**Table S5**: GLMM script and output of recapping rate according to honey bee brood developmental stage in *A. cerana* in Hangzhou, China.

> library(car)

> library(emmeans)

> library(blmeco)

> library(ggforce)

> library(lme4)

> Stagenac <- read.csv(file.choose(),header=TRUE, sep=";")

> Stagenac$Colony <- as.factor(Stagenac$Colony)

> Stagenac$DevelopmentStage <- as.factor(Stagenac$DevelopmentStage)

>

> str(Stagenac)

'data.frame': 42 obs. of 5 variables:

$ Species : chr "Acerana" "Acerana" "Acerana" "Acerana" ...

$ Colony : Factor w/ 6 levels "AcC1","AcC10",..: 1 1 1 1 1 1 1 5 5 5 ...

$ DevelopmentStage: Factor w/ 7 levels "GreyThorax","PinkEye",..: 4 6 2 5 7 1 3 4 6 2 ...

$ NoRecap : int 36 7 3 15 42 16 20 41 9 4 ...

$ Recap : int 1 1 0 3 17 13 13 5 1 1 ...

>

> Stagenac$DevelopmentStage <- factor(Stagenac$DevelopmentStage, levels=c("PrePupa", "WhiteEye", "PinkEye", "PurpleEye", "YellowThorax", "GreyThorax", "PreAdult"))

> plot(Stagenac$DevelopmentStage, Stagenac$Recap/(Stagenac$Recap+Stagenac$NoRecap), ylab="proportion recapped cells", xlab="develpemental stage")

>

> msnac <- glmer(cbind(NoRecap,Recap)~DevelopmentStage+(1|Colony),data=Stagenac,family="binomial")

> summary(msnac)

Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']

Family: binomial ( logit )

Formula: cbind(NoRecap, Recap) ~ DevelopmentStage + (1 | Colony)

Data: Stagenac

AIC BIC logLik deviance df.resid

171.8 185.7 -77.9 155.8 34

Scaled residuals:

Min 1Q Median 3Q Max

-1.79954 -0.60937 0.09823 0.72070 1.62247

Random effects:

Groups Name Variance Std.Dev.

Colony (Intercept) 0.3302 0.5746

Number of obs: 42, groups: Colony, 6

Fixed effects:

Estimate Std. Error z value Pr(>|z|)

(Intercept) 2.91308 0.33758 8.629 < 2e-16 \*\*\*

DevelopmentStageWhiteEye -0.30804 0.49049 -0.628 0.5300

DevelopmentStagePinkEye -0.06782 0.57166 -0.119 0.9056

DevelopmentStagePurpleEye -0.86884 0.34279 -2.535 0.0113 \*

DevelopmentStageYellowThorax -1.46379 0.29899 -4.896 9.79e-07 \*\*\*

DevelopmentStageGreyThorax -1.72273 0.34104 -5.051 4.39e-07 \*\*\*

DevelopmentStagePreAdult -2.08917 0.32211 -6.486 8.82e-11 \*\*\*

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Correlation of Fixed Effects:

(Intr) DvlSWE DvlpmntStgPnE DvlpmntStgPrE DvlSYT DvlSGT

DvlpmntStWE -0.354

DvlpmntStgPnE -0.301 0.219

DvlpmntStgPrE -0.525 0.369 0.314

DvlpmntStYT -0.584 0.405 0.341 0.601

DvlpmntStGT -0.523 0.361 0.304 0.543 0.608

DvlpmntStPA -0.558 0.394 0.333 0.588 0.652 0.586

>

>

> Anova(msnac)

Analysis of Deviance Table (Type II Wald chisquare tests)

Response: cbind(NoRecap, Recap)

Chisq Df Pr(>Chisq)

DevelopmentStage 59.852 6 4.824e-11 \*\*\*

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

>

>

> emmeans(msnac, specs = pairwise ~ DevelopmentStage)

$emmeans

DevelopmentStage emmean SE df asymp.LCL asymp.UCL

PrePupa 2.913 0.338 Inf 2.251 3.57

WhiteEye 2.605 0.487 Inf 1.650 3.56

PinkEye 2.845 0.570 Inf 1.728 3.96

PurpleEye 2.044 0.331 Inf 1.395 2.69

YellowThorax 1.449 0.292 Inf 0.876 2.02

GreyThorax 1.190 0.331 Inf 0.541 1.84

PreAdult 0.824 0.310 Inf 0.216 1.43

Results are given on the logit (not the response) scale.

Confidence level used: 0.95

$contrasts

contrast estimate SE df z.ratio p.value

PrePupa - WhiteEye 0.3080 0.490 Inf 0.628 0.9959

PrePupa - PinkEye 0.0678 0.572 Inf 0.119 1.0000

PrePupa - PurpleEye 0.8688 0.343 Inf 2.535 0.1469

PrePupa - YellowThorax 1.4638 0.299 Inf 4.896 <.0001

PrePupa - GreyThorax 1.7227 0.341 Inf 5.051 <.0001

PrePupa - PreAdult 2.0892 0.322 Inf 6.486 <.0001

WhiteEye - PinkEye -0.2402 0.667 Inf -0.360 0.9998

WhiteEye - PurpleEye 0.5608 0.484 Inf 1.159 0.9092

WhiteEye - YellowThorax 1.1558 0.460 Inf 2.515 0.1538

WhiteEye - GreyThorax 1.4147 0.486 Inf 2.912 0.0555

WhiteEye - PreAdult 1.7811 0.469 Inf 3.800 0.0028

PinkEye - PurpleEye 0.8010 0.567 Inf 1.413 0.7948

PinkEye - YellowThorax 1.3960 0.547 Inf 2.551 0.1414

PinkEye - GreyThorax 1.6549 0.570 Inf 2.904 0.0567

PinkEye - PreAdult 2.0214 0.555 Inf 3.643 0.0050

PurpleEye - YellowThorax 0.5950 0.289 Inf 2.058 0.3783

PurpleEye - GreyThorax 0.8539 0.327 Inf 2.611 0.1224

PurpleEye - PreAdult 1.2203 0.302 Inf 4.035 0.0011

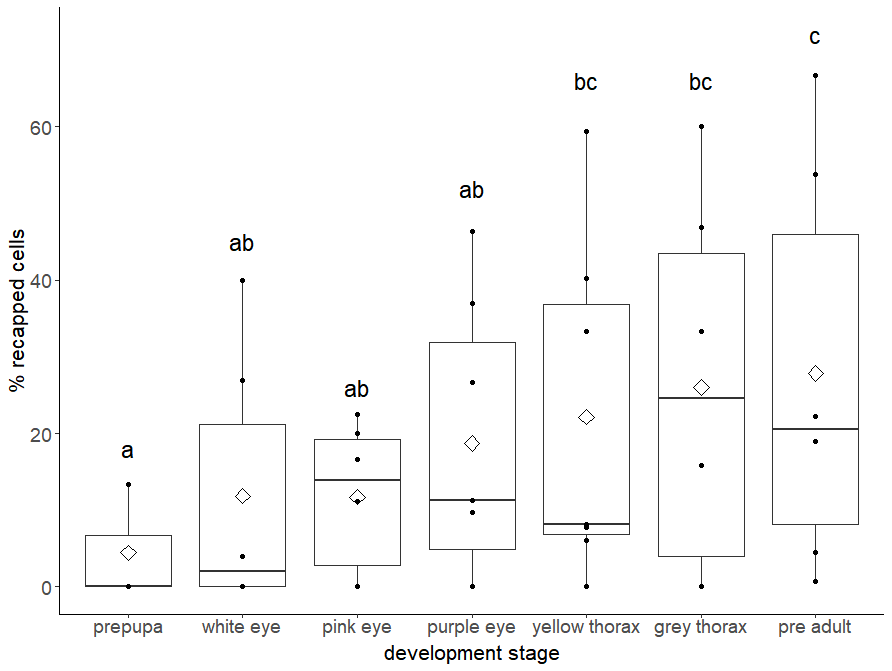
YellowThorax - GreyThorax 0.2589 0.286 Inf 0.906 0.9718

YellowThorax - PreAdult 0.6254 0.260 Inf 2.407 0.1954

GreyThorax - PreAdult 0.3664 0.302 Inf 1.213 0.8896

Results are given on the log odds ratio (not the response) scale.

P value adjustment: tukey method for comparing a family of 7 estimates



> dispersion\_glmer(msnac)

[1] 1.083709

>

> overdisp\_fun(msnac)

chisq ratio rdf p

35.1661089 1.0342973 34.0000000 0.4127192