

Comparative Transcriptomics of Fat Bodies Between Symbiotic and Quasi-Aposymbiotic Adult Females of *Blattella germanica* with Emphasis on the Metabolic Integration with its Endosymbiont *Blattabacterium* and Its Immune System

Francisco J. Silva, Rebeca Domínguez-Santos, Amparo Latorre and Carlos García-Ferris

		*	20	*	40	*	60	*	80	
PGRP-LB_Ime	:	WGARLPK-SVEHFQGEAPYVIIHHSYMPAVCYSTPDCMKSMRDMQDFHQ-LER	GWN	DIGYSFGIGGDMITGRGFNVIGAHAPK	:	83				
PGRP-SB1_Ime	:	WGAVSAR-SPSRISGAVDYVIIHHSNDPNGCSTSEQCKRMINKNIQSDHK-GRRNFS	DIGYNFIVAGDGKVEYEGRGFGLQGSHPN	:	83					
PGRP-SB2_Ime	:	WCPVPISPRMPRLMPVRLIIHHTVT-APCFNPHQCQLVLRQIRADHM--RRKFRD	DIGYNFLIGGDGRIYEGLGFGRGEHAPR	:	82					
PGRP-SC1b_Ime	:	WGGRGAK-WTVGLGNLYLSYAIHHTAG-SYCETRAQCNAVLQSVQNYHM-DSL	GWPDIGYNFLIGGDGNVYEGRGWNMGAAHAAE	:	82					
PGRP-SC2_Ime	:	WGGRSAT-SKTSLANLYLSYAVIHHTAG-NYCSTKAACITQLQNIQAYHM-DSL	GWADIGYNFLIGGDGNVYEGRGWNMGAAHATN	:	82					
PGRP-LB_1_Bge	:	WGAKAPK-QTANITTPVPFVVIHHTYSPAYCNESDTCKKAMREMCHMHQ-DIR	GWWDIGYNFCVGGTGKVEYEGRGWDIQGAHAPR	:	83					
PGRP-SB1-like_Zne	:	WSAKPAKQRDNITSLPVPFVILHHTYIPKDCNSSECKEAMRSMQMHMQ-DLR	GWFDIGYNFCVGETGEVYEGRGWDIQGAHAPR	:	84					
PGRP-SB1_Cse	:	WGTKPAKETDNITSLPVPFVVLHHTHRPRFCNSEDCEAMRTMQYMHQ-DLR	GWFDIGYNFCVGGTGNVYEGRGWDVQGAHAPR	:	84					
PGRP-LB-like_Sgr	:	WGARPPT-ARETMKTPVPFVVIHHTYKPGFCATTEDCKKAMRTMQDMHQ-FQH	KWN	DIGYNFVVGDDGKVEYEGRGWGIVGAHAPN	:	83				
PGRP-LB_2_Bge	:	WKAVSEV-SVKNISNPVPYVVIHHTYQPPACKTRRKCAADMRSMQNFHM-NTK	QWEDIGYNFLIGNGEVYEGRGWGVVGTHAPN	:	83					
PGRP-LB-like_Zne	:	WGAVAAVSIVVLTSLPVPYVVIHHTFLPGFCNTSQTCEAAMRSMQNYHQ-NTN	QWHDIGYHFCIGGTGKVEYEGRGWDVVGTHTPK	:	84					
PGRP-LB_Cse	:	WDARAPVSSQTIPSLPVPYVVIHHTYLPFGFCNTSQACEAAMRSMQNYHQ-NTQ	KWTDIGYNFCIGGTGQVYEGRGWDIVGTHAPN	:	84					
PGRP-LB-like_Sor	:	WGAKPPT-DVENLTLPVPYVVIHHSYIPAACTKEECINDMQWMQKYHQ-QNNS	WCDIGYNFAVGDDNRIYVGRGWDVAVGAHAPR	:	83					
PGRP-LA-like_Bge	:	WYGEPPK-FERQLQLPAPFVVISHTVT-QPCYEFKTCAESMRTMQGVQV-TDND	LPLDLYSFFVVGDDGNVYEGRGWDVTNMHI-G	:	81					
PGRP-LC-like_Sgr	:	WGGRPPL-AVEKVGTPVPFVVIHHTYIPGACNTSDDCQAKMRSMQDFHM--AK	GLNIGYNFIVGGDNRYVYVGRGWDVGAHSPT	:	82					
PGRP-LA-like_Zne	:	WYGVAPK-FERQLKHPTPFVVISHTAT-PACYSPVCAARMRNFQDVHMGDSHNF	PDIGYSFVVGDDGNVYVGRGWDATNMHS-G	:	82					
PGRP-LA_Cse	:	WNGAPAK-YERRIQLPTPYVVISHTAS-EACFSYTVCAAKMRNFQDLHIGGDLN	LPLDIGYSFVVGDDGNVYEGRGWDVTNMHT-G	:	82					
		*	100	*	120	*	140	*	160	
PGRP-LB_Ime	:	YNDKS-VGIVLIGDWRTLEPPKQMLDAAKNLIAFGVFKGYIDPAYKLLGHRQVR	DETECPGRLFAELISSWPH-FTHINDTEG	:	163					
PGRP-SB1_Ime	:	YNRKS-IGIVFIGNFERSAPSAQMLQNAKDLIELAKQRYLKDNITLFGHRQTKA	TSCPGDALYNEIKTWPH-WRQN----	:	158					
PGRP-SB2_Ime	:	YNSQS-IGIAFIGNFQTGLPPSQMLQAARTLIQIAVQRQVSPNYSVVGHCQTKA	TACPGIHLNELLKWPW-WRKP----	:	158					
PGRP-SC1b_Ime	:	WNPYS-IGISFLGNYNWDTLEPNMISAAQQLINDAVNRGQLSSGYILYGHRQVS	ATECPGTHIWNEIRGWSH-WSG-----	:	156					
PGRP-SC2_Ime	:	WNSKS-IGISFLGNYNNTLTLSAQITAAGLLSDAVSRGQIVSGYILYGHRQVG	STECPGTNIWNEIRTSWN-WKA-----	:	156					
PGRP-LB_1_Bge	:	YNNRS-VGICFIGDYMEDIPTEIMTKAGKELIQLGVDGRSIDKDYKLIGHRQVR	DTLCPGDKFFEIQSWEH-YDPIRDVVP	:	163					
PGRP-SB1-like_Zne	:	YNNRS-TGICFIGDFMNSLPTPEMMEAAKDLIKCGVNRSIAEDYKLLGHRQVR	NLCPGDTFYENITTWPH-WDPLQDVVP	:	164					
PGRP-SB1_Cse	:	YNNRS-TGICFIGDFMDSLPTPEMMEAAKDLIKCGVERGSIADVYKLLGHRQVR	DTLCPGDTFYENITTWSH-WDPLADVVT	:	164					
PGRP-LB-like_Sgr	:	YNSRS-IGISFIGDYRTSNVPTPAMLKAGQQLIRCGVARGQIAADYKLLGHRQVR	ATECPGDAFFASIQKWPW-WSPLRDIVP	:	163					
PGRP-LB_2_Bge	:	YNSRS-IGISFIGDYRTELPTAEMLSLAKSMIQCQGVVERGSIADYKLIGHSQVR	RTECPGQALLNEIKKWPW-WEPIK----	:	159					
PGRP-LB-like_Zne	:	YNSNS-TGICFIGDFRTELPTPEMLSAAKSLIECGVERGSIPEYKLLGHSSQTR	NTECPGAALFNEIKTWPH-WDPLNNTSS	:	164					
PGRP-LB_Cse	:	YNNRS-IGICFIGDFRAELPTLEMLATAKSLIECGVERNSTSPDYKLLGHSSQVR	STECPGTALLNEIKTWPH-WDSLNTKTNT	:	164					
PGRP-LB-like_Sor	:	YNSRS-IGIVLIGDWDITLPPESQMLAAQLINMGIRDGYISENYKLIGHRQVR	ETACPGEALYKEIQMWPH-WIPNPDEEV	:	163					
PGRP-LA-like_Bge	:	FVRCNIGIALMGNFVHDEPTIGQINSTQELLELGVLGKGIAPDYKLIPHENATY	ATLSPGKNVVKIIEKWPHEWEPTR----	:	159					
PGRP-LC-like_Sgr	:	YNFKS-VGISFIGDYRTELPTHDMLELAWSLIRCGVARGSISETYKLVGHRQVR	DETECPGDRLYQEIQTWPH-WVAHRDIIP	:	162					
PGRP-LA-like_Zne	:	FVKRCNIGISFIGNFVHDTPTNGQIQAVQELIKLGVSIGKIDKNYKLVAMNET	FTTLSPGVVLYGIIAKWPHEWKPESHDDIG	:	164					
PGRP-LA_Cse	:	FVTRCNIGISFIGNFIRDTPNTNGQIEAVQELIKLGVMKGKIDKYLKLVAMNET	YNTLSPGVVLYAIIISKWPHEWKPRTREDIG	:	164					

Figure S3. Alignment of the PGRP domain superfamily (IPR036505) in several insect proteins. The alignment includes those proteins whose branches were highlighted in colors in the phylogeny of Figure 6, with the addition of several other PGRP proteins, such as *D. melanogaster* PGRP-LB and other *D. melanogaster* PGRP proteins with amidase activity. The residues highlighted in orange are responsible for the Zn²⁺ interaction in *D. melanogaster* PGRP-LB. The residue highlighted in red makes a fourth coordination with Zn²⁺ through a water molecule in *Drosophila* PGRP-LB. Those residues highlighted in green are responsible for the DAP/Lys specificity. The alignment range was from W38 to G200 of *D. melanogaster* PGRP-LB (NP_731575.1). Abbreviations: Dme (*D. melanogaster*), Bge (*B. germanica*) Zne (*Zootermopsis nevadensis*), Cse (*Cryptotermes secundus*) and Sgr (*Schistocerca gregaria*).