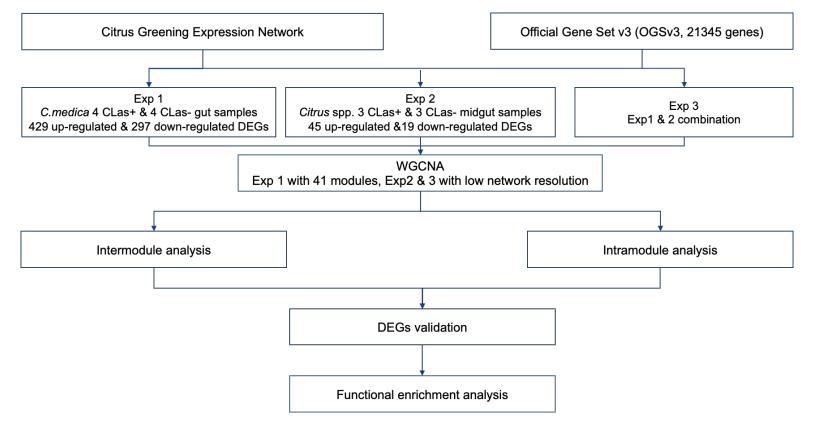
Leveraging co-expression network analysis to establish transcriptional shifts in the gut of the Asian citrus psyllid during *Candidatus* Liberibacter asiaticus infection

Chang Chen, Joshua B. Benoit, Lukas A Mueller and Surya Saha

Workflow



Experiment settings



Exp1:4 CLas infected and 4 healthy psyllid gut samples from host *C. medica*

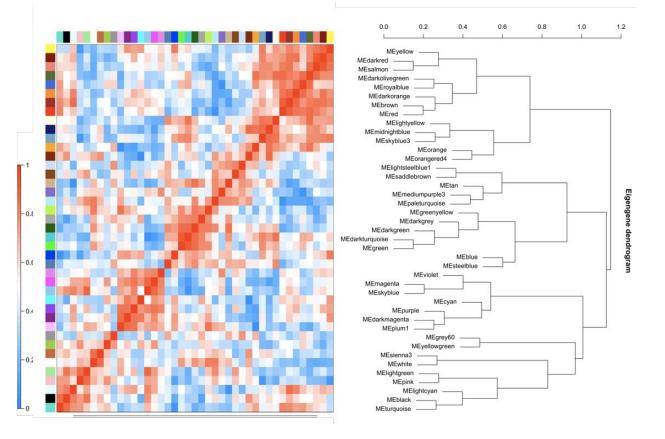


Exp 2:3 CLas infected and 3 healthy psyllid midgut samples from host *Citrus* spp.

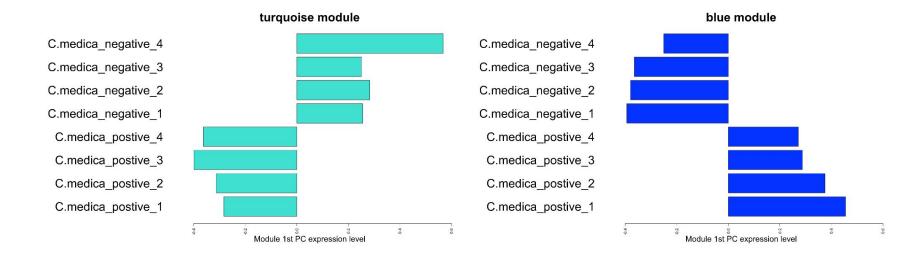


Exp 3 : Combination of Exp 1 & 2

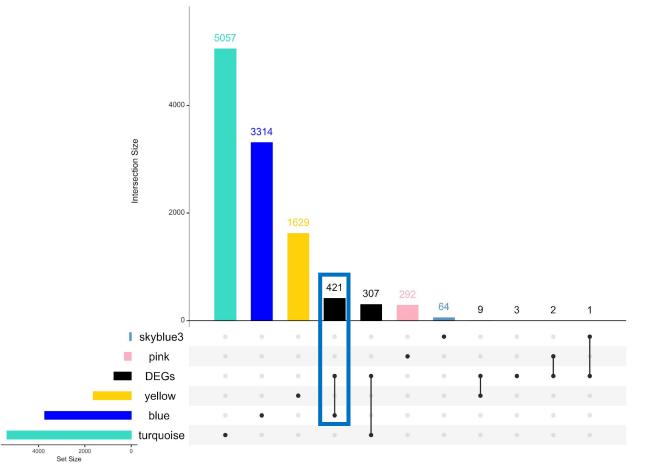
Exp 1 detected 41 modules and intermodule heatmap



Exp 1: Turquoise and blue modules had consistent expression levels between control and infected samples



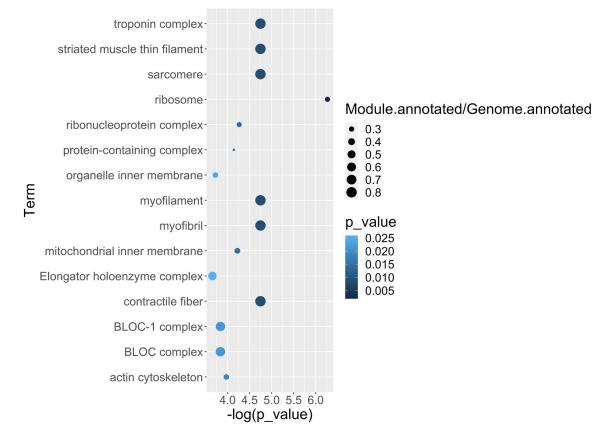
Exp 1: Blue module has the most DEGs



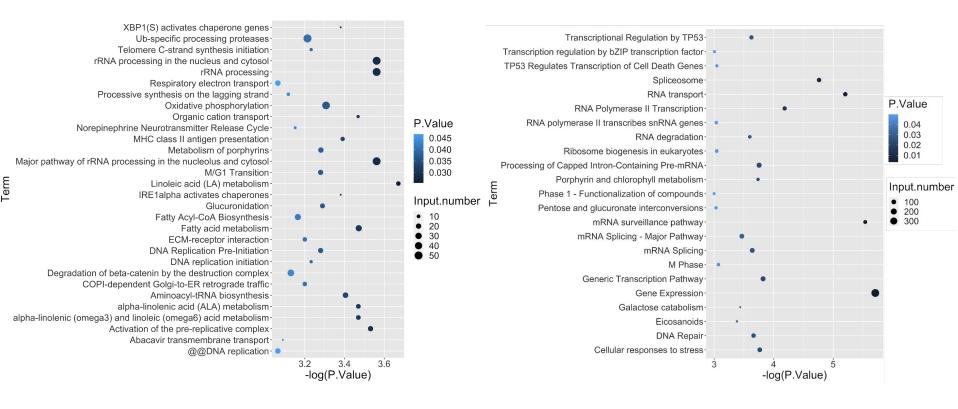
Exp 1: peptidase related functions and iron binding protein expression was up-regulated in GO of DEGs and blue module intersection

	<u>GO.ID</u>	Term	Annotated	Significant	Expected	classic	Aspect
peptidase related functions	GO:0006518	peptide metabolic process	414	36	12.1	2.40E-09	Blue_BP
	GO:0043043	peptide biosynthetic process	391	33	11.43	2.50E-08	Blue_BP
	GO:0004185	serine-type carboxypeptidase activity	18	5	0.51	0.00011	BLue_MF
	GO:0070008	serine-type exopeptidase activity	24	5	0.68	0.00048	BLue_MF
	GO:0008238	exopeptidase activity	58	7	1.65	0.00119	BLue_MF
Iron-binding related functions	GO:0006826	iron ion transport	7	5	0.2	4.10E-07	Blue_BP
	GO:0006879	cellular iron ion homeostasis	7	4	0.2	2.30E-05	Blue_BP
	GO:0000041	transition metal ion transport	14	5	0.41	3.30E-05	Blue_BP
	GO:0055072	iron ion homeostasis	8	4	0.23	4.50E-05	Blue_BP
	GO:0008199	ferric iron binding	6	4	0.17	9.10E-06	BLue_MF

Blue module CC Ontology showed muscle movement related localization



Blue & Turquoise modules KOBAS results revealed core pathways



Turquoise involves in translation-related pathways

Blue involves in metabolism-related pathways

Citrus host-specific psyllid response to CLas infection with distinct DEGs between Exp1 & 2

