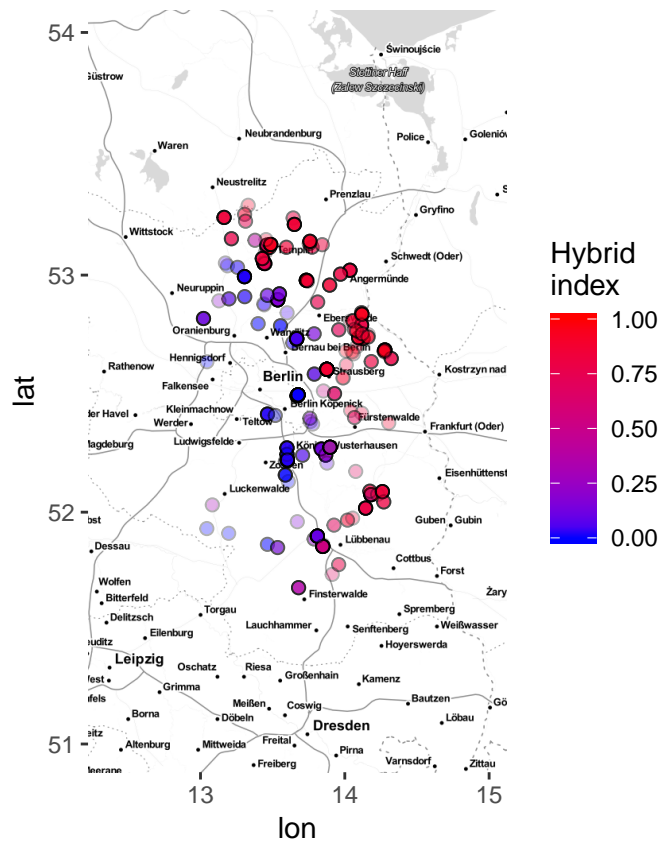
Violin plots on PCR data

PCR positive = one of the 3 markers 18S, COI or ORF470) gave a sequence. Number of Mus musculus caught with PCR performed: 560

General stats on sampling

```
## [1] 577
```

```
## [1] 136
```

```
## [1] 4.222222
```

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

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

AA_0411, AA_0412, AA_0420, AA_0464

General informations on HMHZ

- 577 mice were captured over three years, from 136 farms

- On average, 4.22 mice were caught per farm (95% CI 0.41)

- **Hybrid indexes** were calculated as ratio of M.m.d/M.m.m alleles (between 4 and 14, on average 13 loci)
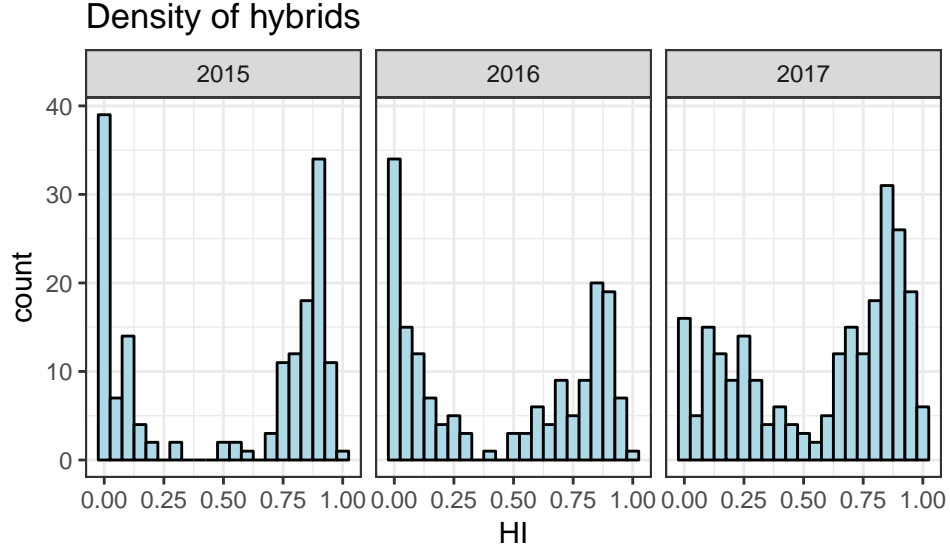
Density of hybrids

Figure 1: Number of animals caught along the hybrid index

Prevalence of our 3 different methods

Prevalence tables

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

	2015	2016	2017
FALSE	92.0	126.00	149.00
TRUE	10.0	25.00	61.00
total	102.0	151.00	210.00
prevalence(%)	9.8	16.56	29.05

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

	2015	2016	2017
FALSE	140.00	148.00	182.00
TRUE	12.00	19.00	59.00
total	152.00	167.00	241.00
prevalence(%)	7.89	11.38	24.48

Table 3: Prevalence of Eimeria per year, based on qPCR in cecum and ileum

	2015	2016	2017
FALSE	0	134.00	160.0
TRUE	0	31.00	39.0

	2015	2016	2017
total	0	165.00	199.0
prevalence(%)	NaN	18.79	19.6

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 in cecum tissue
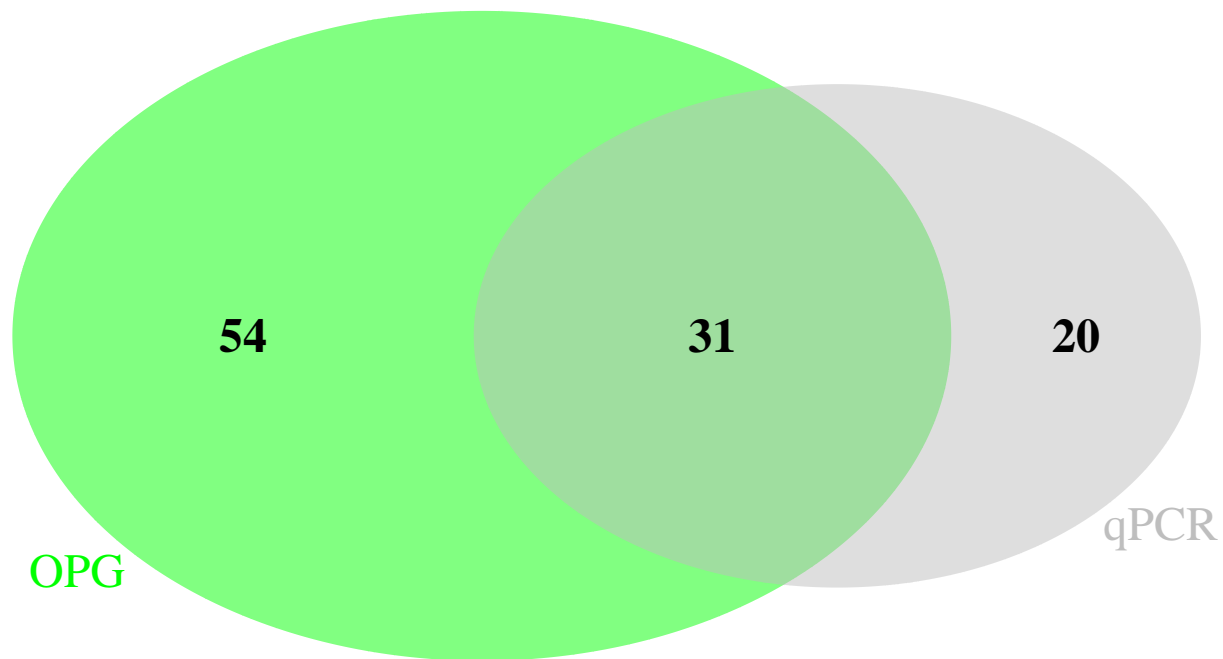
	2015	2016	2017
negative	146.00	122.00	158.00
positive	17.00	45.00	89.00
total	163.00	167.00	247.00
prevalence(%)	10.43	26.95	36.03

OPG-PCR
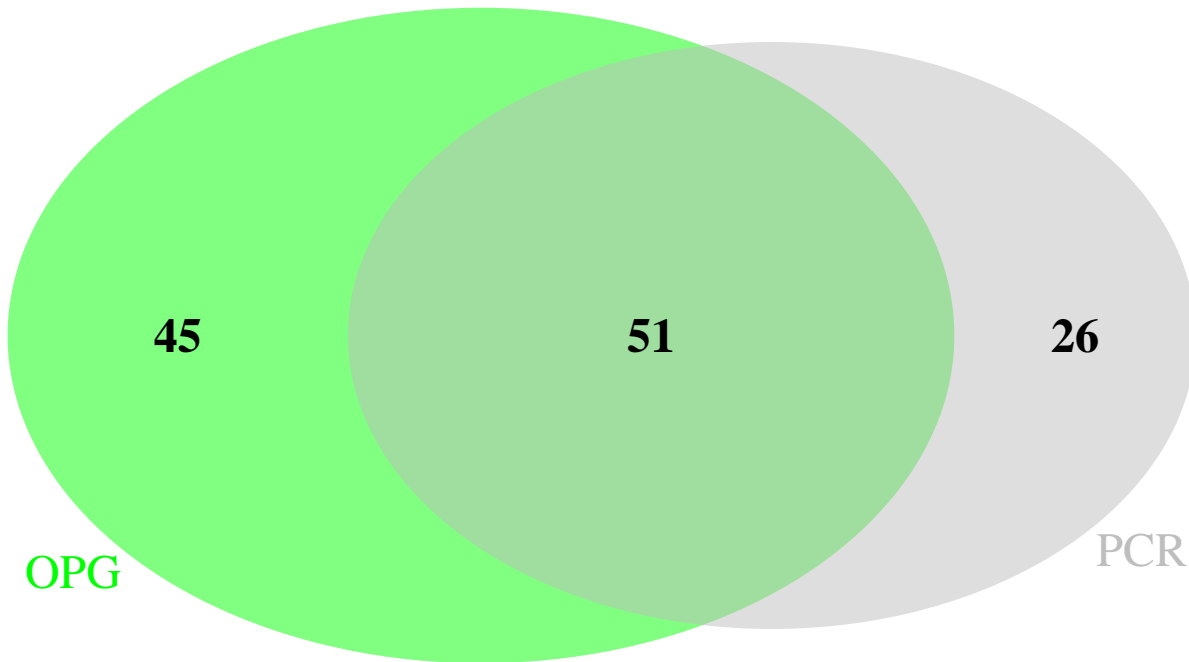
(polygon[GRID.polygon.502], polygon[GRID.polygon.503], polygon[GRID.polygon.504], polygon[GRID.polyg

OPG-qPCR

54   **31**   **20**

OPG

qPCR

```
## (polygon[GRID.polygon.511], polygon[GRID.polygon.512], polygon[GRID.polygon.513], polygon[GRID.polyg
```

OPG-qPCR-PCR

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?)