

Report 1

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Trial data structure

Remarks

missing values

as per preregistration: if measurements were forgotten and cannot be done (e.g. weight not measure immediately before the test), the group average (e.g. among red averse females or among males with red face and red pedipalps) will be attributed to that individual FID 18401 has no weight (had a typo in the weight of both (before after) that could not be corrected)

FID 18401 has no weight (had a typo in the weight of both (before after) that could not be corrected) MID 18228 (paired with FID 18072) and MID 18390 (paired with FID 18478) have no weight averages as described were given to them

note: companion males were IDed but not weighted (only measured at maturity like all spiders)

dependent variables explanations

CopulateYN: copulation that occur at any time, during the video, seen after on the shelf, or extrapolated from the fact that spiderlings emerged

CannibaliseYN: cannibalism that accour during the 2h video or the 46 hours after that (after which male and female were separated)

CopDuringVideo: copulation that occured within the 2h video

EatDuringVideo: cannibalism that occured during the 2h video

decision of dependent variable as preregistered

is frequency of cannibalism within 48h between 15% and 85%?

[1] 36.1991

is frequency of copulation during video between 17% and 83%?

[1] 57.91855

as per preregistration, FTrt and MTrt were recoded as:

Female diet/training

red accustomed/preference group [code (relative to their preference for red) = +0.5]

red averse group [code (relative to their preference for red) = -0.5]

Male color manipulation

AllRed: (face and pedipalps painted red [code (amount of red body parts) = 2]

RedGrey: face painted red and pedipalps painted grey [code (amount of red body parts) = 1]

AllGrey: face and pedipalps painted grey [code (amount of red body parts) = 0]

Covariables explanations

M and **Fcondition** were calculated as $\text{resid}(\text{lm}(\text{Mass} \sim \text{CarapaceWidth}))$

DelayToLay is the difference between the lay date and the trial end date in days

Table structure

Remarks

this table does not include the *20 trials with unmanipulated males*

Out of 221 females tested with a painted male,

221-54 = 167 females laid clutched, of which

221-74 = 147 led to spiderlings (for which the brood size is always known - but for 4 of them the emergence date is not known)

##	FID	FTrt	TrialDate	CopulateYN
##	Min. :18064	RedAverse :109	2018-06-10: 9	Min. :0.0000
##	1st Qu.:18127	RedPreference:112	2018-06-24: 8	1st Qu.:0.0000
##	Median :18327		2018-07-10: 8	Median :1.0000
##	Mean :18306		2018-06-04: 6	Mean :0.6199
##	3rd Qu.:18474		2018-06-29: 6	3rd Qu.:1.0000
##	Max. :18577		2018-07-11: 6	Max. :1.0000
##			(Other) :178	
##	CopDuringVideo	CannibalizeYN	EatDuringVideo	
##	Min. :0.0000	Min. :0.000	Min. :0.0000	
##	1st Qu.:0.0000	1st Qu.:0.000	1st Qu.:0.0000	
##	Median :1.0000	Median :0.000	Median :0.0000	
##	Mean :0.5792	Mean :0.362	Mean :0.1176	
##	3rd Qu.:1.0000	3rd Qu.:1.000	3rd Qu.:0.0000	
##	Max. :1.0000	Max. :1.000	Max. :1.0000	
##				
##		CannibalismTime	CannibalismDate	
##	1899-12-30 08:00:00: 8		2018-06-11: 4	
##	1899-12-30 08:30:00: 7		2018-07-10: 4	
##	1899-12-30 08:15:00: 4		2018-06-05: 3	
##	1899-12-30 09:30:00: 3		2018-06-29: 3	
##	1899-12-30 16:00:00: 3		2018-07-01: 3	
##	(Other) : 48		(Other) : 57	
##	NA's :148		NA's :147	
##				
##			TestRemarks	FMass
##	copulation right after 2h video		: 2	Min. :0.00970
##	24h < cannibalism < 48h		: 1	1st Qu.:0.01660
##	6/26 copulation 8:45AM		: 1	Median :0.01830
##	camera died for one min between 8:30 and 8:31:		: 1	Mean :0.01878
##	camera tilted up		: 1	3rd Qu.:0.02110
##	(Other)		: 27	Max. :0.03390
##	NA's		:188	
##	FCarapaceWidth	MID	MTrt	
##	Min. :1.209	Min. :18140	AllGrey :73	
##	1st Qu.:1.501	1st Qu.:18221	AllRed :75	
##	Median :1.548	Median :18295	RedGrey :73	
##	Mean :1.556	Mean :18320	Unmanipulated: 0	
##	3rd Qu.:1.616	3rd Qu.:18408		
##	Max. :1.847	Max. :18584		
##				

```

##                               MalePaintingRemarks MCarapaceWidth
## picture with scale           : 54      Min.    :1.072
## put to sleep twice           : 9       1st Qu.:1.282
## clean eye with thinner       : 2       Median  :1.339
## put to sleep twice, clean eye with thinner: 2      Mean   :1.332
## a tiny bit of paint on top one chelicerae: 1      3rd Qu.:1.375
## (Other)                      : 26      Max.    :1.580
## NA's                        :127
##      MMass      CompanionID      TrialDateEnd      EmergenceDate
## Min.    :0.0056  Min.    :18140  2018-06-12: 8  2018-09-09: 8
## 1st Qu.:0.0111  1st Qu.:18245  2018-06-24: 7  2018-07-13: 5
## Median :0.0121  Median :18364  2018-07-01: 7  2018-07-26: 5
## Mean   :0.0125  Mean   :18354  2018-07-10: 6  2018-08-06: 5
## 3rd Qu.:0.0131  3rd Qu.:18439  2018-07-19: 6  2018-08-14: 5
## Max.   :0.0651  Max.   :18584  2018-07-30: 6  (Other)   :115
##                               (Other)   :181  NA's     : 78
##      BroodSize      DelaytoLay
## Min.    : 1.00  Min.    : 8.00
## 1st Qu.:16.00  1st Qu.: 12.00
## Median :22.00  Median : 15.00
## Mean   :23.49  Mean   : 21.44
## 3rd Qu.:28.50  3rd Qu.: 18.00
## Max.   :62.00  Max.   :194.00
## NA's   :74    NA's   :54
##                               BroodRemarks      Fcondition
## unsure of hatch date         : 5      Min.    :~-1.166e-02
## end date ealier              : 4      1st Qu.:~-1.282e-03
## end date earlier             : 3      Median  :~-2.292e-04
## a lot of dried out eggs      : 1      Mean    :~-6.833e-05
## about two weeks prior to 7/2. end date ealier: 1    3rd Qu.: 1.063e-03
## (Other)                     : 10     Max.    : 1.629e-02
## NA's                        :197
##      Mcondition      FTrtCode      MTrtCode
## Min.    :~-4.861e-03  Min.    :~-0.500000  Min.    :0.000
## 1st Qu.:~-1.127e-03  1st Qu.:~-0.500000  1st Qu.:0.000
## Median :~-4.316e-04  Median : 0.500000  Median :1.000
## Mean   : 1.878e-05  Mean   : 0.006787  Mean   :1.009
## 3rd Qu.: 3.694e-04  3rd Qu.: 0.500000  3rd Qu.:2.000
## Max.   : 4.848e-02  Max.   : 0.500000  Max.   :2.000
##

```

Results Raw Data

Sample sizes of tests

```

##      FTrt AllGrey AllRed RedGrey Unmanipulated
## 1      RedAverse    36    37    36          10
## 2 RedPreference    37    38    37          10

```

Number of tests (and percentages) where copulation was seen during the video (note that this may change slightly as we havent finish watching them so we may have misidentified a copulation when watching live or missed one - both these events are rare)

```

##      FTrt AllGrey AllRed RedGrey Unmanipulated
## 1      RedAverse    23    18    25          6
## 2 RedPreference    22    22    18          6

```

```
##           FTrt AllGrey AllRed RedGrey Unmanipulated
## 1 RedAverse 63.88889 48.64865 69.44444          60
## 2 RedPreference 59.45946 57.89474 48.64865          60
```

Number of tests where cannibalism occurred during the 48h allocated

```
##           FTrt AllGrey AllRed RedGrey Unmanipulated
## 1 RedAverse      12      15      16          6
## 2 RedPreference      12      10      15          4

##           FTrt AllGrey AllRed RedGrey Unmanipulated
## 1 RedAverse 33.33333 40.54054 44.44444          60
## 2 RedPreference 32.43243 26.31579 40.54054          40
```

Preregistered Analyses on Copulation and Cannibalism

in preregistration

Model 1: glm (CannibalismY/N ~ male treatment * female treatment + female body condition, family = binomial).

Model 2: glm (CannibalismY/N ~ female treatment + female body condition, family = binomial)

Model 3: glm (CopulationY/N ~ male treatment * female treatment + male size + male body condition, family = binomial).

Model 4: glm (CopulationY/N ~ female treatment + male size + male body condition, family = binomial).

If Fcondition is significantly leading to more cannibalism this should be removed (Preregistered)

FCondition was positively significant in the cannibalism model so it is silenced in the models below

```
# Model 1
modCannibalism <- glm (CannibalizeYN ~ FTrtCode* MTrtCode
                      #+ Fcondition
                      , family = "binomial", data = MY_TABLE)

summary(modCannibalism)
```

```
##
## Call:
## glm(formula = CannibalizeYN ~ FTrtCode * MTrtCode, family = "binomial",
##      data = MY_TABLE)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.0604  -0.9480  -0.8952   1.3652   1.5522
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -0.57403    0.22255  -2.579   0.0099 **
## FTrtCode         0.01430    0.44511   0.032   0.9744
## MTrtCode        0.00454    0.17197   0.026   0.9789
```

```
## FTrtCode:MTrtCode -0.29045    0.34393  -0.844   0.3984
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 289.31  on 220  degrees of freedom
## Residual deviance: 287.61  on 217  degrees of freedom
## AIC: 295.61
##
## Number of Fisher Scoring iterations: 4
```

```
# Model 2
modCannibalism2 <- glm (CannibalizeYN ~ FTrtCode
                        #+ Fcondition
                        , family = "binomial", data = MY_TABLE)

summary(modCannibalism2)
```

```
##
## Call:
## glm(formula = CannibalizeYN ~ FTrtCode, family = "binomial",
##      data = MY_TABLE)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.0017  -1.0017  -0.8956   1.3639   1.4883
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -0.5675     0.1403  -4.044 5.25e-05 ***
## FTrtCode      -0.2781     0.2807  -0.991   0.322
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 289.31  on 220  degrees of freedom
## Residual deviance: 288.33  on 219  degrees of freedom
## AIC: 292.33
##
## Number of Fisher Scoring iterations: 4
```

```
# Model 3
modCop <- glm (CopDuringVideo ~ FTrtCode* MTrtCode + MCarapaceWidth + Mcondition
              , family = "binomial", data = MY_TABLE)

summary(modCop)
```

```
##
## Call:
## glm(formula = CopDuringVideo ~ FTrtCode * MTrtCode + MCarapaceWidth +
##      Mcondition, family = "binomial", data = MY_TABLE)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.651  -1.251   0.915   1.070   1.296
```

```
##
## Coefficients:
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -1.7654     2.6427  -0.668   0.504
## FTrtCode      -0.5422     0.4455  -1.217   0.224
## MTrtCode      -0.1809     0.1691  -1.070   0.285
## MCarapaceWidth  1.7080     1.9806   0.862   0.388
## Mcondition    -7.2680    33.2151  -0.219   0.827
## FTrtCode:MTrtCode  0.3122     0.3376   0.925   0.355
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 300.80  on 220  degrees of freedom
## Residual deviance: 297.58  on 215  degrees of freedom
## AIC: 309.58
##
## Number of Fisher Scoring iterations: 4
# Model 4
modCop2 <- glm (CopDuringVideo ~ FTrtCode + MCarapaceWidth + Mcondition
               , family = "binomial", data = MY_TABLE)
summary(modCop2)

##
## Call:
## glm(formula = CopDuringVideo ~ FTrtCode + MCarapaceWidth + Mcondition,
##      family = "binomial", data = MY_TABLE)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.4855  -1.2911   0.9732   1.0511   1.2682
##
## Coefficients:
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -1.7851     2.6160  -0.682   0.495
## FTrtCode      -0.2203     0.2743  -0.803   0.422
## MCarapaceWidth  1.5827     1.9632   0.806   0.420
## Mcondition    -4.4557    33.1516  -0.134   0.893
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 300.80  on 220  degrees of freedom
## Residual deviance: 299.53  on 217  degrees of freedom
## AIC: 307.53
##
## Number of Fisher Scoring iterations: 4
```