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Research article

Analysis of immune-related genes during Nora virus infection of *Drosophila melanogaster* using next generation sequencing

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Supplementary

Table S1. Statistical analysis of PANTHER analysis of differentially expressed genes across time points for NV+ and NV− flies. The numbers in the columns indicate a hypergeometric p-value for the PANTHER analysis for days 2, 10, 20 and 30. *The numbers in the table are unmapped IDs, NA = Not applicable because 0 genes were in this specific category. A value of 0 means that the exponent of the p-value was so high (indicating an extremely low p-value), that the p-value cannot be depicted properly by the operating system.

Category name (gene ontology accession number)	Day 2		Day 10		Day 20		Day 30		FlyBase [1]
	Up	Down	Up	Down	Up	Down	Up	Down	# Genes in GO Category
	97*	2*	477*	32*	304*	75*	512*	324*	
Biological adhesion (GO: 0022610)	4.64e−07	NA	2.59e−30	NA	1.27e−19	NA	2.22e−31	1.63e−47	669
Biological regulation (GO: 0065007)	0	NA	0	0	0	0	0	0	16394
Cellular component organization or biogenesis (GO: 0071840)	4.71e−242	NA	0	6.70e−33	0	1.28e−113	0	0	7995
Cellular process (GO: 0009987)	0	NA	0	0	0	0	0	0	43160
Developmental process (GO: 0032502)	4.50e−130	NA	0	5.30e−28	0	2.00e−97	0	0	5667
Growth (GO: 0040007)	3.04e−10	NA	2.78e−39	0.023156	6.23e−28	3.72e−09	1.10e−46	2.80e−46	556
Immune system process (GO:0002376)	NA	NA	2.31e−49	NA	2.37e−37	NA	8.21e−52	4.96e−42	743
Localization (GO: 0051179)	0	NA	0	8.55e−109	0	0	0	0	12057
Locomotion (GO: 0040011)	7.46e−15	NA	1.05e−56	NA	1.44e−39	5.79e−13	2.74e−58	2.30e−58	846
Metabolic process (GO: 0008152)	0	NA	0	0	0	0	0	0	45390
Multicellular organism process (GO: 0032501)	9.58e−226	NA	0	NA	0	4.77e−179	0	0	8101
Reproduction (GO: 0000003)	1.18e−69	NA	1.58e−257	NA	1.43e−183	1.50e−38	4.71e−272	6.57e−191	2773
Response to stimulus (GO: 0050896)	0	NA	0	1.19e−68	0	1.02e−256	0	0	10778
Rhythmic process (GO: 0048511)	0.087659	NA	7.51e−05	NA	8.45e−07	NA	5.34e−06	NA	164

Table S2. PANTHER analysis of differentially expressed genes across time points for NV+ vs. NV− flies. The numbers in the column indicate the total number of genes found either upregulated or downregulated for the immune system processes that were able to be mapped from PANTHER. *This gene is an orthologue described by PANTHER databases.

Day 2		**Day 10**		**Day 20**		**Day 30**	
Up	Down	Up	Down	Up	Down	Up	Down
9	0	26	2	21	3	23	8
CG11319		*Aplip1*	*CG5568*	*Aplip1*	*CG5568*	*Aplip1*	*CG3394*
CG11407		*CG11319*	*Hsp27*	*CG11319*	*Hsp26*	*CG11319*	*CG5568*
CG11407*		*CG11391*		*CG11407*	*Hsp27*	*CG11407*	*CG5708*
CG4461		*CG11407*		*CG11407**		*CG11407**	*dos*
CG45002		*CG11407**		*CG11453*		*CG11453*	*Duox*
Fatp		*CG11453*		*CG15611*		*CG15611*	*Hsp26*
hig		*CG15611*		*CG30456*		*CG17999*	*Hsp27*
Mlp60A		*CG17684*		*CG42673*		*CG30456*	*Jafrac2*
wry		*CG17999*		*CG4328*		*CG42673*	
		CG30456		*CG4461*		*CG4328*	
		CG42673		*CG45002*		*CG4461*	
		CG4328		*CG8834*		*CG45002*	
		CG4461		*CG9993*		*CG4830*	
		CG45002		*Fatp*		*CG8834*	
		CG7409		*fw*		*CG9993*	
		CG8834		*hig*		*Fatp*	
		CG9993		*l(2)efl*		*fw*	
		Fatp		*Lim3**		*hig*	
		fw		*Lim3,Mlp84B*		*l(2)efl*	
		hig		*Mlp60A*		*Lim3**	
		Hsp67Bc		*wry*		*Lim3,Mlp84B*	
		l(2)efl				*Mlp60A*	
		Lim3*				*wry*	
		Lim3,Mlp84B					
		Mlp60A					
		wry					

Table S3. Gene list of differentially expressed immune related genes across time points for NV+ and NV− flies from the manual analysis using a list of *Drosophila* genes with potential relevance to the immune response [2], FlyBase [1], The Inter*active* Fly list of RNAi genes [3]. The red highlighted genes represent the upregulated genes, whereas the green highlighted genes represent the downregulated genes for each comparison.

Table S4. The excel file depicts the data for Nora virus infected (NV+) or uninfected (NV−) flies for each time point (10, 20 and 30) compared to the control time point (day 2). These are comparisons NV+ day 2 vs. day 10, 20 and 30. The comparisons for NV+ vs. NV− for each time point (2, 10, 20 and 30) are also given. The red highlighted genes represent the upregulated genes, whereas the green highlighted genes represent the downregulated genes for each comparison.

References

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2. Lemaitre Lab Uplem, List of *Drosophila* gene potentially involved in the immune response, 2007. Available from: https://lemaitrelab.epfl.ch/page-7767-en.html.
3. Society for Developmental Biology, the Interactive Fly: RNAi and posttranscriptional gene silencing, 2017. Available from: http://www.sdbonline.org/sites/fly/aignfam/rnaistuf.htm.