Electronic Supplementary Material, Datafile S1:

AIC estimates of full models and final (selected) models

Post-copulatory genetic matchmaking: HLA-dependent effects of cervical mucus on human sperm function

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Proceedings of the Royal Society B (DOI: 10.1098/rspb.2020.1682)

1. Overall models for the effect of HLA-dissimilarity on sperm swimming velocity (VCL)

Model 5A: Full model with Timepoint * HLA dissimilarity interaction

 $Model_5A = lmer (VCL \sim 1 + Timepoint * HLA_dissimilarity + (Timepoint|Sub-sample) + (Timepoint|Sub-sample:Replicate) + (Timepoint|Male) + (Timepoint|Female) + (Timepoint|Male:Female), data = All_timepoints) \\ AIC = 6965.6$

Model 5B: Like Model 5A, but without Timepoint * HLA dissimilarity interaction

 $Model_5B = lmer (VCL \sim 1 + Timepoint + HLA_dissimilarity + (Timepoint|Sub-sample) + (Timepoint|Sub-sample:Replicate) + (Timepoint|Male) + (Timepoint|Female) + (Timepoint|Male:Female), data = All_timepoints) \\ AIC = 6965.4 (Final model)$

2. Overall models for the effect of Genomic dissimilarity on sperm swimming velocity (VCL)

Model 6A: Full model with Timepoint * Genomic dissimilarity interaction

 $\label{eq:model_6A} Model_6A = lmer (VCL \sim 1 + Timepoint * Genomic_dissimilarity + (Timepoint|Sub-sample) + (Timepoint|Sub-sample:Replicate) + (Timepoint|Male) + (Timepoint|Female) + (Timepoint|Male:Female), data = All_timepoints) \\ AIC = 6929.6$

Model 6B: Like Model 6A, but random slope, (Timepoint|Sub-sample:replicate), replaced with random intercept, (1|Sub-sample:replicate)

 $Model_6B = lmer (VCL \sim 1 + Timepoint * Genomic_dissimilarity + (Timepoint|Sub-sample) + (1|Sub-sample:Replicate) + (Timepoint|Male) + (Timepoint|Female) + (Timepoint|Male:Female), data = All_timepoints) \\ AIC = 6919.6 (Final model)$

Model 6C: Like Model 6B, but without Timepoint * Genomic dissimilarity interaction

 $Model_6C = lmer (VCL \sim 1 + Timepoint + Genomic_dissimilarity + (Timepoint|Sub-sample) + (1|Sub-sample:Replicate) + (Timepoint|Male) + (Timepoint|Female) + (Timepoint|Male:Female), data = All_timepoints) \\ AIC = 6941.7$

${\bf 3.\ Overall\ models\ for\ the\ effect\ of\ HLA-dissimilarity\ on\ sperm\ hyperactivation}$

Model 2A: Full model with Timepoint * HLA dissimilarity interaction

 $Model_2A = lmer \ (Hyperactivation \sim 1 + Timepoint * HLA_dissimilarity + (Timepoint|Sub-sample) + (Timepoint|Sub-sample:Replicate) + (Timepoint|Male) + (Timepoint|Female) + (Timepoint|Male:Female), \ data = All_timepoints) \\ AIC = 5651.3$

Model 2B: Like Model 2A, but without Timepoint * HLA dissimilarity interaction

 $Model_2B = lmer \ (Hyperactivation \sim 1 + Timepoint + HLA_dissimilarity + (Timepoint|Sub-sample) + (Timepoint|Sub-sample:Replicate) + (Timepoint|Male) + (Timepoint|Female) + (Timepoint|Male:Female), \ data = All_timepoints) \\ AIC = 5647.7 \ (Final model)$

4. Overall models for the effect of Genomic dissimilarity on sperm hyperactivation

Model 3A: Full model with Timepoint * Genomic dissimilarity interaction

 $Model_3A = lmer \ (Hyperactivation \sim 1 + Timepoint * Genomic_dissimilarity + (Timepoint|Sub-sample) + (Timepoint|Sub-sample:Replicate) + (Timepoint|Male) + (Timepoint|Female) + (Timepoint|Male:Female), data = All_timepoints) \\ AIC = 5616.9$

Model 3B: Like Model 3A, but random slope, (Timepoint|Sub-sample:replicate), replaced with random intercept, (1|Sub-sample:replicate)

 $\label{eq:model_3B} Model_3B = lmer \ (Hyperactivation \sim 1 + Timepoint * Genomic_dissimilarity + (Timepoint|Sub-sample) + (1|Sub-sample:Replicate) + (Timepoint|Male) + (Timepoint|Female) + (Timepoint|Male:Female), \ data = All_timepoints) \\ AIC = 5607.1 \ (Final model)$

Model 3C: Like Model 3B, but without Timepoint * Genomic dissimilarity interaction

 $\label{eq:model_3C} \begin{aligned} & Model_3C = lmer \ (Hyperactivation \sim 1 + Timepoint + Genomic_dissimilarity + (Timepoint | Sub-sample) + (1 | Sub-sample: Replicate) + (Timepoint | Male) + (Timepoint | Female) + (Timepoint | Male: Female), \ data = All_timepoints) \\ & AIC = 5625.5 \end{aligned}$

5. Overall models for the effect of Grantham distance on sperm swimming velocity (VCL)

Model 4A: Full model with Timepoint * Grantham interaction

 $\label{eq:model_4A} Model_4A = lmer (VCL \sim 1 + Timepoint * Grantham + (Timepoint | Sub-sample) + (Timepoint | Sub-sample: Replicate) + (Timepoint | Male) + (Timepoint | Female) + (Timepoint | Male: Female), data = All_timepoints) \\ AIC = 6949.8 (Final model)$

Model 4B: Like Model 4A, but without Timepoint * Grantham interaction

 $\begin{aligned} & Model_4B = lmer \ (VCL \sim 1 + Timepoint + Grantham + (Timepoint | Sub-sample) + (Timepoint | Sub-sample: Replicate) + \\ & + (Timepoint | Male) + (Timepoint | Female) + (Timepoint | Male: Female), \ data = All_timepoints) \\ & AIC = 6962.1 \end{aligned}$

6. Overall models for the effect of Grantham distance on sperm hyperactivation

Model 1A: Full model with Timepoint * Grantham interaction

 $Model_1A = lmer \ (Hyperactivation \sim 1 + Timepoint * Grantham + (Timepoint | Sub-sample) + (Timepoint | Sub-sample: Replicate) + (Timepoint | Male) + (Timepoint | Female) + (Timepoint | Male: Female), data = All_timepoints) \\ AIC = 5634.4 \ (Final model)$

Model 1B: Like Model 1A, but without Timepoint * Grantham interaction

 $Model_1B = lmer \ (Hyperactivation \sim 1 + Timepoint + Grantham + (Timepoint | Sub-sample) + (Timepoint | Sub-sample: Replicate) + (Timepoint | Male) + (Timepoint | Female) + (Timepoint | Male: Female) , data = All_timepoints) \\ AIC = 5643.3$

7. The effect of Grantham distance on sperm swimming velocity (VCL) at 180 min

Model 8A: Full model with random slope, (Grantham male)

```
\label{eq:model_8A} Model_8A = lmer (VCL \sim 1 + (1|Sub\text{-sample}) + (1|Sub\text{-sample}:Replicate) + Grantham + (Grantham|Male) + (1|Male) + (1|Female) + (1|Male:Female), data = Time_180) \\ AIC = 2377.6
```

Model 8B: Like Model 8A, but without (1|male)

```
\label{eq:model_8B} Model\_8B = lmer (VCL \sim 1 + (1|Sub\text{-sample}) + (1|Sub\text{-sample}:Replicate) + Grantham + (Grantham|Male) + (1|Female) + (1|Male:Female), data = Time\_180) \\ AIC = 2375.6 (Final model)
```

Model 8C: Like Model 8A, but without (Grantham male)

```
\label{eq:model_8C} \begin{split} & Model\_8C = lmer \ (VCL\_180 \sim 1 + (1|Sub\text{-sample}) + (1|Sub\text{-sample}:Replicate) + Grantham + (1|Male) + \\ & (1|Female) + (1|Male:Female), \ data = Time\_180) \\ & AIC = 2382.5 \end{split}
```

8. The effect of Grantham distance on sperm hyperactivation at 180 min

Model 7A: Full model with random slope, (Grantham|male)

```
\label{eq:model_7A} Model\_7A = lmer (Hyperactivation \sim 1 + (1|Sub\text{-sample}) + (1|Sub\text{-sample}:Replicate) + Grantham + (Grantham|Male) + \\ + (1|Male) + (1|Female) + (1|Male:Female), \ data = Time\_180) \\ AIC = 1925.9
```

Model 7B: Like Model 7A, but without (1|male)

```
\begin{aligned} & Model\_7B = lmer \ (Hyperactivation \sim 1 + (1|Sub\text{-}sample) + (1|Sub\text{-}sample:Replicate) + Grantham + (Grantham|Male) + \\ & (1|Female) + (1|Male:Female), \ data = Time\_180) \\ & AIC = 1923.9 \ (Final \ model) \end{aligned}
```

Model 7C: Like Model 7A, but without (Grantham|male)

```
\label{eq:model_7C} \begin{split} & Model\_7C = lmer \ (Hyperactivation \sim 1 + (1|Sub\text{-sample}) + (1|Sub\text{-sample}:Replicate) + Grantham + (1|Male) + \\ & + (1|Female) + (1|Male:Female), \ data = Time\_180) \\ & AIC = 1934.2 \end{split}
```

9. The effect of HLA-dissimilarity on sperm viability

Model 10A: Full model with random slope, (HLA dissimilarity|male)

```
\label{eq:model_10A} \begin{split} & Model\_10A = lmer \ (Viability \sim 1 + (1|Sub\text{-sample}) + (1|Sub\text{-sample}:Replicate) + HLA\_dissimilarity + \\ & (HLA\_dissimilarity|Male) + (1|Male) + \ (1|Female) + (1|Male:Female), \ data = Viability) \\ & AIC = 1552.7 \end{split}
```

Model 10B: Like Model 10A, but without (HLA_dissimilarity|male)

```
\begin{aligned} & Model\_10B = lmer \ (Viability \sim 1 + (1|Sub\text{-sample}) + (1|Sub\text{-sample}:Replicate) + HLA\_dissimilarity + \\ & + (1|Male) + (1|Female) + (1|Male:Female), \ data = Viability) \\ & AIC = 1551.3 \ (Final \ model) \end{aligned}
```

10. The effect of Grantham distance on sperm viability

Model 9A: Full model with random slope, (Grantham|male)

```
\begin{aligned} & Model\_9A = lmer \ (Viability \sim 1 + (1|Sub\text{-}sample) + (1|Sub\text{-}sample:Replicate) + Grantham + (Grantham|Male) + \\ & + (1|Male) + (1|Female) + (1|Male:Female), \ data = Viability) \\ & AIC = 1556.0 \end{aligned}
```

Model 9B: Like Model 9A, but without (Grantham male)

```
\begin{aligned} &Model\_9B = lmer \ (Viability \sim 1 + (1|Sub\text{-sample}) + (1|Sub\text{-sample}:Replicate) + Grantham + (1|Male) + \\ &+ (1|Female) + (1|Male:Female), \ data = Viability) \\ &AIC = 1555.3 \ (Final \ model) \end{aligned}
```

11. The effect of Genomic dissimilarity on sperm viability

Model 11A: Full model with random slope, (Genomic_dissimilarity|male)

```
\label{eq:model_11A} Model_11A = lmer \ (Viability \sim 1 + (1|Sub\text{-sample}) + (1|Sub\text{-sample}:Replicate) + Genomic\_dissimilarity + (Genomic\_dissimilarity|Male) + (1|Male) + (1|Female) + (1|Male:Female), \ data = Viability) \\ AIC = 1559.9
```

Model 11B: Like Model 11A, but without (Genomic dissimilarity|male)

```
\label{eq:model_1B} \begin{split} & Model\_11B = lmer \ (Viability \sim 1 + (1|Sub\text{-sample}) + (1|Sub\text{-sample}:Replicate) + Genomic\_dissimilarity + \\ & + (1|Male) + (1|Female) + (1|Male:Female), \ data = Viability) \\ & AIC = 1554.6 \ (Final \ model) \end{split}
```