

# Separate sex PCAs with model estimates – checking effect of P:C ratio

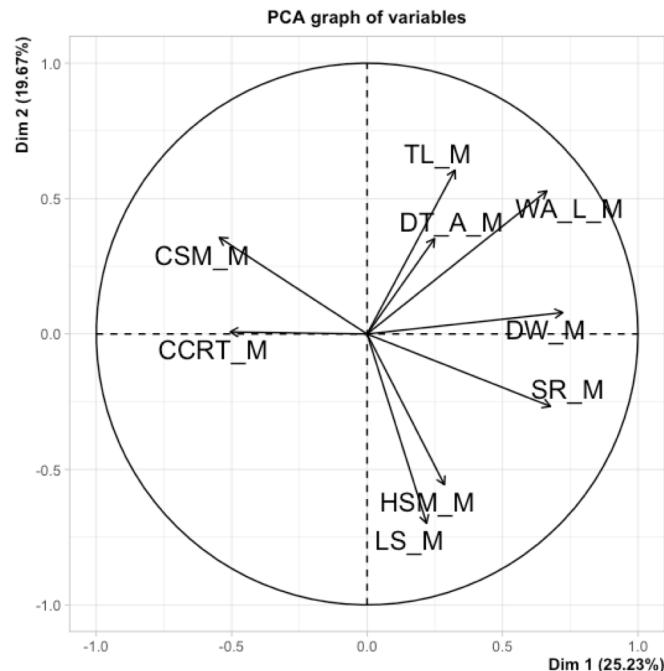
05/10/2022

# Notes

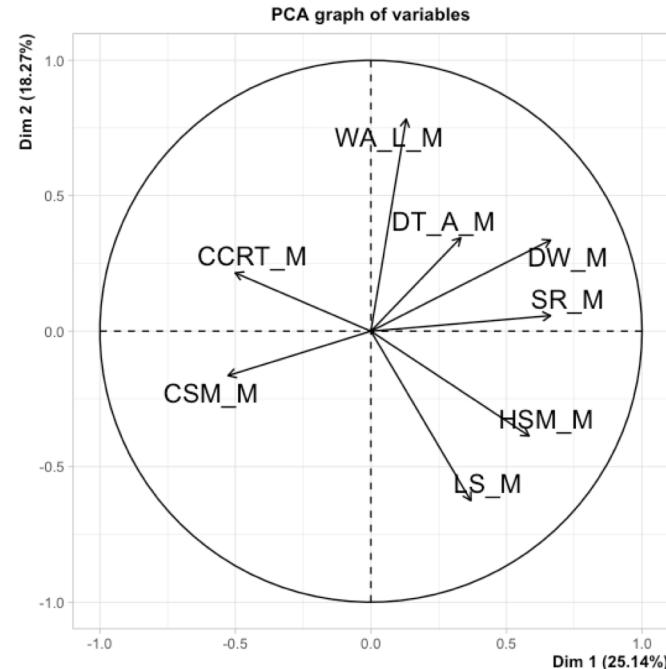
- Using model estimates for line rather than raw data (scaled to unit variance).
- Comparing **all data** (i.e. the previous analysis) with estimates from a single lab but with similar **P:C ratio** in diet.
- TL is missing from males
- Lmer estimates (rather than glmer estimates used for dia)
- Sexes dealt with separately
  - PCA1 (M9) – male PCA with 9 traits
  - PCA2 (F9) – female PCA with 9 traits equivalent to males
  - PCA3 (Fmax) – female PCA with all 12 female traits
  - PCA4 (FmaxPlus) – female PCA with 13 traits (12 female traits + via)
- Loadings of traits on to PCs are considered of interest if greater than  $> 0.4$  (or  $< -0.4$ ).
  - Loadings  $> 0.6$  are in **bold red**
  - Loadings from  $0.4 - 0.59$  are in dark red

# 1: Male PCA - 9 traits (M9)

All data



P:C ctrl data v2

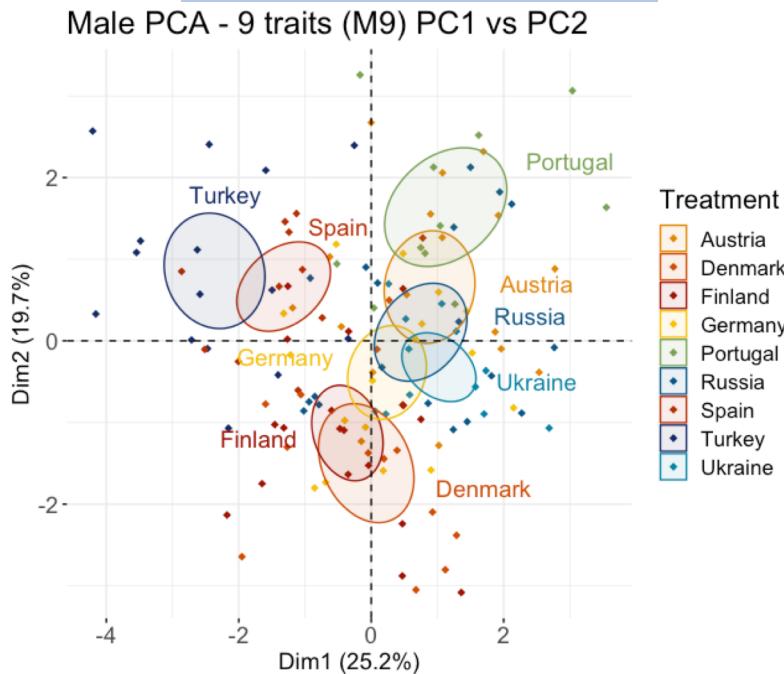


	eigenval	% var	cum % var
comp 1	2.271	25.231	25.231
comp 2	1.770	19.670	44.902
comp 3	1.211	13.452	58.353
comp 4	1.055	11.723	70.076
comp 5	0.818	9.084	79.160
comp 6	0.680	7.551	86.710
comp 7	0.462	5.139	91.849
comp 8	0.387	4.297	96.146
comp 9	0.347	3.854	100.000

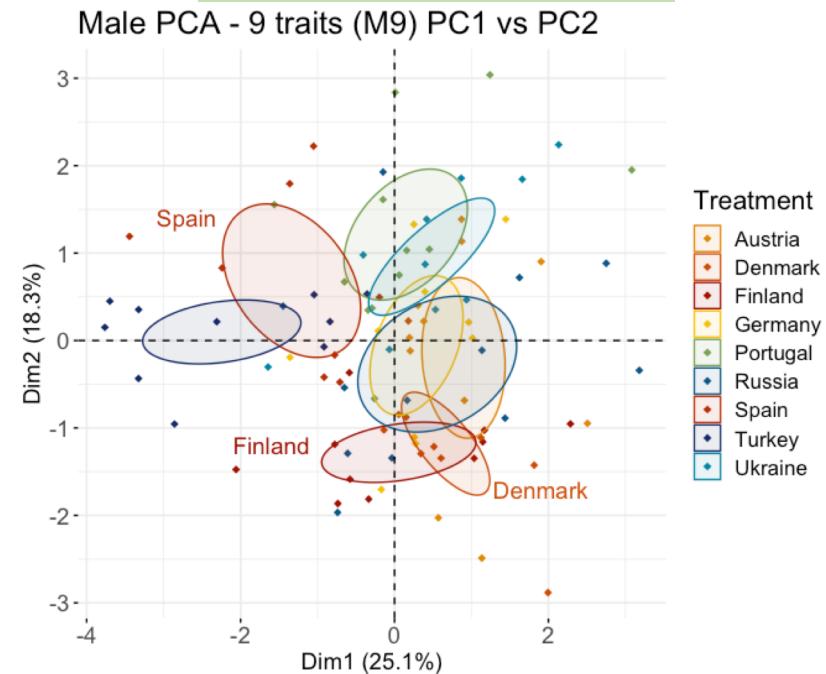
	eigenval	% var	cum % var
comp 1	2.011	25.140	25.140
comp 2	1.462	18.272	43.412
comp 3	1.137	14.215	57.627
comp 4	0.882	11.028	68.656
comp 5	0.838	10.471	79.127
comp 6	0.775	9.683	88.810
comp 7	0.520	6.495	95.306
comp 8	0.376	4.694	100.000

# 1: Male PCA - 9 traits (M9)

## All data



## P:C ctrl data v2



	<b>Dim.1</b>	<b>Dim.2</b>	<b>Dim.3</b>	<b>Dim.4</b>
CCRT_M	<b>-0.505</b>	0.007	<b>0.598</b>	0.295
CSM_M	<b>-0.545</b>	0.356	0.367	0.080
DT_A_M	0.249	0.352	0.038	0.812
DW_M	<b>0.722</b>	0.079	0.380	-0.260
HSM_M	0.286	<b>-0.556</b>	<b>-0.412</b>	0.345
LS_M	0.220	<b>-0.699</b>	0.171	0.181
SR_M	<b>0.677</b>	-0.267	<b>0.517</b>	0.105
TL_M	0.324	<b>0.605</b>	-0.316	0.219
WA_L_M	<b>0.664</b>	0.528	0.077	-0.154

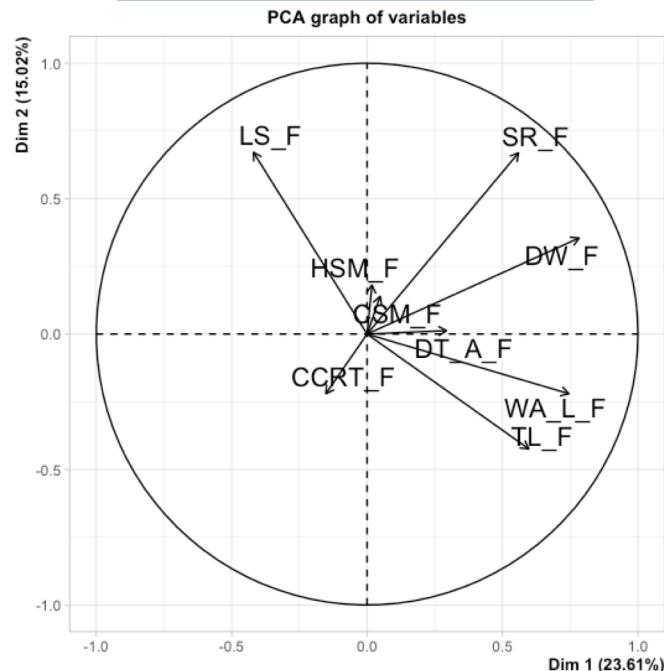
	<b>Dim.1</b>	<b>Dim.2</b>	<b>Dim.3</b>	<b>Dim.4</b>
CCRT_M	<b>-0.501</b>	0.215	<b>0.608</b>	0.158
CSM_M	<b>-0.527</b>	-0.164	-0.221	0.709
DT_A_M	0.331	0.345	<b>0.433</b>	0.422
DW_M	<b>0.663</b>	0.337	-0.250	0.362
HSM_M	<b>0.584</b>	-0.387	-0.318	0.169
LS_M	0.368	<b>-0.625</b>	0.334	0.041
SR_M	<b>0.663</b>	0.057	<b>0.455</b>	-0.038
TL_M	.	.	.	.
WA_L_M	0.130	<b>0.783</b>	-0.220	-0.118

# PCA 1 differences

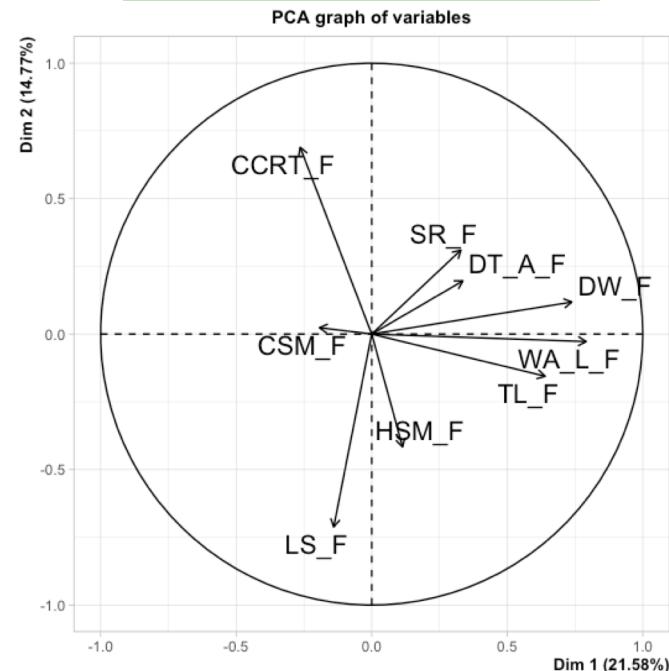
- Whether using **all data** or **P:C control** the result is similar
- There is a slight difference in PC1: in the **P:C control** analysis, WA no longer loads on to PC1, but HSM does
- For PC2 the result is similar (negative correlation of LS and WA).
- For PC3 the negative correlation between CCRT and HSM is less strong in **P:C control** than **all data**, but the positive correlation between CCRT and SR is maintained

## 2: Female PCA – 9 traits (F9)

All data



P:C ctrl data v2

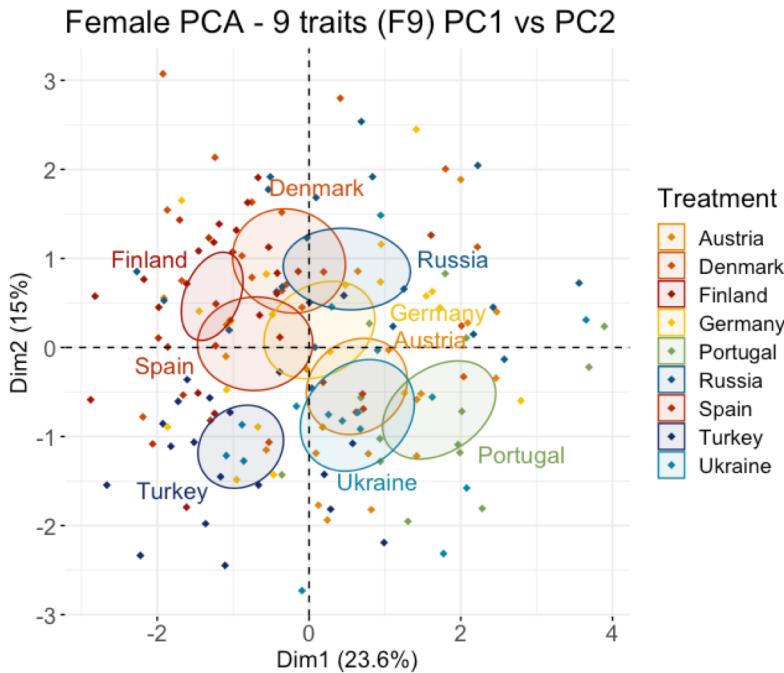


	eigenval	% var	cum % var
comp 1	2.125	23.612	23.612
comp 2	1.352	15.022	38.634
comp 3	1.210	13.441	52.075
comp 4	0.993	11.033	63.108
comp 5	0.950	10.554	73.662
comp 6	0.891	9.903	83.565
comp 7	0.659	7.327	90.892
comp 8	0.505	5.609	96.502
comp 9	0.315	3.498	100.000

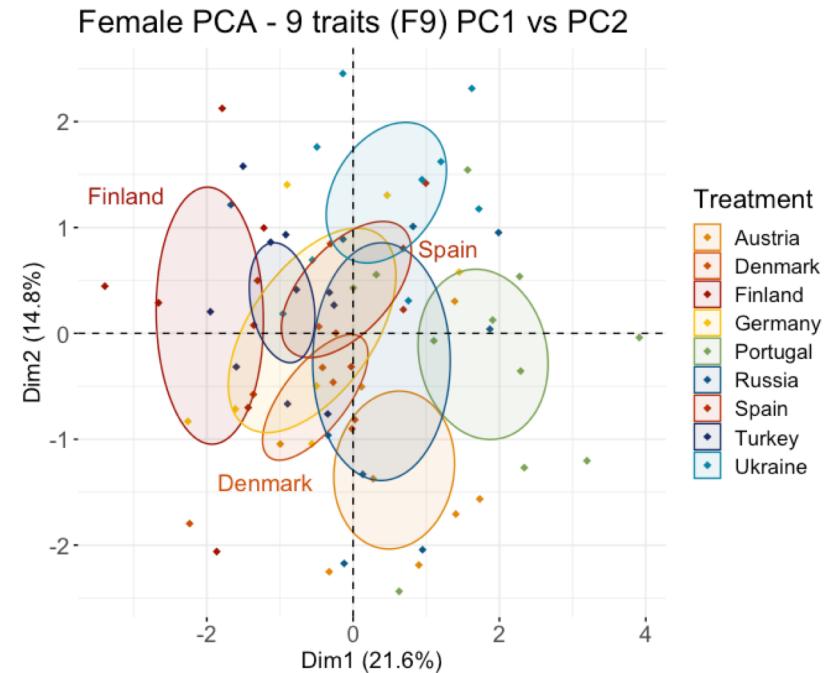
	eigenval	% var	cum % var
comp 1	1.942	21.575	21.575
comp 2	1.329	14.768	36.343
comp 3	1.279	14.217	50.560
comp 4	1.144	12.713	63.273
comp 5	0.874	9.709	72.982
comp 6	0.780	8.663	81.644
comp 7	0.693	7.700	89.344
comp 8	0.507	5.634	94.978
comp 9	0.452	5.022	100.000

## 2: Female PCA – 9 traits (F9)

All data



P:C ctrl data v2



	<b>Dim.1</b>	<b>Dim.2</b>	<b>Dim.3</b>	<b>Dim.4</b>
CCRT_F	-0.152	-0.220	<b>0.625</b>	0.396
CSM_F	0.048	0.139	<b>-0.564</b>	0.357
DT_A_F	0.293	0.013	0.333	0.673
DW_F	<b>0.783</b>	0.355	0.039	-0.100
HSM_F	0.018	0.181	<b>0.553</b>	-0.416
LS_F	<b>-0.420</b>	<b>0.671</b>	-0.097	0.108
SR_F	<b>0.559</b>	<b>0.669</b>	0.102	0.105
TL_F	<b>0.597</b>	<b>-0.424</b>	-0.249	0.109
WA_L_F	<b>0.745</b>	-0.220	0.047	-0.197

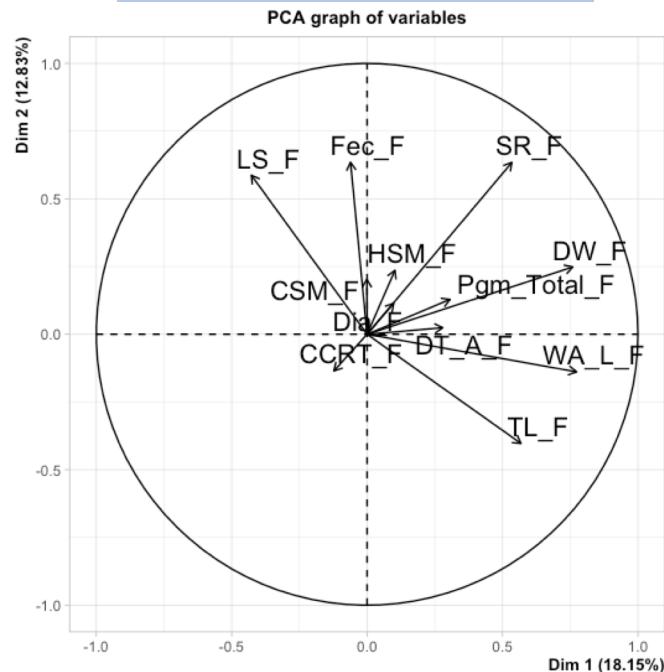
	<b>Dim.1</b>	<b>Dim.2</b>	<b>Dim.3</b>	<b>Dim.4</b>
CCRT_F	-0.264	<b>0.689</b>	0.055	-0.461
CSM_F	-0.193	0.024	0.116	0.880
DT_A_F	0.337	0.196	<b>0.676</b>	0.115
DW_F	<b>0.739</b>	0.118	0.124	0.088
HSM_F	0.114	<b>-0.416</b>	<b>0.508</b>	-0.292
LS_F	-0.140	<b>-0.712</b>	0.273	-0.177
SR_F	0.329	0.310	<b>0.449</b>	0.063
TL_F	<b>0.640</b>	-0.156	<b>-0.471</b>	0.042
WA_L_F	<b>0.791</b>	-0.027	-0.187	-0.120

# PCA 2 results

- The main axis of variation (PC1) is fairly similar
  - In both **all data** and **P:C control** size traits (DW, TL and WA) positively correlate. In **all data** they also negatively correlate to LS
- The negative correlation between SR and TL moves from PC2 in **all data** to PC3 in **P:C control**. In **P:C control** the positive correlation of LS (with SR) is weaker, but there is now a positive correlation between DT\_A, HSM and SR.
- The negative correlation of CSM and HSM has moved from PC3 in **all data** to PC4 in **P:C control** (and is weaker)
- Some trait correlations along PC2 and PC3 are weaker or have broken down, e.g. positive correlation between CCRT and HSM in **all data** PC3 is now negative correlation in **P:C control** PC2

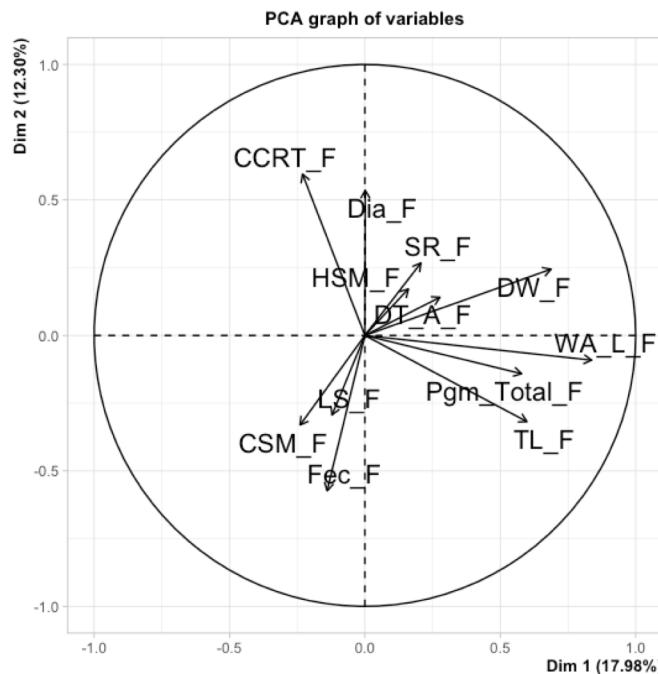
### 3: Female PCA – 12 traits (Fmax)

All data



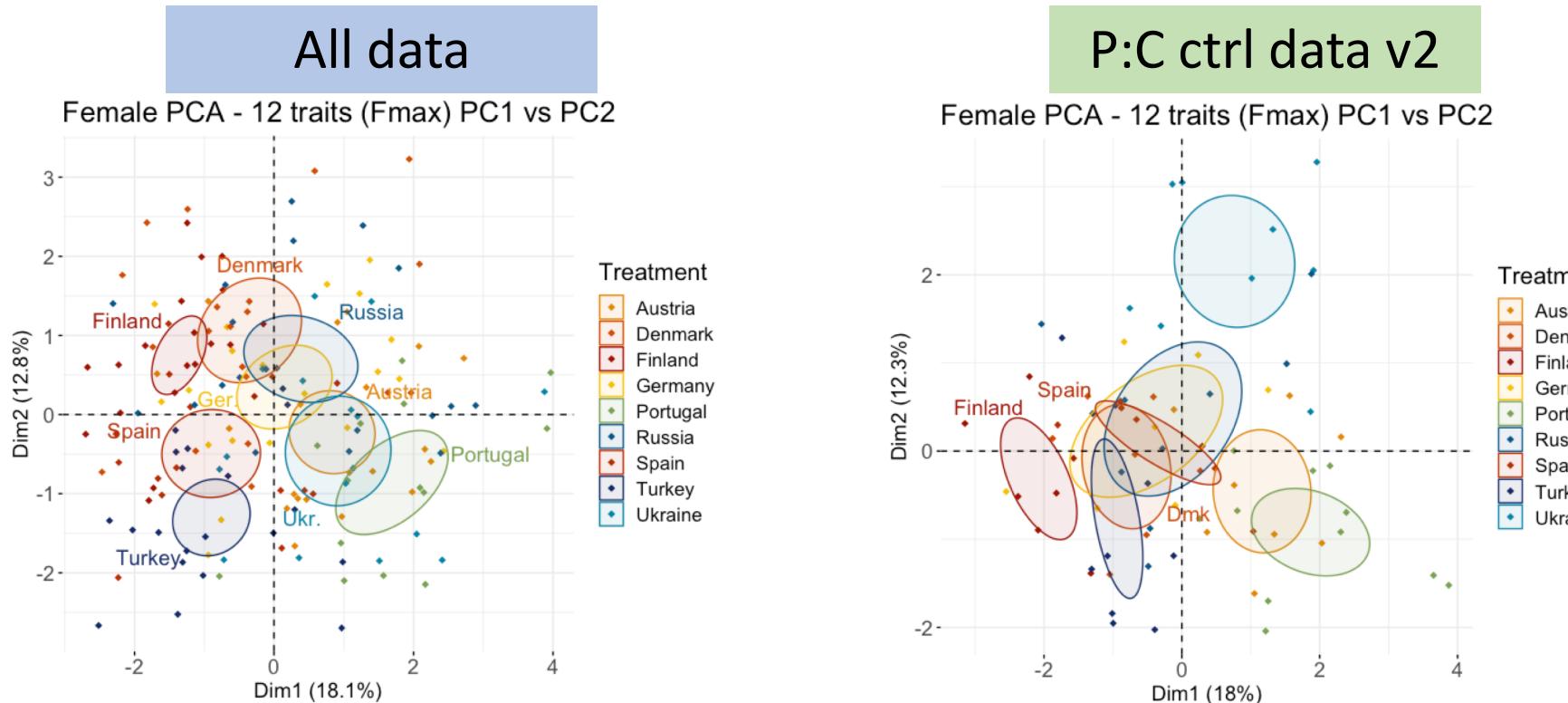
	<b>eigenval</b>	<b>% var</b>	<b>cum % var</b>
comp 1	2.178	18.149	18.149
comp 2	1.540	12.834	30.983
comp 3	1.470	12.250	43.233
comp 4	1.116	9.300	52.534
comp 5	1.072	8.931	61.465
comp 6	1.000	8.332	69.797
comp 7	0.829	6.906	76.704
comp 8	0.787	6.557	83.260
comp 9	0.664	5.537	88.797
comp 10	0.605	5.044	93.842
comp 11	0.438	3.647	97.488
comp 12	0.301	2.512	100.000

P:C ctrl data v2



	<b>eigenval</b>	<b>% var</b>	<b>cum % var</b>
comp 1	2.157	17.976	17.976
comp 2	1.476	12.298	30.274
comp 3	1.330	11.080	41.354
comp 4	1.305	10.876	52.230
comp 5	1.083	9.024	61.254
comp 6	1.033	8.609	69.863
comp 7	0.816	6.800	76.664
comp 8	0.709	5.908	82.571
comp 9	0.674	5.617	88.188
comp 10	0.608	5.067	93.254
comp 11	0.450	3.750	97.005
comp 12	0.359	2.995	100.000

### 3: Female PCA – 12 traits (Fmax)



	<b>Dim.1</b>	<b>Dim.2</b>	<b>Dim.3</b>	<b>Dim.4</b>
CCRT_F	-0.122	-0.135	<b>0.426</b>	0.591
CSM_F	-0.001	0.203	<b>-0.405</b>	0.099
DT_A_F	0.280	0.024	-0.036	0.232
Dia_F	0.098	0.114	<b>0.546</b>	0.383
DW_F	<b>0.759</b>	0.248	-0.155	0.131
Fec_F	-0.061	<b>0.635</b>	-0.087	-0.022
HSM_F	0.103	0.236	<b>0.639</b>	-0.190
LS_F	<b>-0.427</b>	<b>0.587</b>	-0.148	-0.245
Pgm_Tl_F	0.306	0.129	<b>0.518</b>	-0.541
SR_F	<b>0.535</b>	<b>0.635</b>	-0.103	0.305
TL_F	<b>0.568</b>	<b>-0.403</b>	-0.286	-0.063
WA_L_F	<b>0.774</b>	-0.139	0.066	-0.229

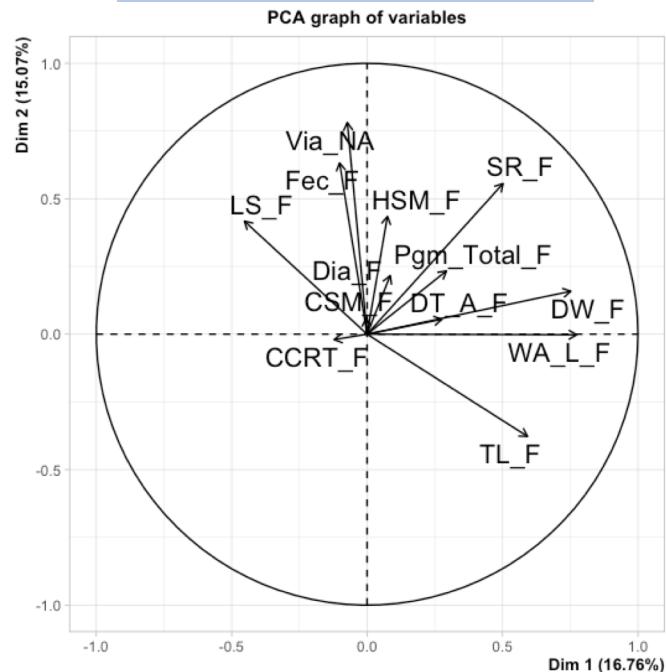
	<b>Dim.1</b>	<b>Dim.2</b>	<b>Dim.3</b>	<b>Dim.4</b>
CCRT_F	-0.230	<b>0.595</b>	0.013	-0.363
CSM_F	-0.239	-0.331	<b>0.593</b>	0.038
DT_A_F	0.277	0.141	<b>0.551</b>	0.340
Dia_F	0.002	<b>0.536</b>	0.053	0.185
DW_F	<b>0.687</b>	0.245	0.243	0.056
Fec_F	-0.140	<b>-0.574</b>	<b>0.412</b>	-0.013
HSM_F	0.160	0.171	-0.168	0.711
LS_F	-0.121	-0.294	-0.301	0.644
Pgm_Tl_F	<b>0.579</b>	-0.141	-0.211	-0.004
SR_F	0.207	0.267	<b>0.518</b>	0.114
TL_F	<b>0.598</b>	-0.318	-0.075	-0.263
WA_L_F	<b>0.838</b>	-0.091	-0.081	-0.130

# PCA 3 results

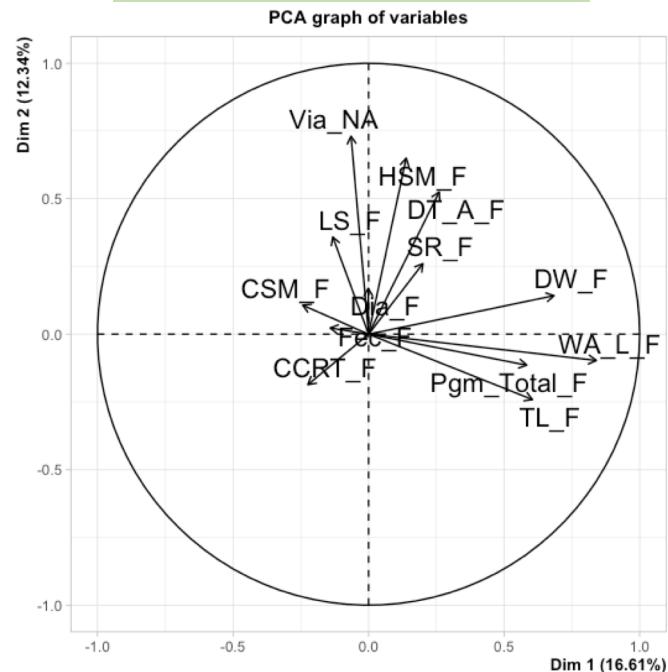
- Similar to PCA 2 results in some ways: the main axis of variation (PC1) is again a size correlation:
  - In both **all data** and **P:C control** size traits (DW, TL and WA) positively correlate. In **all data** they negatively correlate to LS, and in **P:C control** they positively correlate with Pigm.
- The positive correlation between CCRT and Dia moves from PC3 in **all data** to PC2 in **P:C control**
- The positive correlation between Fec and Pigm moves from PC2 in **all data** to PC3 in **P:C control**
- Loss of some other trait correlations (including LS correlations)

## 4: Female PCA – 13 traits (Fmax+)

All data



P:C ctrl data v2

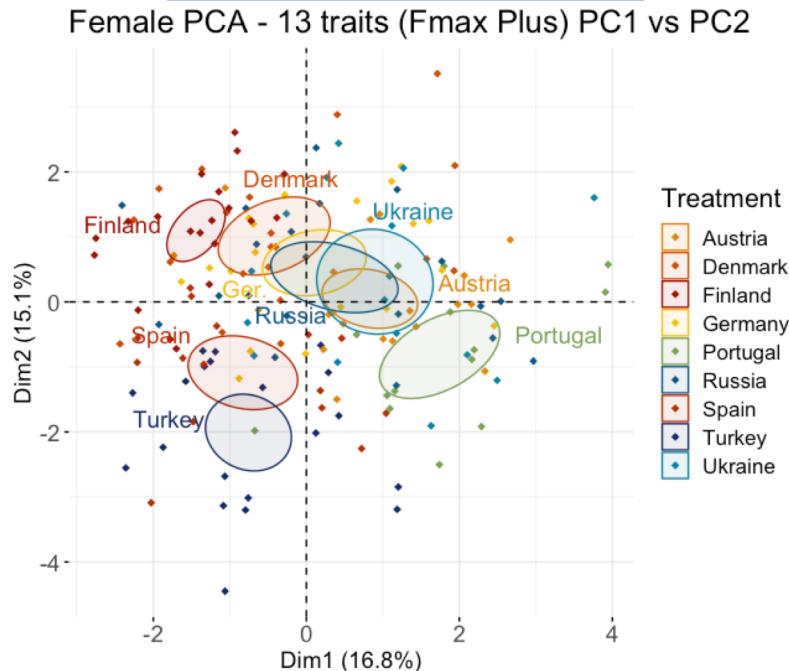


	eigenval	% var	cum % var
comp 1	2.179	16.763	16.763
comp 2	1.959	15.069	31.832
comp 3	1.477	11.361	43.194
comp 4	1.117	8.589	51.783
comp 5	1.072	8.245	60.028
comp 6	1.016	7.817	67.844
comp 7	0.847	6.512	74.356
comp 8	0.789	6.066	80.421
comp 9	0.761	5.855	86.276
comp 10	0.606	4.664	90.940
comp 11	0.487	3.743	94.684
comp 12	0.413	3.173	97.857
comp 13	0.279	2.143	100.000

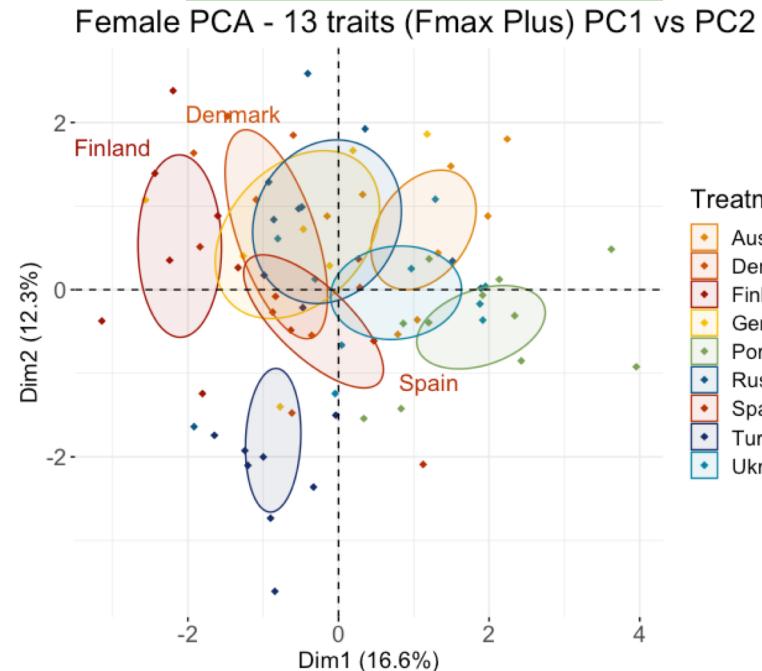
	eigenval	% var	cum % var
comp 1	2.159	16.607	16.607
comp 2	1.605	12.343	28.951
comp 3	1.474	11.339	40.289
comp 4	1.327	10.210	50.500
comp 5	1.085	8.349	58.848
comp 6	1.036	7.970	66.818
comp 7	0.830	6.385	73.203
comp 8	0.816	6.276	79.479
comp 9	0.696	5.356	84.835
comp 10	0.615	4.728	89.563
comp 11	0.550	4.231	93.794
comp 12	0.450	3.461	97.255
comp 13	0.357	2.745	100.000

## 4: Female PCA – 13 traits (Fmax+)

All data



P:C ctrl data v2



	<b>Dim.1</b>	<b>Dim.2</b>	<b>Dim.3</b>	<b>Dim.4</b>
CCRT_F	-0.122	-0.020	<b>0.446</b>	0.587
CSM_F	-0.004	0.059	<b>-0.447</b>	0.096
DT_A_F	0.276	0.055	-0.038	0.219
Dia_F	0.085	0.216	<b>0.483</b>	0.399
DW_F	<b>0.753</b>	0.159	-0.228	0.147
Fec_F	-0.102	<b>0.633</b>	-0.264	-0.020
HSM_F	0.075	<b>0.435</b>	<b>0.543</b>	-0.180
LS_F	<b>-0.453</b>	<b>0.417</b>	-0.319	-0.225
Pgm_Tl_F	0.293	0.233	<b>0.454</b>	-0.529
SR_F	<b>0.502</b>	<b>0.556</b>	-0.288	0.327
TL_F	<b>0.592</b>	-0.377	-0.150	-0.084
WA_L_F	<b>0.774</b>	-0.002	0.109	-0.239
Via_NA	-0.073	<b>0.782</b>	0.040	-0.027

	<b>Dim.1</b>	<b>Dim.2</b>	<b>Dim.3</b>	<b>Dim.4</b>
CCRT_F	-0.224	-0.186	<b>-0.633</b>	0.125
CSM_F	-0.243	0.107	0.356	0.553
DT_A_F	0.261	<b>0.525</b>	-0.060	0.415
Dia_F	-0.001	0.169	<b>-0.511</b>	-0.001
DW_F	<b>0.684</b>	0.142	-0.225	0.216
Fec_F	-0.142	0.023	<b>0.586</b>	0.393
HSM_F	0.139	<b>0.650</b>	-0.074	-0.382
LS_F	-0.132	0.359	0.357	-0.485
Pgm_Tl_F	<b>0.584</b>	-0.114	0.125	-0.198
SR_F	0.200	0.261	-0.226	0.458
TL_F	<b>0.605</b>	-0.241	0.280	0.009
WA_L_F	<b>0.840</b>	-0.097	0.073	-0.038
Via_NA	-0.065	<b>0.731</b>	0.066	-0.020

# PCA 4 results

- Similar results to PCA 2 and PCA 3.
- Positive correlation between HSM and Via maintained for PC2
- Negative correlation between CCRT and Dia maintained in PC3
- Negative correlation between LS and SR moves from PC1 in **all data** to PC4 in **P:C control**
- Loss of some other trait correlations

# Summary

- Some important changes to trait correlations between **all data** and **P:C controlled data**. Some patterns remain similar, but the North/South divide (at least in females) is less clear.
- Development time has a stronger effect. Could within-population DT\_A variability be more influenced by diet than other traits? Perhaps not surprising, given nutritional/resource thresholds for metamorphosis?