Sequence-based decomposition of genomic variance for starvation resistance in *Drosophila melanogaster*

Stefan McKinnon Høj-Edwards

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CENTER FOR QUANTITATIVE GENETICS AND GENOMICS

$$y = X\beta + g_F + g + e$$

$$\begin{pmatrix} g_F \\ g \end{pmatrix} \sim N\left[0, \begin{pmatrix} G_F\sigma_F^2 & 0 \\ 0 & G\sigma_g^2 \end{pmatrix}\right]$$

$$\begin{pmatrix} y_T \\ \{y_P\} \end{pmatrix} = \begin{pmatrix} X_T\beta \\ X_P\beta \end{pmatrix} + \begin{pmatrix} g_{F,T} \\ g_{F,P} \end{pmatrix} + \begin{pmatrix} g_T \\ g_P \end{pmatrix} + \begin{pmatrix} e_T \\ e_P \end{pmatrix}$$

$$\hat{y}_P = E[y_P|y_T] = X_P\beta + \left(G_{F,TP}\sigma_F^2 + G_{TP}\sigma_g^2\right)\left[G_{F,T}\sigma_S^2 + G_T\sigma_g^2 + I\sigma_e^2\right]^{-1}(y_T - X_T\beta)$$

$$PA = \frac{1}{n}\sum_{n} \mathrm{Cor}(\hat{y}_P, y_P)$$

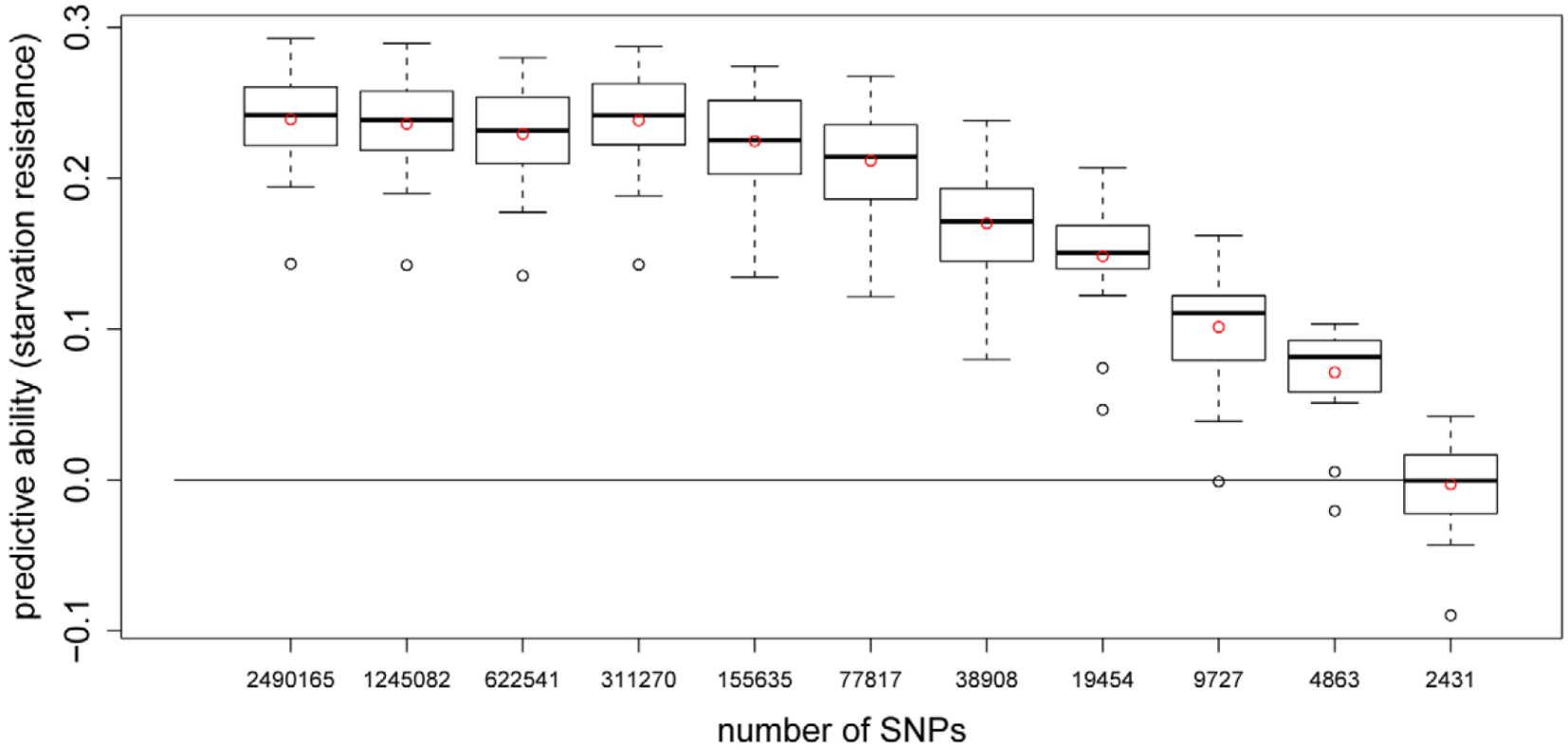
Prediction ability in *D. melanogaster*

Drosophila melanogaster

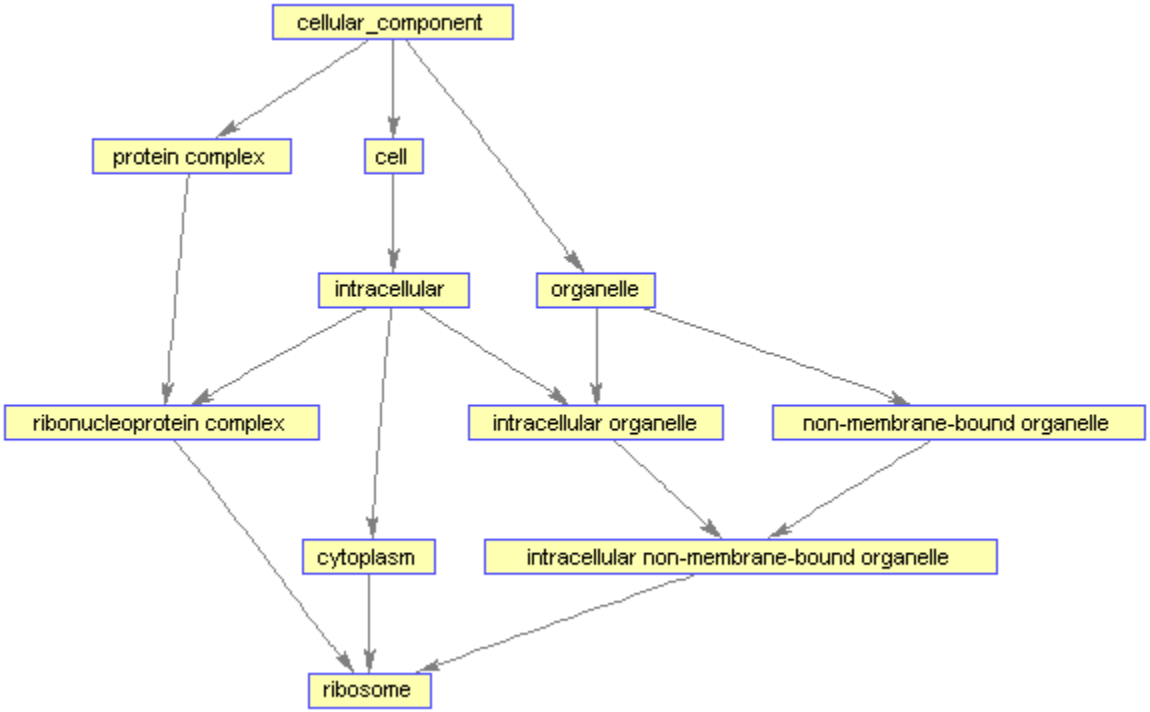
D. melanogaster Genetic Reference Panel

197 homogenous lines

Starvation Resistance



Ober et al. (2012)
doi: 10.1371/journal.pgen.1002685


cellular_component
protein complex
cell
intracellular
organelle
ribonucleoprotein complex
intracellular organelle
non-membrane-bound organelle
cytoplasm
intracellular non-membrane-bound organelle
ribosome

	PA ± std.err	LR	H^2_{set}	Markers	Term
GO:0007474	0.394 ± 0.0266	8.05	85%	29,018	Imaginal disc-derived wing vein specification
GO:0042742	0.373 ± 0.0329	8.64	51%	6,225	Defense response to bacterium
GO:0007464	0.357 ± 0.0283	6.90	48%	14,263	R3/R4 cell fate commitment
GO:0048747	0.355 ± 0.0349	5.38	25%	5,256	Muscle fiber development
GO:0048103	0.352 ± 0.0408	5.92	34%	2,468	Somatic stem cell division
GO:0007465	0.532 ± 0.0373	4.72	31%	5,541	R7 cell fate commitment
GO:0045893	0.351 ± 0.0276	7.40	69%	24,874	Positive regulation of transcription, DNA-dependent
GO:0007458	0.350 ± 0.0278	6.05	39%	3,739	Progression of morphogenetic furrow involved in (…)
GO:0008587	0.349 ± 0.0253	6.10	61%	16,124	Imaginal disc-derived wing margin morphogenesis
GO:0010389	0.348 ± 0.0263	5.19	19%	682	Regulation of G2/M transition of mitotic cell cycle

PA of union of top 10 GO terms:
0.536 ± 0.0233

Predictive ability in cattle

Danish Holstein dairy cattle

4,497 genotyped bulls
(partially by imputation)

621,217 SNPs, 1-5 kb apart

Clinical records of mastitis in daughters

Pathway	Trait	Markers	H^2_{set}	p-value	LR
Pentose phosphate pathway	Mastitis 1.1	182	2.3%	$4 \cdot 10^{-2}$	11.6
Excretory System	Mastitis 1.1	1,639	3.6%	$4 \cdot 10^{-2}$	11.2
Proximal tubule bicarbonate reclamation	Udder-health	187	1.2%	$8 \cdot 10^{-2}$	11.9
Proximal tubule bicarbonate reclamation	Mastitits 1.1	187	2.2%	$1 \cdot 10^{-4}$	24.1

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Discussion

- Bias from biological pathways as prior information
- Population structure

Conclusions

- Workable model for examining genomic features
- Can improve predictive ability
- Improved predictive ability important for both breeding and personalised medicine

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- Per Madsen
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