**PCA**

Vegetarian finch (*Platyspiza crassirostris*)

Pearson correlation matrix

|  |  |  |  |
| --- | --- | --- | --- |
|  | FST | ∆ Tajima’s D | ∆AF |
| FST | 1.000 | 0.098 | 0.355 |
| ∆ Tajima’s D | 0.098 | 1.000 | 0.144 |
| |∆AF| | 0.355 | 0.144 | 1.000 |

PCA loadings / rotations

|  |  |  |  |
| --- | --- | --- | --- |
|  | PC1 | PC2 | PC3 |
| Z FST | 0. 644 | -0. 338 | 0. 686 |
| Z |∆AF| | 0. 666 | -0. 192 | 0. 720 |
| Z ∆ Tajima’s D | -0. 375 | -0. 921 | -0. 101 |

PC Importances

|  |  |  |  |
| --- | --- | --- | --- |
|  | PC1 | PC2 | PC3 |
| Standard deviation | 1.194 | 0.966 | 0.801 |
| Proportion of variance | 0.475 | 0.311 | 0.214 |
| Cumulative proportion | 0.475 | 0.786 | 1.000 |

GO terms (PANTHER)

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| PANTHER GO-Slim Biological Process | Background genes | Selected genes | Fold enrichment | P-value | FDR |
| angiogenesis (GO:0001525) | 32 | 4 | 29.73 | 9.12E-06 | 1.89E-02 |
| blood vessel morphogenesis (GO:0048514) | 36 | 4 | 26.42 | 1.48E-05 | 1.53E-02 |
| blood vessel development (GO:0001568) | 37 | 4 | 25.71 | 1.65E-05 | 1.14E-02 |
| vasculature development (GO:0001944) | 38 | 4 | 25.03 | 1.84E-05 | 9.55E-03 |
| tube morphogenesis (GO:0035239) | 38 | 4 | 25.03 | 1.84E-05 | 7.64E-03 |
| tube development (GO:0035295) | 40 | 4 | 23.78 | 2.26E-05 | 7.83E-03 |

Significant Genes:

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Symbol | Name | Chr\_# | Chr\_std | Start | Stop |
| HPSE | Heparanase | 4 | NC\_044574.1 | 59804605 | 59815556 |
| ANGPT1 | Angiopoietin 1 | 2 | NC\_044572.1 | 133469688 | 133623609 |
| ITGA2B | Integrin subunit alpha 2b | 27 | NC\_044597.1 | 1174211 | 1182568 |

Notes:

If we remove all significant genes linked to these angiogenesis genes, we find two additional significant GO terms: “regulation of cell adhesion mediated by integrin” and “cell-matrix adhesion.” The first term is influenced by HPSE and ITGA2B only, but the second is PODXL

Medium ground finch (*Geospiza fortis*)

Pearson correlation matrix

|  |  |  |  |
| --- | --- | --- | --- |
|  | FST | ∆ Tajima’s D | ∆AF |
| FST | 1.000 | 0.060 | 0.470 |
| ∆ Tajima’s D | 0.060 | 1.000 | 0.027 |
| |∆AF| | 0.470 | 0.027 | 1.000 |

PCA loadings / rotations

|  |  |  |  |
| --- | --- | --- | --- |
|  | PC1 | PC2 | PC3 |
| Z FST | -0.704 | 0.055 | -0.709 |
| Z |∆AF| | -0.699 | 0.126 | 0.704 |
| Z ∆ Tajima’s D | 0.128 | 0.990 | -0.050 |

PC Importances

|  |  |  |  |
| --- | --- | --- | --- |
|  | PC1 | PC2 | PC3 |
| Standard deviation | 1.216 | 0.997 | 0.727 |
| Proportion of variance | 0.493 | 0.331 | 0.176 |
| Cumulative proportion | 0.493 | 0.824 | 1.000 |

GO Terms PANTHER

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| PANTHER GO-Slim Biological Process | Background genes | Selected genes | Fold enrichment | P-value | FDR |
| skeletal muscle tissue development (GO:0007519) | 14 | 3 | 84.93 | 5.18E-06 | 1.08E-02 |
| skeletal muscle organ development (GO:0060538) | 16 | 3 | 74.31 | 7.94E-06 | 8.25E-03 |
| muscle organ development (GO:0007517) | 20 | 3 | 59.45 | 1.61E-05 | 1.11E-02 |
| muscle tissue development (GO:0060537) | 30 | 3 | 39.63 | 5.62E-05 | 2.92E-02 |
| positive regulation of cell development (GO:0010720) | 33 | 3 | 36.03 | 7.51E-05 | 3.12E-02 |

Significant Genes

|  |  |
| --- | --- |
| MYF5 | Myogenic factor 5 |
| MYF6 | Myogenic factor 6 |

Small tree finch (*Camarhynchus parvulus*)

Pearson correlation matrix

|  |  |  |  |
| --- | --- | --- | --- |
|  | FST | ∆ Tajima’s D | ∆AF |
| FST | 1.000 | 0.031 | 0.49 |
| ∆ Tajima’s D | 0.031 | 1.000 | -0.004 |
| |∆AF| | 0.459 | -0.004 | 1.000 |

PCA loadings / rotations

|  |  |  |  |
| --- | --- | --- | --- |
|  | PC1 | PC2 | PC3 |
| Z FST | -0.707 | -0.008 | -0.707 |
| Z |∆AF| | 0.706 | 0.067 | 0.705 |
| Z ∆ Tajima’s D | -0.042 | 0.998 | -0.053 |

PC Importances

|  |  |  |  |
| --- | --- | --- | --- |
|  | PC1 | PC2 | PC3 |
| Standard deviation | 1.208 | 1.000 | 0.735 |
| Proportion of variance | 0.487 | 0.334 | 0.180 |
| Cumulative proportion | 0.487 | 0.820 | 1.000 |

GO Terms PANTHER

NONE

Combined analyses

GO Terms of all “selected gene” lists combined

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| PANTHER GO-Slim Biological Process | Background genes | Selected genes | Fold enrichment | P-value | FDR |
| angiogenesis (GO:0001525) | 32 | 5 | 16.89 | 1.02E-05 | 2.12E-02 |
| blood vessel morphogenesis (GO:0048514) | 36 | 5 | 15.01 | 1.86E-05 | 1.28E-02 |
| blood vessel development (GO:0001568) | 37 | 5 | 14.61 | 2.13E-05 | 1.11E-02 |
| vasculature development (GO:0001944) | 38 | 5 | 14.22 | 2.43E-05 | 1.01E-02 |
| tube morphogenesis (GO:0035239) | 38 | 5 | 14.22 | 2.43E-05 | 8.43E-03 |
| tube development (GO:0035295) | 40 | 5 | 13.51 | 3.14E-05 | 9.33E-03 |
| anatomical structure formation involved in morphogenesis (GO:0048646) | 83 | 7 | 9.12 | 1.11E-05 | 1.16E-02 |

Genes involved:

Angiogenesis stuff: HPSE, ANGPT1, ITGA2B, VEGFC

Morphogenesis: HPSE, ANGPT1, COL12A1, ITGA2B, VEGFC

VEGFC and COL12A1 are in PAR

If we look at overlapping lists of pathways identified by panther, one is identified in all three species (), and two are identified in CRA and PAR (Integrin signaling pathway and platelet-derived-growth factor (PDGF) signaling pathway). The first is involved in cell growth, and the latter has obvious implications for parasite tolerance/resistance.

Integrin signaling pathway genes:

ITGA2B (CRA)

COL12A1 (PAR)

LIMS1 (PAR)

PDGF genes:

ARHGAP27

STARD13 (PAR)

DLC1 (PAR)