

**S1A Table.** Summary of genes involved in pigmentation of insect wings and other body parts identified within the *M. caerulatus* transcriptome. For each gene the corresponding Unigene ID, FPKM values and their one of their main functions are shown.

gene	Unigene ID	read count	FPKM	Main function
Aristaless ( <i>al</i> )	TR167515	8	0.77	<i>Homeobox</i> protein, precedes <i>wg</i> expression - wing pattern evolution
Black ( <i>b</i> )	TR93729	12	0.65	Cysteine sulfinic acid decarboxylase, melanin pathway
Ebony ( <i>e</i> )	TR1248	35	1.40	Inhibits melanization in non-black wing regions
Tan ( <i>t</i> )	TR192472	44	1.81	Melanin pathway
Yellow ( <i>yellow</i> )	TR182547	2,205	61.44	Melanin pathway
	TR183295	2,866	71.30	
Ecdysone Receptor ( <i>EcR</i> )	TR215139	1,262	41.31	Ligand-dependent transcription factor, steroid receptor super family
Araucan ( <i>ara</i> )	TR162214	32	2.24	Transcription factor, imaginal disc-derived and wing vein specification
Henna ( <i>Hn</i> )	TR231264	874	24.74	Pteridine pathway - regulates phenylalanine
bric a brac 1 ( <i>bab</i> )	TR165906	61	3.00	Axis patterning, involved in female specific pigmentation in <i>Drosophila</i> sp.
bric a brac 2 ( <i>bab</i> )	TR206843	149	8.67	
Dor ( <i>dor</i> )	TR165868	1,574	28.41	Pigment granule gene, vacuolar protein sorting-associated protein 18 homolog
Pale protein ( <i>ple</i> )	TR106565	217	4.18	Tyrosine 3-monooxygenase, melanin pathway
	TR158701	32,165	606.37	
	TR200723	10,582	181.28	
Phenoloxidase 2 ( <i>PO</i> )	TR201540	441	8.99	Melanization, final polymerization cuticular pigments, immune response
	TR177287	1,035	13.73	
Rosy ( <i>ry</i> )	TR202403	136	3.21	Xanthine dehydrogenase, pteridine pathway
	TR203851	93	4.56	
White ( <i>w</i> )	TR217941	774	23.58	Ommochrome pathway - ommochrome precursor transporter gene
Scarlet ( <i>st</i> )	TR182410	189	4.21	
	TR16501	89	4.20	Pigment granule gene, organ pigmentation
Mal ( <i>mal</i> )	TR151410	97	2.23	Molybdenum cofactor sulfurase, cofactor for synthetic processes: essential for xanthine dehydrogenase (XDH) and aldehyde oxidase (ADO)
	TR151410	35	1.51	
Prat ( <i>Prat</i> )	TR15147	21	1.54	Amidophosphoribosyltransferase, purine metabolism, pteridine pathway
Vermillion ( <i>v</i> )	TR155117	845	30.07	Ommochrome pathway, ommochrome enzyme gene, brown eye pigment, tryptophan 2,3-dioxygenase

**S1B Table.** Genes of the wing-patterning gene network found in *M. caerulatus* with their corresponding Unigene ID, FPKM values and some of their main functions.

gene	Unigene ID	read count	FPKM	Main function
Hedgehog ( <i>Hh</i> )	TR219975	265	10.63	Short range signaling molecule, embryonic segmentation, segment polarity
Decapentaplegic ( <i>Dpp</i> )	TR23365	19	1.98	Long range signaling molecule; embryonic dorsal/ventral patterning; boundaries between appendage compartments
	TR199155	67	2.56	
Optomotor-blind ( <i>bi</i> [ <i>Omb</i> ])	TR174327	226	20.03	Transcription factor, wing differentiation and wing formation
Spalt major ( <i>salm</i> )	TR119349	79	2.93	Transcription factor, <i>Dpp</i> signaling, controls vein-specific expression of knirps and iroquois gene complex - controls position of the wing veins
	TR211792	132	6.63	
Serrate ( <i>Ser</i> )	TR178981	1,344	28.57	Short range signaling molecule, notch ligand; initiation of wing margin (dorsal-ventral) by controlling cell proliferation
Cut ( <i>cut</i> )	TR148092	98	3.88	Selector gene (homeodomain transcription factor), wing and follicle cell morphogenesis
Achaete / Scute ( <i>ac/sc</i> )	TR159427	610	20.65	Transcription factor, involved in the determination of the neural fate; (scute alone responsible for sex determination)
Wingless ( <i>wg</i> )	TR153309	159	9.53	Long range signaling molecule, segment polarity gene, wing morphogenesis, mediating dorso-ventral compartment boundary
Scalloped ( <i>sd</i> )	TR191046	573	19.87	Selector gene (homeodomain transcription factor), downstream effector molecule (wingless pathway)
Blistered [Serum Response Factor] ( <i>bs</i> [ <i>srf</i> ])	TR175967	390	15.56	Selector gene (homeodomain transcription factor), vein / intervein formation
	TR175378	67	2.22	
Spitz ( <i>spi</i> )	TR160328	60	2.67	Ligand for the epidermal growth factor receptor, differentiation of ommatidial cell types
Ultrabithorax ( <i>Ubx</i> )	TR214266	21	1.88	Selector gene ( <i>Hox</i> gene), 'correct' dorsal and ventral appendage patterning in the third thoracic segment
Sex combs reduced ( <i>Scr</i> )	TR157439	65	4.37	Selector gene ( <i>Hox</i> gene), first thoracic segment development
Extradenticle ( <i>exd</i> )	TR187890	498	31.83	Transcription factor, interacts with homeotic proteins for specificity of homeotic protein binding to DNA - cofactor of <i>Ubx</i> , transformation of segmental identities