

# Development and characterization of microsatellite markers for the tsetse species *Glossina brevipalpis* and preliminary population genetics analyses

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```
setwd("C:/Users/GSTOTTENMF/OneDrive - IAEA/Desktop/Manuscript V7/Submission/D
ata_repository")

library(ggplot2)
library(MASS)
library(rmarkdown)
library(knitr)
library(lme4)
library(MuMIn)
library(ggthemes)
library(datasets)
library(plyr)
library(dplyr)
library(tidyverse)
library(coin)

### Analysis of all loci on all samples
### Linkage disequilibrium: BY correction for all loci
p.adjust(c(0.3229, 0.5156, 1, 0.001, 0.6289, 0.8639, 0.7811, 0.8109, 0.874
9, 0.3022, 0.6471, 0.1094, 0.0072, 0.0763, 0.0103, 0.079, 0.9676, 0.2757, 0.
1998, 0.544, 0.5839, 0.0206, 0.3982, 0.2224, 1, 0.9607, 0.3872, 0.1506, 0.4
215, 0.2636, 1, 0.4142, 0.5945, 0.2685, 0.3466, 0.0648, 0.4681, 0.5652, 0.86
01, 0.4104, 0.3353, 0.8572, 0.4667, 0.8822, 0.6735), method = "BY")

## [1] 1.0000000 1.0000000 1.0000000 0.1977727 1.0000000 1.0000000 1.0000000
## [8] 1.0000000 1.0000000 1.0000000 1.0000000 1.0000000 0.6790195 1.0000000
## [15] 0.6790195 1.0000000 1.0000000 1.0000000 1.0000000 1.0000000 1.0000000
## [22] 1.0000000 1.0000000 1.0000000 1.0000000 1.0000000 1.0000000 1.0000000
## [29] 1.0000000 1.0000000 1.0000000 1.0000000 1.0000000 1.0000000 1.0000000
## [36] 1.0000000 1.0000000 1.0000000 1.0000000 1.0000000 1.0000000 1.0000000
## [43] 1.0000000 1.0000000 1.0000000

### Correlation between FIS and FST for all loci on all samples
FISFST <- read.csv("FISFST_allloci_allsamples.csv", sep=",", row.names=NULL)
FISFST
```

```

##      Locus   FST   FIS
## 1     Gb5 0.099 0.053
## 2     Gb28 0.121 0.109
## 3     Gb35 0.122 0.435
## 4     Gb48 0.108 0.052
## 5     Gb66 0.057 0.046
## 6     Gb72 0.082 -0.056
## 7     Gb73 0.155 0.285
## 8     Gb92 0.132 0.026
## 9     Gb158 0.123 -0.070
## 10    Gb165 0.167 -0.131

with(FISFST, cor.test(FST, FIS, alternative="greater", method="spearman"))

##
## Spearman's rank correlation rho
##
## data:  FST and FIS
## S = 184, p-value = 0.6336
## alternative hypothesis: true rho is greater than 0
## sample estimates:
##      rho
## -0.1151515

### Correlation between FIS and number of blanks for all Loci on all samples
FISblanksall <- read.csv("FISblanks_allloci_allsamples.csv", sep=",", row.names=NULL)
FISblanksall

##      Locus Nb   FIS
## 1     Gb5  2 0.053
## 2     Gb28  8 0.109
## 3     Gb35 10 0.435
## 4     Gb48 20 0.052
## 5     Gb66  1 0.046
## 6     Gb72  4 -0.056
## 7     Gb73  5 0.285
## 8     Gb92  8 0.026
## 9     Gb158 8 -0.070
## 10    Gb165 8 -0.131

with(FISblanksall, cor.test(Nb, FIS, alternative="greater", method="spearman"))

## Warning in cor.test.default(Nb, FIS, alternative = "greater", method =
## "spearman"): Cannot compute exact p-value with ties

##
## Spearman's rank correlation rho
##
## data:  Nb and FIS

```

```

## S = 146.43, p-value = 0.3784
## alternative hypothesis: true rho is greater than 0
## sample estimates:
##      rho
## 0.112555

### Correlation between FIS and number of blanks for 7 Loci (Gb5, 28, 35, 66,
73, 92, 165) on all samples
FISblanks7lociall <- read.csv("FISblanks_7loci_allsamples.csv", sep=",", row.
names=NULL)
FISblanks7lociall

##   Locus Nb    FIS
## 1   Gb5  2  0.053
## 2  Gb28  8  0.109
## 3  Gb35 10  0.435
## 4  Gb66  1  0.046
## 5  Gb73  5  0.285
## 6  Gb92  8  0.026
## 7 Gb165  8 -0.131

with(FISblanks7lociall, cor.test(Nb, FIS, alternative="greater", method="spea
rman"))

## Warning in cor.test.default(Nb, FIS, alternative = "greater", method =
## "spearman"): Cannot compute exact p-value with ties

##
## Spearman's rank correlation rho
##
## data:  Nb and FIS
## S = 43.547, p-value = 0.3159
## alternative hypothesis: true rho is greater than 0
## sample estimates:
##      rho
## 0.2223748

### Correlation between FIS and number of blanks for 4 Loci (Gb 5, 35, 66, 73
) on all samples
FISblanks4lociall <- read.csv("FISblanks_4loci_allsamples.csv", sep=",", row.
names=NULL)
FISblanks4lociall

##   Locus Nb    FIS
## 1   Gb5  2  0.053
## 2  Gb35 10  0.435
## 3  Gb66  1  0.046
## 4  Gb73  5  0.285

with(FISblanks4lociall, cor.test(Nb, FIS, alternative="greater", method="spea
rman"))

```

```
##
## Spearman's rank correlation rho
##
## data: Nb and FIS
## S = 0, p-value = 0.04167
## alternative hypothesis: true rho is greater than 0
## sample estimates:
## rho
## 1
```

### Short allele dominance

```
SAD <- read.csv("SAD.csv", sep=",", row.names=NULL)
```

```
SAD
```

##	loci	Allele	Capf	p..All.W.	Smallf	Weights
## 1	Gb28	227	0.297	NA	NA	NA
## 2	Gb28	228	-0.033	NA	NA	NA
## 3	Gb28	229	0.099	NA	NA	NA
## 4	Gb28	231	0.368	NA	NA	NA
## 5	Gb28	233	0.281	NA	NA	NA
## 6	Gb28	235	0.020	NA	NA	NA
## 7	Gb28	237	-0.004	NA	NA	NA
## 8	Gb28	239	0.010	NA	NA	NA
## 9	Gb28	247	0.478	NA	NA	NA
## 10	Gb28	249	-0.009	NA	NA	NA
## 11	Gb28	257	-0.005	NA	NA	NA
## 12	Gb28	281	0.055	NA	NA	NA
## 13	Gb35	193	1.000	0.014	NA	0.014198783
## 14	Gb35	199	0.413	0.049	NA	0.051524711
## 15	Gb35	205	0.430	0.118	NA	0.133786848
## 16	Gb35	221	0.468	0.153	NA	0.180637544
## 17	Gb35	223	0.027	0.007	NA	0.007049345
## 18	Gb35	227	0.387	0.035	NA	0.036269430
## 19	Gb35	229	0.431	0.326	NA	0.483679525
## 20	Gb35	233	0.643	0.208	NA	0.262626263
## 21	Gb35	235	0.549	0.049	NA	0.051524711
## 22	Gb35	239	0.658	0.042	NA	0.043841336
## 23	Gb48	229	-0.004	0.025	-0.059	0.024375000
## 24	Gb48	251	0.072	0.008	-0.286	0.007936000
## 25	Gb48	253	0.150	0.083	0.091	0.076111000
## 26	Gb48	255	0.183	0.358	0.149	0.229836000
## 27	Gb48	257	0.454	0.217	0.281	0.169911000
## 28	Gb48	259	0.005	0.008	-0.014	0.007936000
## 29	Gb48	261	0.003	0.025	-0.080	0.024375000
## 30	Gb48	264	-0.024	0.042	-0.070	0.040236000
## 31	Gb48	265	0.008	0.008	-0.024	0.007936000
## 32	Gb48	266	-0.096	0.117	-0.212	0.103311000
## 33	Gb48	268	-0.007	0.025	-0.047	0.024375000
## 34	Gb48	269	-0.013	0.017	0.005	0.016711000
## 35	Gb48	277	0.018	0.042	-0.223	0.040236000

##	36	Gb48	279	0.026	0.025	-0.167	0.024375000
##	37	Gb5	219	0.027	0.006	NA	0.006036217
##	38	Gb5	225	0.266	0.043	NA	0.044932079
##	39	Gb5	227	0.461	0.116	NA	0.131221719
##	40	Gb5	229	-0.080	0.098	NA	0.108647450
##	41	Gb5	231	-0.027	0.037	NA	0.038421599
##	42	Gb5	233	0.265	0.043	NA	0.044932079
##	43	Gb5	235	0.217	0.183	NA	0.223990208
##	44	Gb5	237	-0.019	0.024	NA	0.024590164
##	45	Gb5	239	0.046	0.098	NA	0.108647450
##	46	Gb5	241	-0.030	0.037	NA	0.038421599
##	47	Gb5	243	0.275	0.146	NA	0.170960187
##	48	Gb5	245	-0.117	0.116	NA	0.131221719
##	49	Gb5	247	0.199	0.055	NA	0.058201058
##	50	Gb66	202	0.006	0.006	NA	0.006036217
##	51	Gb66	211	-0.049	0.183	NA	0.223990208
##	52	Gb66	214	-0.007	0.006	NA	0.006036217
##	53	Gb66	220	0.005	0.037	NA	0.038421599
##	54	Gb66	223	-0.005	0.055	NA	0.058201058
##	55	Gb66	226	0.069	0.085	NA	0.092896175
##	56	Gb66	229	0.221	0.049	NA	0.051524711
##	57	Gb66	232	0.155	0.140	NA	0.162790698
##	58	Gb66	235	-0.008	0.043	NA	0.044932079
##	59	Gb66	241	0.078	0.079	NA	0.085776330
##	60	Gb66	244	0.204	0.250	NA	0.333333333
##	61	Gb66	247	0.322	0.037	NA	0.038421599
##	62	Gb66	256	0.003	0.018	NA	0.018329939
##	63	Gb66	259	0.000	0.012	NA	0.012145749
##	64	Gb72	207	-0.030	0.056	NA	0.059322034
##	65	Gb72	211	0.516	0.025	NA	0.025641026
##	66	Gb72	213	0.109	0.075	NA	0.081081081
##	67	Gb72	215	-0.026	0.044	NA	0.046025105
##	68	Gb72	217	-0.024	0.038	NA	0.039501040
##	69	Gb72	219	0.113	0.206	NA	0.259445844
##	70	Gb72	221	-0.067	0.300	NA	0.428571429
##	71	Gb72	223	0.064	0.119	NA	0.135073780
##	72	Gb72	225	-0.039	0.063	NA	0.067235859
##	73	Gb72	227	-0.014	0.019	NA	0.019367992
##	74	Gb72	231	-0.018	0.031	NA	0.031991744
##	75	Gb72	235	-0.008	0.006	NA	0.006036217
##	76	Gb72	239	-0.005	0.013	NA	0.013171226
##	77	Gb72	245	0.008	0.006	NA	0.006036217
##	78	Gb158	187	-0.075	0.086	NA	0.094091904
##	79	Gb158	191	0.012	0.026	NA	0.026694045
##	80	Gb158	193	0.115	0.336	NA	0.506024096
##	81	Gb158	195	0.070	0.257	NA	0.345895020
##	82	Gb158	197	-0.025	0.132	NA	0.152073733
##	83	Gb158	199	0.243	0.099	NA	0.109877913
##	84	Gb158	201	0.027	0.007	NA	0.007049345
##	85	Gb158	205	-0.056	0.059	NA	0.062699256

```

## 86 Gb165 210 -0.152 0.547 NA 1.207505519
## 87 Gb165 212 0.280 0.267 NA 0.364256480
## 88 Gb165 214 0.269 0.087 NA 0.095290252
## 89 Gb165 218 -0.007 0.007 NA 0.007049345
## 90 Gb165 220 -0.066 0.093 NA 0.102535832
## 91 Gb73 228 0.369 0.095 NA 0.104972376
## 92 Gb73 230 0.132 0.070 NA 0.075268817
## 93 Gb73 238 -0.010 0.013 NA 0.013171226
## 94 Gb73 240 0.806 0.089 NA 0.097694841
## 95 Gb73 242 0.495 0.095 NA 0.104972376
## 96 Gb73 244 -0.044 0.051 NA 0.053740780
## 97 Gb73 246 0.396 0.089 NA 0.097694841
## 98 Gb73 248 0.543 0.247 NA 0.328021248
## 99 Gb73 250 0.334 0.228 NA 0.295336788
## 100 Gb73 254 0.005 0.013 NA 0.013171226
## 101 Gb73 256 -0.001 0.013 NA 0.013171226
## 102 Gb92 278 -0.011 NA NA NA
## 103 Gb92 282 0.330 NA NA NA
## 104 Gb92 284 0.005 NA NA NA
## 105 Gb92 286 -0.005 NA NA NA
## 106 Gb92 290 -0.045 NA NA NA
## 107 Gb92 292 0.326 NA NA NA
## 108 Gb92 294 0.073 NA NA NA
## 109 Gb92 300 -0.018 NA NA NA
## 110 Gb92 302 0.069 NA NA NA
## 111 Gb92 304 0.256 NA NA NA
## 112 Gb92 306 0.013 NA NA NA
## 113 Gb92 314 -0.010 NA NA NA

```

```
SAD_Gb28 <- subset(SAD, loci=="Gb28")
```

```
SAD_Gb28
```

```

##   loci Allele  Capf p..All.W. Smallf Weights
## 1 Gb28 227 0.297 NA NA NA
## 2 Gb28 228 -0.033 NA NA NA
## 3 Gb28 229 0.099 NA NA NA
## 4 Gb28 231 0.368 NA NA NA
## 5 Gb28 233 0.281 NA NA NA
## 6 Gb28 235 0.020 NA NA NA
## 7 Gb28 237 -0.004 NA NA NA
## 8 Gb28 239 0.010 NA NA NA
## 9 Gb28 247 0.478 NA NA NA
## 10 Gb28 249 -0.009 NA NA NA
## 11 Gb28 257 -0.005 NA NA NA
## 12 Gb28 281 0.055 NA NA NA

```

```
with(SAD_Gb28, cor.test(Allele, Capf, alternative="less", method="spearman"))
```

```

##
## Spearman's rank correlation rho
##

```

```

## data: Allele and Capf
## S = 352, p-value = 0.2355
## alternative hypothesis: true rho is less than 0
## sample estimates:
##      rho
## -0.2307692

SAD_Gb35 <- subset(SAD,loci=="Gb35")
SAD_Gb35

##   loci Allele  Capf p..All.W. Smallf  Weights
## 13 Gb35   193 1.000   0.014    NA 0.014198783
## 14 Gb35   199 0.413   0.049    NA 0.051524711
## 15 Gb35   205 0.430   0.118    NA 0.133786848
## 16 Gb35   221 0.468   0.153    NA 0.180637544
## 17 Gb35   223 0.027   0.007    NA 0.007049345
## 18 Gb35   227 0.387   0.035    NA 0.036269430
## 19 Gb35   229 0.431   0.326    NA 0.483679525
## 20 Gb35   233 0.643   0.208    NA 0.262626263
## 21 Gb35   235 0.549   0.049    NA 0.051524711
## 22 Gb35   239 0.658   0.042    NA 0.043841336

with(SAD_Gb35, cor.test(Allele, Capf, alternative="less", method="spearman"))

##
## Spearman's rank correlation rho
##
## data: Allele and Capf
## S = 128, p-value = 0.7431
## alternative hypothesis: true rho is less than 0
## sample estimates:
##      rho
## 0.2242424

SAD_Gb48 <- subset(SAD,loci=="Gb48")
SAD_Gb48

##   loci Allele  Capf p..All.W. Smallf  Weights
## 23 Gb48   229 -0.004   0.025 -0.059 0.024375
## 24 Gb48   251 0.072   0.008 -0.286 0.007936
## 25 Gb48   253 0.150   0.083 0.091 0.076111
## 26 Gb48   255 0.183   0.358 0.149 0.229836
## 27 Gb48   257 0.454   0.217 0.281 0.169911
## 28 Gb48   259 0.005   0.008 -0.014 0.007936
## 29 Gb48   261 0.003   0.025 -0.080 0.024375
## 30 Gb48   264 -0.024   0.042 -0.070 0.040236
## 31 Gb48   265 0.008   0.008 -0.024 0.007936
## 32 Gb48   266 -0.096   0.117 -0.212 0.103311
## 33 Gb48   268 -0.007   0.025 -0.047 0.024375
## 34 Gb48   269 -0.013   0.017 0.005 0.016711

```

```

## 35 Gb48      277  0.018      0.042 -0.223 0.040236
## 36 Gb48      279  0.026      0.025 -0.167 0.024375

with(SAD_Gb48, cor.test Allele, Capf, alternative="less", method="spearman"))

##
## Spearman's rank correlation rho
##
## data: Allele and Capf
## S = 622, p-value = 0.09867
## alternative hypothesis: true rho is less than 0
## sample estimates:
##      rho
## -0.367033

with(SAD_Gb48, cor.test(Smallf, Weights, alternative="less", method="spearman
"))

## Warning in cor.test.default(Smallf, Weights, alternative = "less", method
=
## "spearman"): Cannot compute exact p-value with ties

##
## Spearman's rank correlation rho
##
## data: Smallf and Weights
## S = 331.95, p-value = 0.8251
## alternative hypothesis: true rho is less than 0
## sample estimates:
##      rho
## 0.270429

lm_SAD_Gb48 <- lm(Smallf ~ Allele, data=SAD_Gb48, Weights=weight)

## Warning: In lm.fit(x, y, offset = offset, singular.ok = singular.ok, ...)
:
## extra argument 'Weights' will be disregarded

summary(lm_SAD_Gb48)

##
## Call:
## lm(formula = Smallf ~ Allele, data = SAD_Gb48, Weights = weight)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.270353 -0.100216  0.004299  0.066836  0.315508
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.773365   0.897041   0.862   0.406
## Allele      -0.003143   0.003434  -0.915   0.378

```



```

##
## Residual standard error: 0.1531 on 12 degrees of freedom
## Multiple R-squared: 0.06526, Adjusted R-squared: -0.01263
## F-statistic: 0.8378 on 1 and 12 DF, p-value: 0.3781

SAD_Gb5 <- subset(SAD,loci=="Gb5")
SAD_Gb5

## loci Allele Capf p..All.W. Smallf Weights
## 37 Gb5 219 0.027 0.006 NA 0.006036217
## 38 Gb5 225 0.266 0.043 NA 0.044932079
## 39 Gb5 227 0.461 0.116 NA 0.131221719
## 40 Gb5 229 -0.080 0.098 NA 0.108647450
## 41 Gb5 231 -0.027 0.037 NA 0.038421599
## 42 Gb5 233 0.265 0.043 NA 0.044932079
## 43 Gb5 235 0.217 0.183 NA 0.223990208
## 44 Gb5 237 -0.019 0.024 NA 0.024590164
## 45 Gb5 239 0.046 0.098 NA 0.108647450
## 46 Gb5 241 -0.030 0.037 NA 0.038421599
## 47 Gb5 243 0.275 0.146 NA 0.170960187
## 48 Gb5 245 -0.117 0.116 NA 0.131221719
## 49 Gb5 247 0.199 0.055 NA 0.058201058

with(SAD_Gb5, cor.test(Allele, Capf, alternative="less", method="spearman"))

##
## Spearman's rank correlation rho
##
## data: Allele and Capf
## S = 440, p-value = 0.2467
## alternative hypothesis: true rho is less than 0
## sample estimates:
## rho
## -0.2087912

SAD_Gb66 <- subset(SAD,loci=="Gb66")
SAD_Gb66

## loci Allele Capf p..All.W. Smallf Weights
## 50 Gb66 202 0.006 0.006 NA 0.006036217
## 51 Gb66 211 -0.049 0.183 NA 0.223990208
## 52 Gb66 214 -0.007 0.006 NA 0.006036217
## 53 Gb66 220 0.005 0.037 NA 0.038421599
## 54 Gb66 223 -0.005 0.055 NA 0.058201058
## 55 Gb66 226 0.069 0.085 NA 0.092896175
## 56 Gb66 229 0.221 0.049 NA 0.051524711
## 57 Gb66 232 0.155 0.140 NA 0.162790698
## 58 Gb66 235 -0.008 0.043 NA 0.044932079
## 59 Gb66 241 0.078 0.079 NA 0.085776330
## 60 Gb66 244 0.204 0.250 NA 0.333333333
## 61 Gb66 247 0.322 0.037 NA 0.038421599

```

```

## 62 Gb66      256  0.003      0.018      NA 0.018329939
## 63 Gb66      259  0.000      0.012      NA 0.012145749

with(SAD_Gb66, cor.test Allele, Capf, alternative="less", method="spearman"))

##
## Spearman's rank correlation rho
##
## data: Allele and Capf
## S = 298, p-value = 0.8895
## alternative hypothesis: true rho is less than 0
## sample estimates:
##      rho
## 0.3450549

SAD_Gb72 <- subset(SAD, loci=="Gb72")
SAD_Gb72

##      loci Allele  Capf p..All.W. Smallf      Weights
## 64 Gb72      207 -0.030      0.056      NA 0.059322034
## 65 Gb72      211  0.516      0.025      NA 0.025641026
## 66 Gb72      213  0.109      0.075      NA 0.081081081
## 67 Gb72      215 -0.026      0.044      NA 0.046025105
## 68 Gb72      217 -0.024      0.038      NA 0.039501040
## 69 Gb72      219  0.113      0.206      NA 0.259445844
## 70 Gb72      221 -0.067      0.300      NA 0.428571429
## 71 Gb72      223  0.064      0.119      NA 0.135073780
## 72 Gb72      225 -0.039      0.063      NA 0.067235859
## 73 Gb72      227 -0.014      0.019      NA 0.019367992
## 74 Gb72      231 -0.018      0.031      NA 0.031991744
## 75 Gb72      235 -0.008      0.006      NA 0.006036217
## 76 Gb72      239 -0.005      0.013      NA 0.013171226
## 77 Gb72      245  0.008      0.006      NA 0.006036217

with(SAD_Gb72, cor.test Allele, Capf, alternative="less", method="spearman"))

##
## Spearman's rank correlation rho
##
## data: Allele and Capf
## S = 454, p-value = 0.506
## alternative hypothesis: true rho is less than 0
## sample estimates:
##      rho
## 0.002197802

SAD_Gb158 <- subset(SAD, loci=="Gb158")
SAD_Gb158

##      loci Allele  Capf p..All.W. Smallf      Weights
## 78 Gb158      187 -0.075      0.086      NA 0.094091904
## 79 Gb158      191  0.012      0.026      NA 0.026694045

```

```

## 80 Gb158      193  0.115      0.336      NA 0.506024096
## 81 Gb158      195  0.070      0.257      NA 0.345895020
## 82 Gb158      197 -0.025      0.132      NA 0.152073733
## 83 Gb158      199  0.243      0.099      NA 0.109877913
## 84 Gb158      201  0.027      0.007      NA 0.007049345
## 85 Gb158      205 -0.056      0.059      NA 0.062699256

with(SAD_Gb158, cor.test(Allele, Capf, alternative="less", method="spearman")
)

##
## Spearman's rank correlation rho
##
## data: Allele and Capf
## S = 72, p-value = 0.6483
## alternative hypothesis: true rho is less than 0
## sample estimates:
##      rho
## 0.1428571

SAD_Gb73 <- subset(SAD,loci=="Gb73")
SAD_Gb73

##      loci Allele  Capf p..All.W. Smallf  Weights
## 91  Gb73    228  0.369    0.095     NA 0.10497238
## 92  Gb73    230  0.132    0.070     NA 0.07526882
## 93  Gb73    238 -0.010    0.013     NA 0.01317123
## 94  Gb73    240  0.806    0.089     NA 0.09769484
## 95  Gb73    242  0.495    0.095     NA 0.10497238
## 96  Gb73    244 -0.044    0.051     NA 0.05374078
## 97  Gb73    246  0.396    0.089     NA 0.09769484
## 98  Gb73    248  0.543    0.247     NA 0.32802125
## 99  Gb73    250  0.334    0.228     NA 0.29533679
## 100 Gb73    254  0.005    0.013     NA 0.01317123
## 101 Gb73    256 -0.001    0.013     NA 0.01317123

with(SAD_Gb73, cor.test(Allele, Capf, alternative="less", method="spearman"))

##
## Spearman's rank correlation rho
##
## data: Allele and Capf
## S = 250, p-value = 0.3468
## alternative hypothesis: true rho is less than 0
## sample estimates:
##      rho
## -0.1363636

SAD_Gb92 <- subset(SAD,loci=="Gb92")
SAD_Gb92

```

```

##      loci Allele   Capf p..All.W. Smallf Weights
## 102 Gb92    278 -0.011      NA      NA      NA
## 103 Gb92    282  0.330      NA      NA      NA
## 104 Gb92    284  0.005      NA      NA      NA
## 105 Gb92    286 -0.005      NA      NA      NA
## 106 Gb92    290 -0.045      NA      NA      NA
## 107 Gb92    292  0.326      NA      NA      NA
## 108 Gb92    294  0.073      NA      NA      NA
## 109 Gb92    300 -0.018      NA      NA      NA
## 110 Gb92    302  0.069      NA      NA      NA
## 111 Gb92    304  0.256      NA      NA      NA
## 112 Gb92    306  0.013      NA      NA      NA
## 113 Gb92    314 -0.010      NA      NA      NA

with(SAD_Gb92, cor.test(Allele, Capf, alternative="less", method="spearman"))

##
## Spearman's rank correlation rho
##
## data: Allele and Capf
## S = 276, p-value = 0.5481
## alternative hypothesis: true rho is less than 0
## sample estimates:
##      rho
## 0.03496503

SAD_Gb165 <- subset(SAD,loci=="Gb165")
SAD_Gb165

##      loci Allele   Capf p..All.W. Smallf Weights
## 86 Gb165    210 -0.152    0.547      NA 1.207505519
## 87 Gb165    212  0.280    0.267      NA 0.364256480
## 88 Gb165    214  0.269    0.087      NA 0.095290252
## 89 Gb165    218 -0.007    0.007      NA 0.007049345
## 90 Gb165    220 -0.066    0.093      NA 0.102535832

with(SAD_Gb165, cor.test(Allele, Capf, alternative="less", method="spearman")
)

##
## Spearman's rank correlation rho
##
## data: Allele and Capf
## S = 20, p-value = 0.525
## alternative hypothesis: true rho is less than 0
## sample estimates:
## rho
## 0

### Linkage disequilibrium: BY correction for 9 selected Loci
p.adjust(c(0.3265, 0.5193, 0.0006, 0.6329, 0.864, 0.7794, 0.821, 0.8735, 0

```

```
.2963, 0.1097, 0.0085, 0.0715, 0.0115,
      0.081, 0.9701, 0.2031, 0.5426, 0.5946, 0.0201, 0.4044, 0.2177, 1
, 0.3921, 0.5911, 0.269, 0.3584, 0.0654,
      0.4602, 0.5638, 0.8668, 0.4043, 0.3298, 0.8541, 0.4636, 0.8868, 0
.6678), method="BY")
```

```
## [1] 1.00000000 1.00000000 0.09017048 1.00000000 1.00000000 1.00000000
## [7] 1.00000000 1.00000000 1.00000000 1.00000000 0.57608917 1.00000000
## [13] 0.57608917 1.00000000 1.00000000 1.00000000 1.00000000 1.00000000
## [19] 0.75517776 1.00000000 1.00000000 1.00000000 1.00000000 1.00000000
## [25] 1.00000000 1.00000000 1.00000000 1.00000000 1.00000000 1.00000000
## [31] 1.00000000 1.00000000 1.00000000 1.00000000 1.00000000 1.00000000
```

### ### Correlation between FIS and FST for 9 selected Loci on all samples

```
FISFST9loci <- read.csv("FISFST_9loci_allsamples.csv", sep=",", row.names=NULL)
```

```
FISFST9loci
```

```
## Locus FST FIS
## 1 Gb5 0.099 0.053
## 2 Gb28 0.121 0.109
## 3 Gb35 0.122 0.435
## 4 Gb66 0.057 0.046
## 5 Gb72 0.082 -0.056
## 6 Gb73 0.155 0.285
## 7 Gb92 0.132 0.026
## 8 Gb158 0.123 -0.070
## 9 Gb165 0.167 -0.131
## 10 All 0.116 0.082
```

```
with(FISFST9loci, cor.test(FST, FIS, alternative="greater", method="spearman"))
```

```
##
## Spearman's rank correlation rho
##
## data: FST and FIS
## S = 182, p-value = 0.6206
## alternative hypothesis: true rho is greater than 0
## sample estimates:
## rho
## -0.1030303
```

### ### Correlation between FIS and FST for 9 selected Loci on field samples only

```
FISFST9locifieldsamples <- read.csv("FISFST_9loci_fieldsamples.csv", sep=",", row.names=NULL)
```

```
FISFST9locifieldsamples
```

```
## Locus FST FIS
## 1 Gb5 0.056 0.057
## 2 Gb28 0.079 0.055
```

```

## 3  Gb35 0.171  0.308
## 4  Gb66 0.040 -0.016
## 5  Gb72 0.058 -0.054
## 6  Gb73 0.080  0.318
## 7  Gb92 0.007  0.107
## 8  Gb158 0.022 -0.080
## 9  Gb165 0.103 -0.118

with(FISFST9locifieldsamples, cor.test(FST, FIS, alternative="greater", metho
d="spearman"))

##
## Spearman's rank correlation rho
##
## data:  FST and FIS
## S = 100, p-value = 0.3389
## alternative hypothesis: true rho is greater than 0
## sample estimates:
##      rho
## 0.1666667

### Correlation between FIS and number of blanks for selected 9 loci on field
samples
FISblanks9loci_fieldsamples <- read.csv("FISblanks_9loci_fieldsamples.csv", s
ep=",", row.names=NULL)
FISblanks9loci_fieldsamples

##   Locus Nb    FIS
## 1   Gb5  0  0.057
## 2   Gb28 8  0.055
## 3   Gb35 6  0.308
## 4   Gb66 1 -0.016
## 5   Gb72 3 -0.054
## 6   Gb73 3  0.318
## 7   Gb92 5  0.107
## 8  Gb158 4 -0.080
## 9  Gb165 4 -0.118

with(FISblanks9loci_fieldsamples, cor.test(Nb, FIS, alternative="greater", me
thod="spearman"))

## Warning in cor.test.default(Nb, FIS, alternative = "greater", method =
## "spearman"): Cannot compute exact p-value with ties

##
## Spearman's rank correlation rho
##
## data:  Nb and FIS
## S = 108.91, p-value = 0.4065
## alternative hypothesis: true rho is greater than 0
## sample estimates:

```

```

##          rho
## 0.09244024

### Correlation between FIS and number of blanks for Loci without null alleles
(Gb5, 35, 66, 73, 92)
FISblankslocinonulls_fieldsamples <- read.csv("FISblanks_locinonulls_fieldsam
ples.csv", sep=",", row.names=NULL)
FISblankslocinonulls_fieldsamples

##   Locus Nb FIS_nulls
## 1  Gb5  0    0.057
## 2  Gb28 8     NA
## 3  Gb35 6    0.308
## 4  Gb66 1   -0.016
## 5  Gb72 3     NA
## 6  Gb73 3    0.318
## 7  Gb92 5    0.107
## 8 Gb158 4     NA
## 9 Gb165 4     NA

with(FISblankslocinonulls_fieldsamples, cor.test(Nb, FIS_nulls, alternative="
greater", method="spearman"))

##
## Spearman's rank correlation rho
##
## data:  Nb and FIS_nulls
## S = 8, p-value = 0.175
## alternative hypothesis: true rho is greater than 0
## sample estimates:
## rho
## 0.6

```