

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

05/10/2022

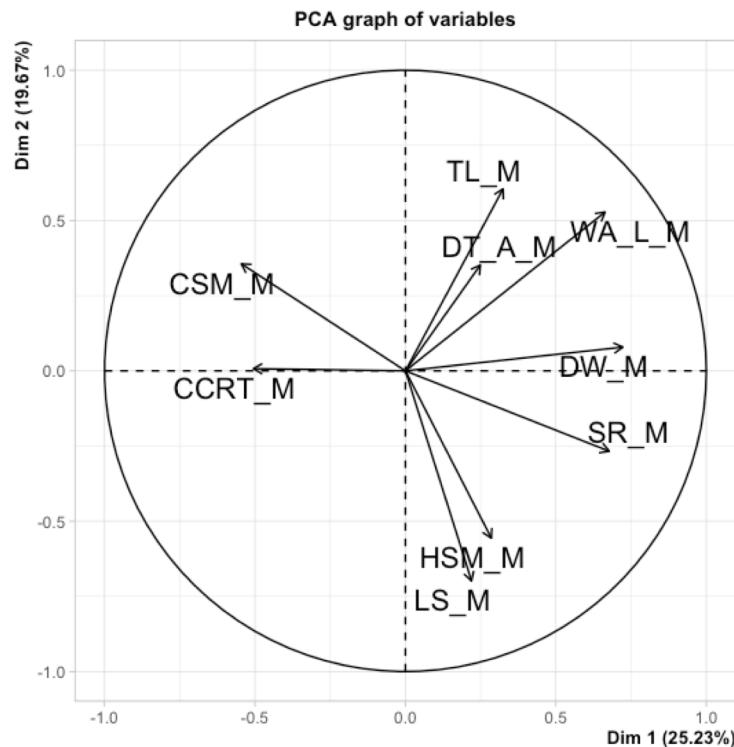
Notes

- 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

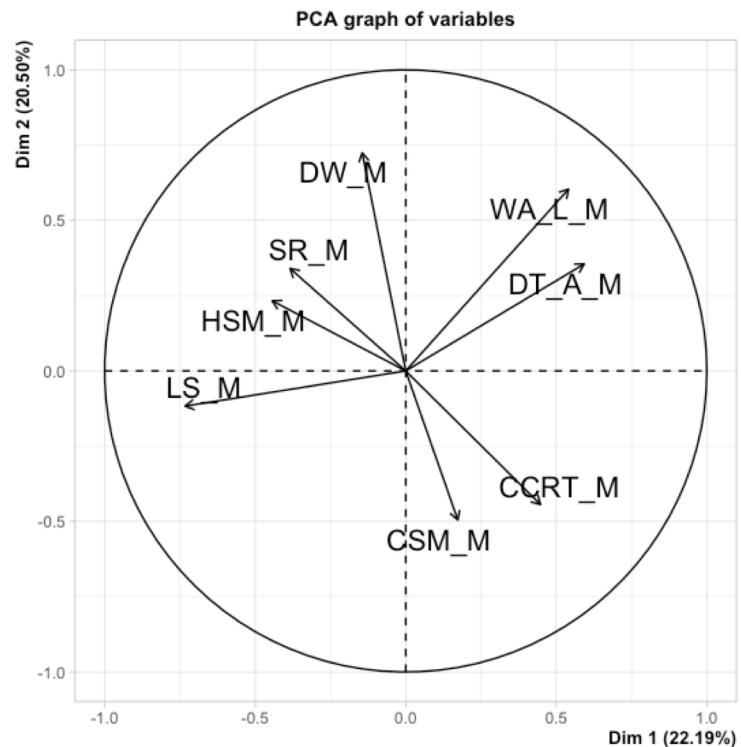
All data

1: Male PCA - 9 traits (M9)

P:C control data



	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



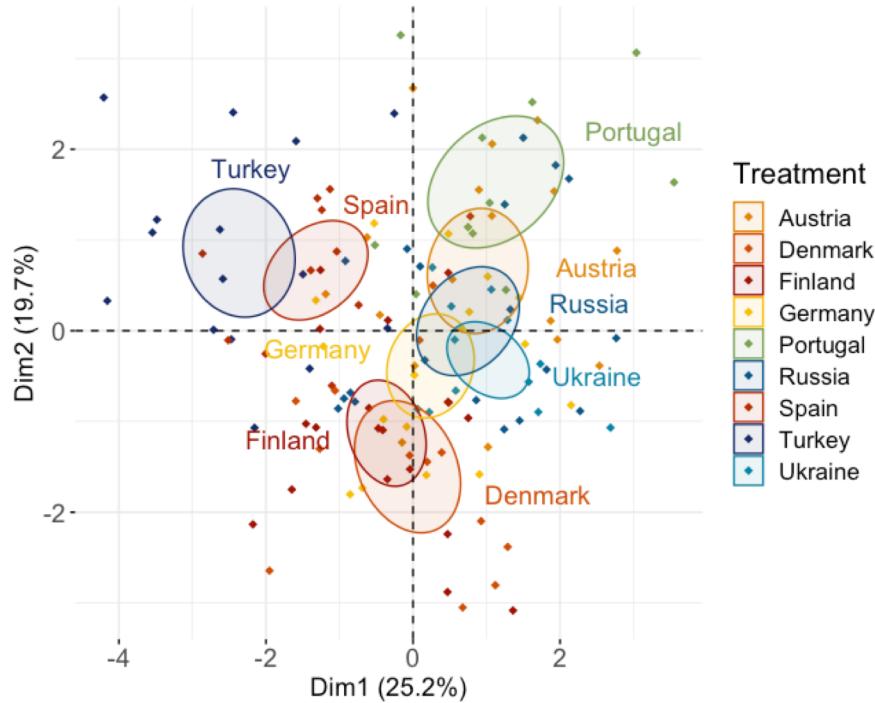
	eigenval	% var	cum % var
comp 1	1.775	22.189	22.189
comp 2	1.640	20.504	42.693
comp 3	1.395	17.443	60.136
comp 4	0.831	10.388	70.524
comp 5	0.748	9.354	79.878
comp 6	0.669	8.363	88.241
comp 7	0.525	6.564	94.805
comp 8	0.416	5.195	100.000

All data

1: Male PCA - 9 traits (M9)

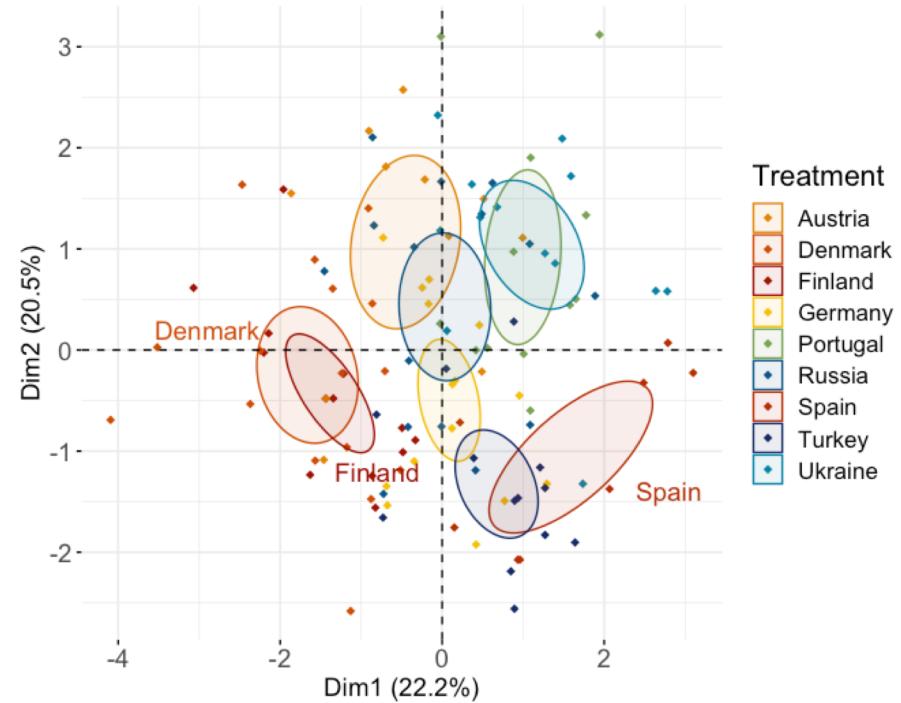
P:C control data

Male PCA - 9 traits (M9) PC1 vs PC2



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

Male PCA - 9 traits (M9) PC1 vs PC2



	Dim.1	Dim.2	Dim.3	Dim.4
CCRT_M	0.447	-0.444	0.263	0.553
CSM_M	0.173	-0.495	0.522	-0.437
DT_A_M	0.593	0.355	-0.093	0.379
DW_M	-0.145	0.724	0.386	-0.137
HSM_M	-0.443	0.233	-0.600	0.082
LS_M	-0.732	-0.117	0.191	0.298
SR_M	-0.384	0.340	0.701	0.247
TL_M
WA_L_M	0.541	0.604	0.086	-0.123

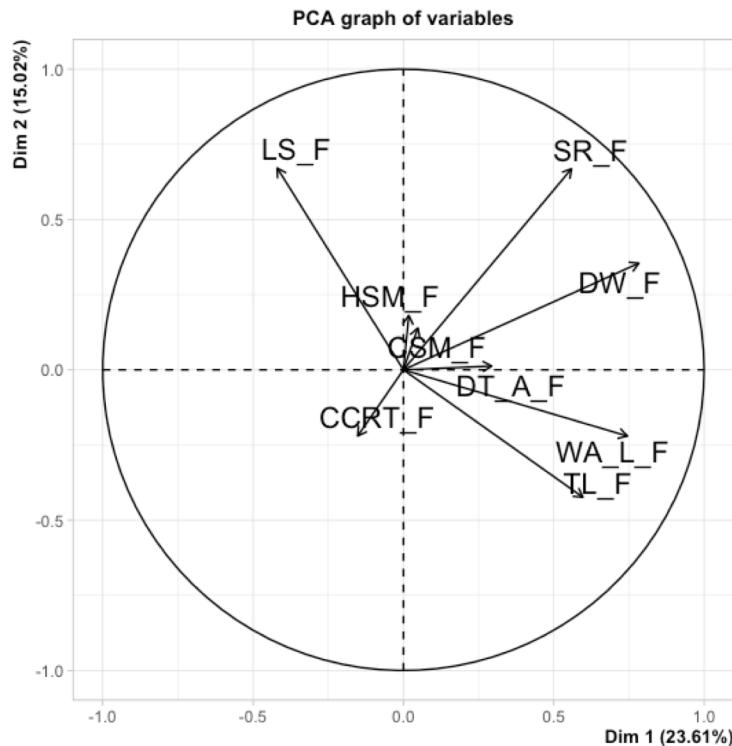
PCA 1 differences

- The main axes of variation have ‘swapped’.
 - In the **all data** analysis, CCRT + CSM (-ve) and DW + WA (+ve) load on to PC1, in the **P:C control**, they load onto PC2.
 - In **all data**, HSM + LS (-ve) and WA (+ve) load on to PC2, in the **P:C control** they load onto PC1
 - A direct inverse correlation between HSM and CSM + SR has strengthened for PC3 in the **P:C control**
- What could be driving changes?
 - There is no TL in **P:C control**, so the body size correlations may be less strong?
 - In the **P:C control** DT_A loads onto PC1 (but in **all data** it only loads strongly onto PC4)

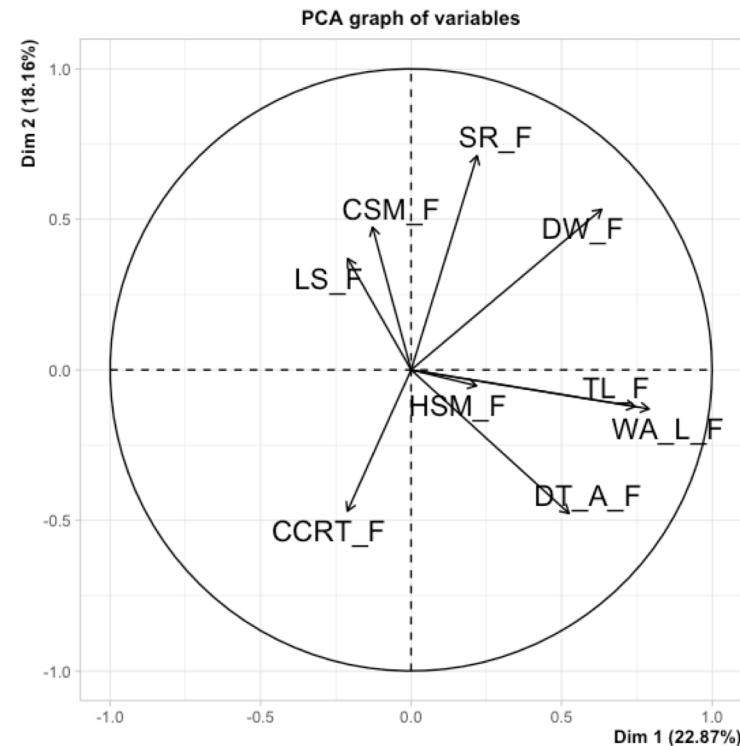
All data

2: Female PCA – 9 traits (F9)

P:C control data



	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

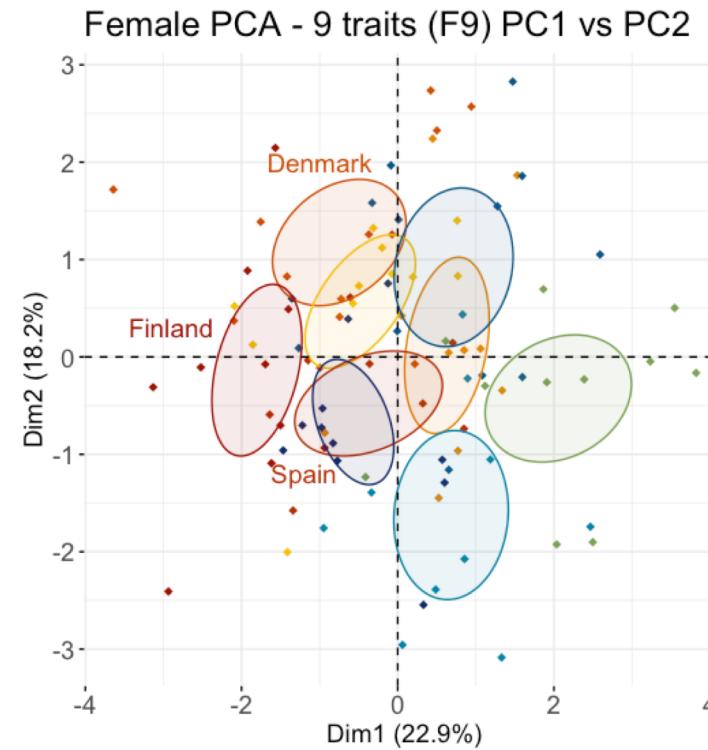
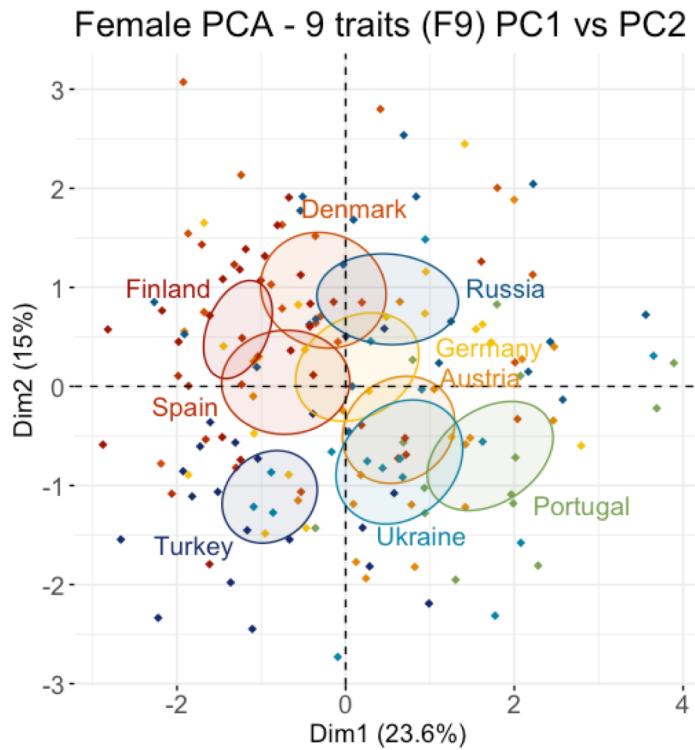


	eigenval	% var	cum % var
comp 1	2.058	22.866	22.866
comp 2	1.634	18.155	41.021
comp 3	1.289	14.327	55.348
comp 4	1.035	11.501	66.849
comp 5	0.905	10.054	76.903
comp 6	0.749	8.325	85.228
comp 7	0.513	5.701	90.930
comp 8	0.476	5.294	96.224
comp 9	0.340	3.776	100.000

All data

2: Female PCA – 9 traits (F9)

P:C control data



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

	Dim.1	Dim.2	Dim.3	Dim.4
CCRT_F	-0.212	-0.469	0.518	0.532
CSM_F	-0.128	0.474	0.366	-0.567
DT_A_F	0.525	-0.477	0.257	-0.165
DW_F	0.633	0.533	0.198	0.239
HSM_F	0.217	-0.053	-0.534	0.394
LS_F	-0.211	0.370	-0.581	0.054
SR_F	0.219	0.712	0.341	0.397
TL_F	0.745	-0.122	-0.205	-0.142
WA_L_F	0.791	-0.130	-0.041	-0.101

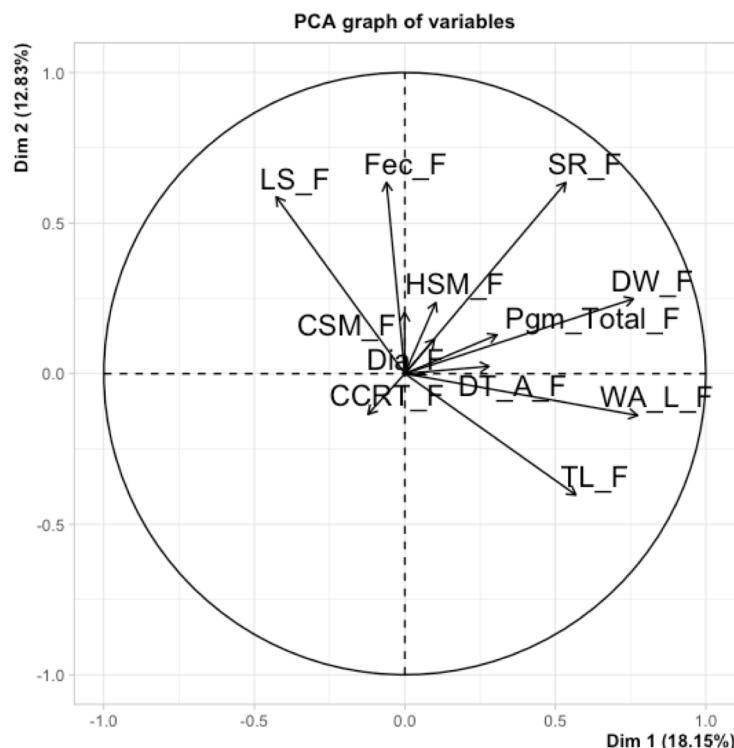
PCA 2 results

- 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 negatively correlate to LS, and in **P:C control** they positively correlate with DT_A.
- The negative correlation between CCRT and CSM moves from PC2 in **all data** to PC3 in **P:C control**, and the negative correlation between CSM and HSM is weaker (loading < 0.4)
- Some trait correlations along PC2 and PC3 appear to have broken down
- Again, it seems like DT_A is driving these changes (it correlates with both PC1 and PC2 in **P:C control**, but only PC4 in **all data**)

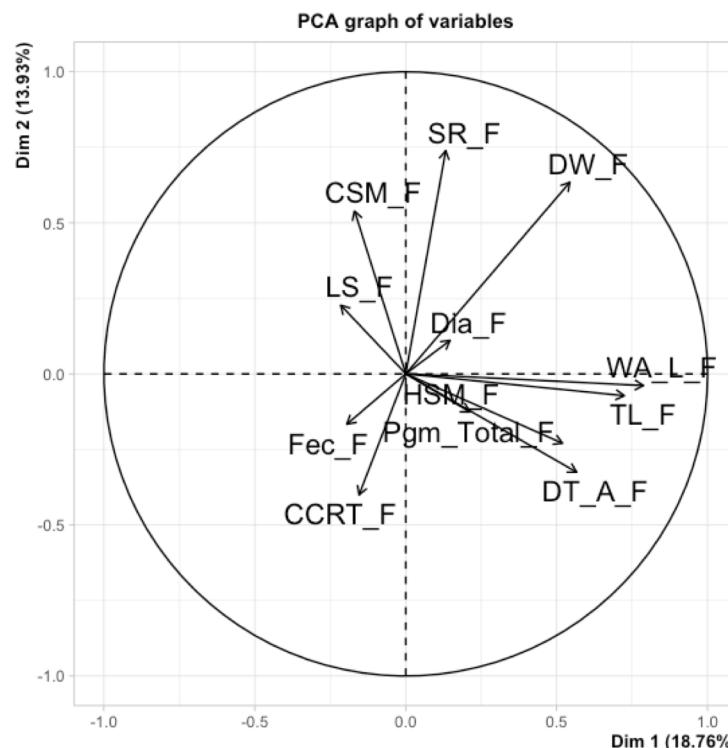
All data

3: Female PCA – 12 traits (Fmax)

P:C control data



	eigenval	% var	cum % var
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

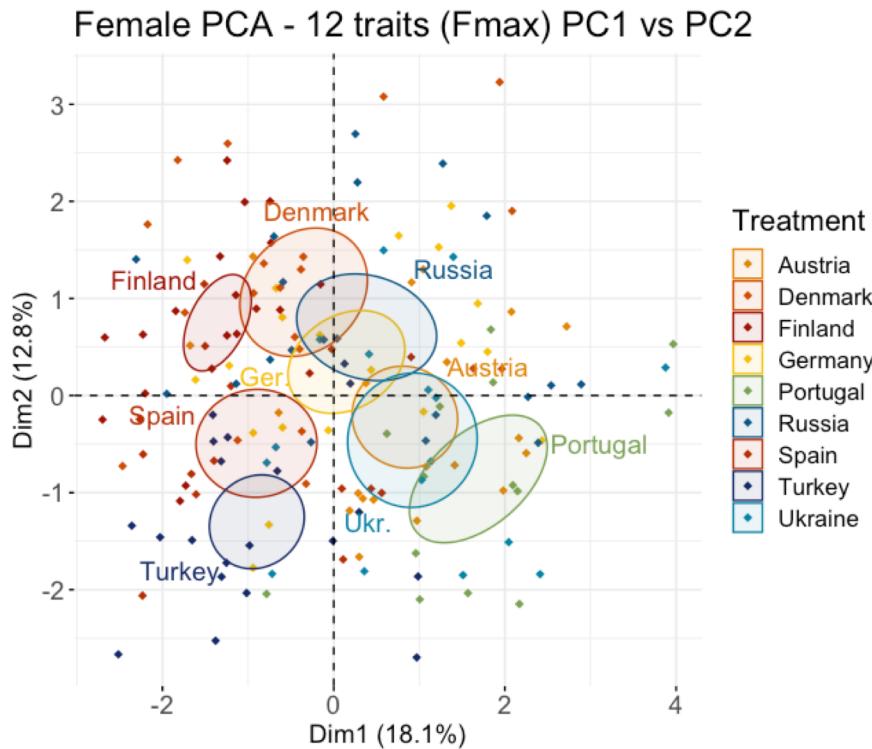


	eigenval	% var	cum % var
comp 1	2.251	18.761	18.761
comp 2	1.672	13.931	32.693
comp 3	1.554	12.951	45.643
comp 4	1.093	9.112	54.755
comp 5	0.972	8.099	62.855
comp 6	0.952	7.931	70.785
comp 7	0.864	7.202	77.987
comp 8	0.759	6.329	84.316
comp 9	0.597	4.976	89.293
comp 10	0.507	4.221	93.514
comp 11	0.450	3.748	97.262
comp 12	0.329	2.738	100.000

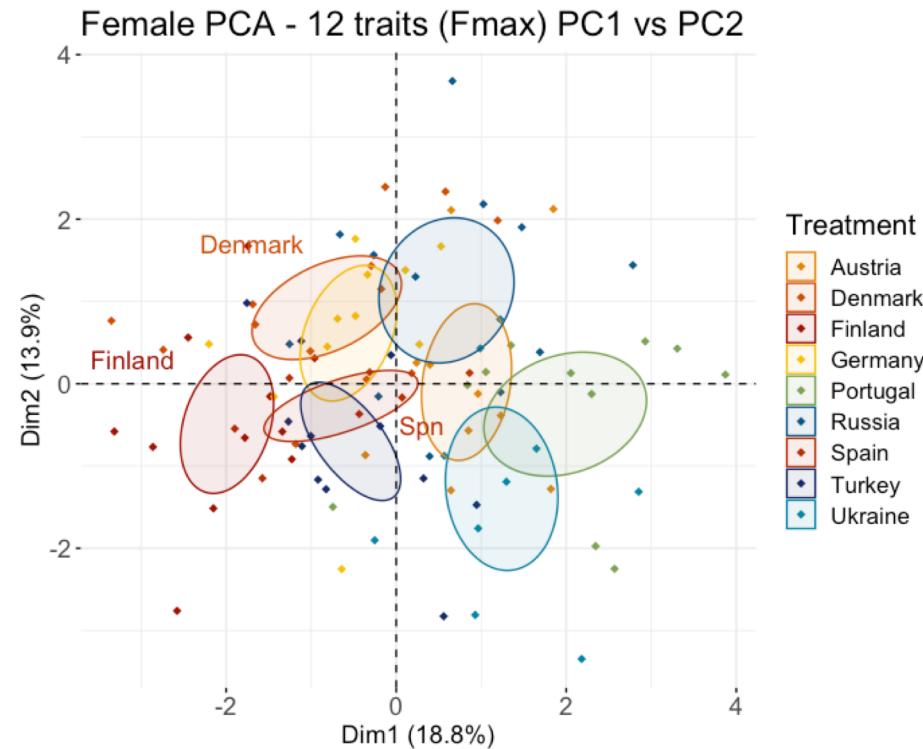
All data

3: Female PCA – 12 traits (Fmax)

P:C control data



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



	Dim.1	Dim.2	Dim.3	Dim.4
CCRT_F	-0.155	-0.401	0.473	0.553
CSM_F	-0.170	0.539	0.326	-0.339
DT_A_F	0.566	-0.325	0.409	-0.049
Dia_F	0.146	0.110	0.670	-0.250
DW_F	0.544	0.634	0.014	0.265
Fec_F	-0.195	-0.167	-0.293	0.419
HSM_F	0.212	-0.126	-0.489	0.055
LS_F	-0.215	0.227	-0.465	-0.316
Pgm_Total_F	0.519	-0.230	-0.102	-0.139
SR_F	0.132	0.739	0.023	0.488
TL_F	0.724	-0.072	-0.225	-0.039
WA_L_F	0.787	-0.039	-0.064	-0.018

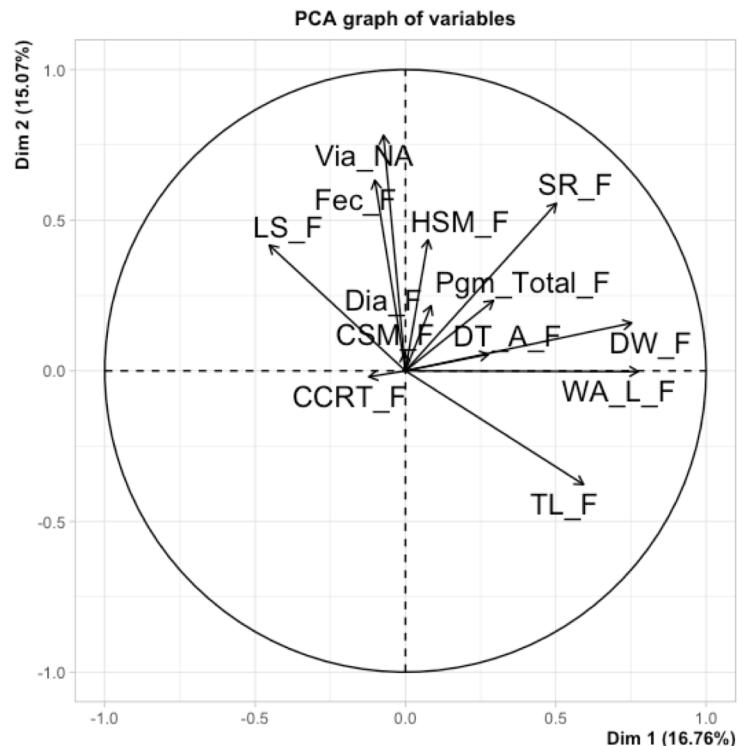
PCA 3 results

- 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 DT_A and Pigm.
- The negative correlation between CCRT and CSM moves from PC3 in **all data** to PC2 in **P:C control** (similar but inverse to PCA 2 result).
- Possible negative correlation between CSM and HSM, but weaker (loading < 0.4)
- DT_A effect? Loss of fecundity correlations?

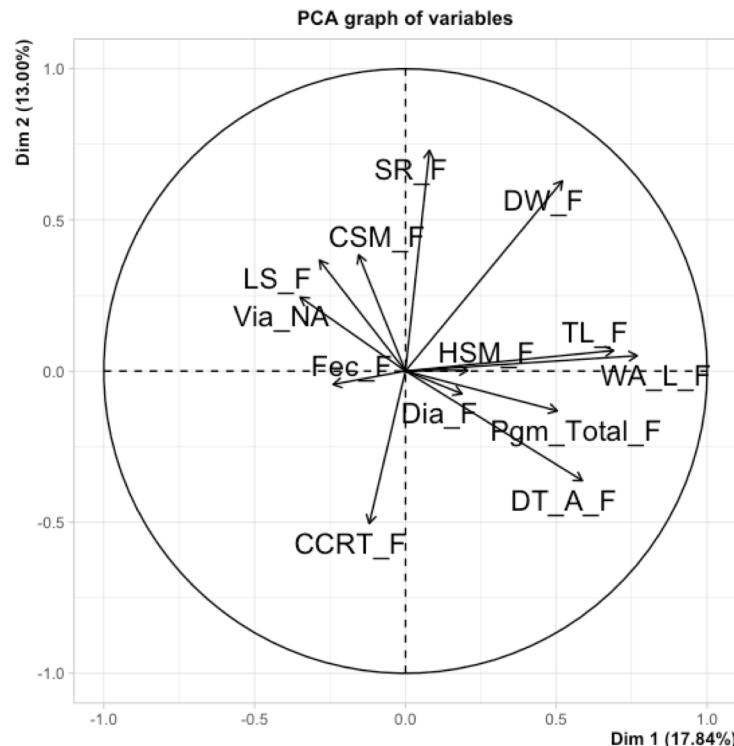
All data

4: Female PCA – 13 traits (Fmax+)

P:C control data



	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

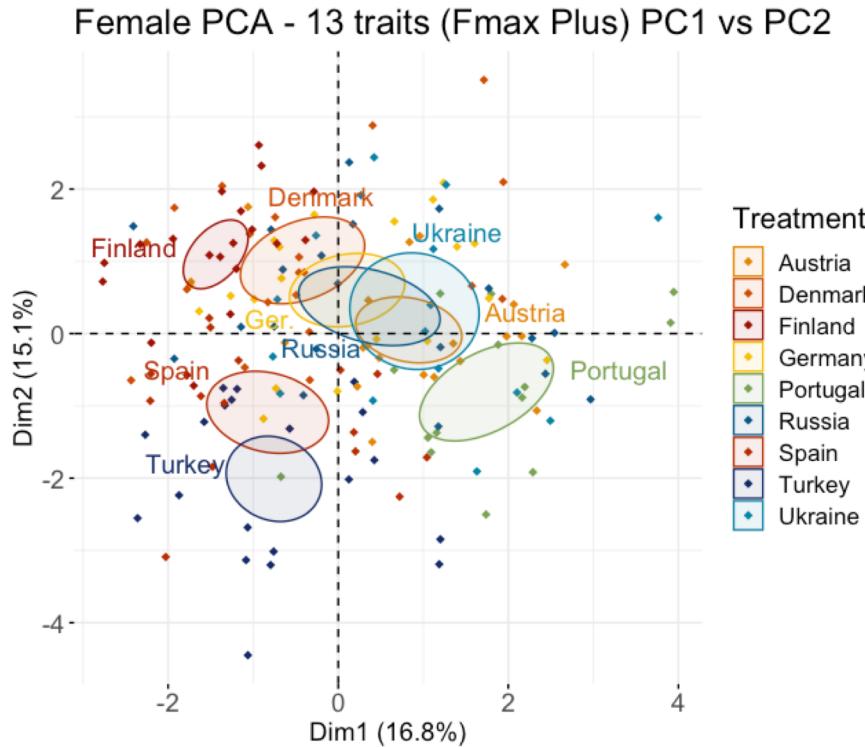


	eigenval	% var	cum % var
comp 1	2.319	17.836	17.836
comp 2	1.690	13.000	30.836
comp 3	1.607	12.362	43.198
comp 4	1.157	8.898	52.096
comp 5	1.068	8.219	60.314
comp 6	0.972	7.476	67.791
comp 7	0.865	6.651	74.441
comp 8	0.782	6.012	80.453
comp 9	0.707	5.437	85.890
comp 10	0.562	4.322	90.212
comp 11	0.504	3.876	94.088
comp 12	0.446	3.428	97.516
comp 13	0.323	2.484	100.000

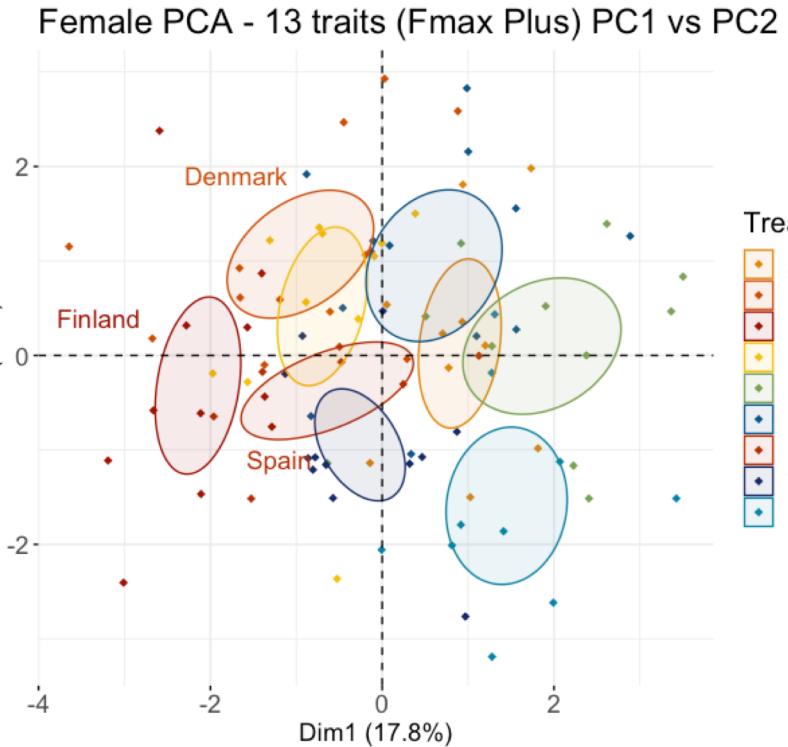
All data

4: Female PCA – 13 traits (Fmax+)

P:C control data



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



	Dim.1	Dim.2	Dim.3	Dim.4
CCRT_F	-0.120	-0.504	-0.286	0.464
CSM_F	-0.155	0.384	-0.510	-0.255
DT_A_F	0.587	-0.363	-0.198	0.231
Dia_F	0.188	-0.075	-0.633	0.118
DW_F	0.520	0.629	-0.182	0.069
Fec_F	-0.240	-0.044	0.367	0.448
HSM_F	0.207	0.002	0.455	-0.372
LS_F	-0.285	0.367	0.383	-0.013
Pgm_Total_F	0.503	-0.132	0.231	0.104
SR_F	0.080	0.731	-0.206	0.381
TL_F	0.690	0.068	0.309	0.083
WA_L_F	0.768	0.051	0.146	0.070
Via_NA	-0.349	0.245	0.302	0.545

PCA 4 results

- Similar results to PCA 2 and PCA 3.
- Negative correlation between CSM and HSM on PC3 is now maintained with highish loadings (> 0.4), although correlation of dia has switched signs.
 - Across PCA 3 and PCA 4 there is a disassociation of the **all data** PC3 (+CCRT +dia +HSM -CSM)
- Again, DT_A is strong, viability and fecundity do not retain high loading for PC1, 2 or 3

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.
- Strong effect of development time, suggesting that DT_A variability may be more influenced by diet than other traits? Perhaps not surprising, given nutritional/resource thresholds for metamorphosis?
- On the other hand, fecundity, viability (and to a lesser extent life span) lose importance – why might this be?
 - Could inter-line (genotypic) variability be more important in these traits than diet-induced variability?