

RESEARCH LETTER

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Hexamerin-like protein 2, a cricket allergen involved in occupational and food allergy

Insects are increasingly being considered as occupational and food allergens. Occupational allergy to crickets may be triggered in factory workers who manufacture food for reptiles, in professionals who raise reptiles as pets or in the zoos, and in cooks who make culinary recipes with insects. Additionally, edible insects are gradually being included in the western diet. Crickets have been reported, in several publications, either as occupational allergens^{1,2} or being related to cross-reactivity with seafood.³⁻⁵

Although no allergen from crickets has yet been included in the WHO/IUIS (World Health Organization and International Union of Immunological Societies) Allergen Database (<http://www.allergen.org/>), some of their proteins have indeed demonstrated the capacity to bind IgE. In 2008, Bartra et al.¹ had reported various potential allergens in the cricket species *Acheta campestris* with molecular weights (MW) of approximately 17, 32, 47 and 62 kDa. Tropomyosin has been reported as a major allergen related to cross-reactivity with seafood^{3,4} and house dust mites.⁴ Hexamerin 1B precursor and arginine kinase have also been identified in *Gryllus bimaculatus*.⁵ The current study aimed to identify the allergens involved in the allergic reactions experienced by two patients, after handling or ingestion of crickets, respectively, and to investigate whether the allergens involved were the same or specific, depending on the sensitization route.

The first patient was a 37-year-old cricket breeder, who presented with rhinoconjunctivitis, dyspnoea and contact dermatitis after manual contact with the exoskeletons of crickets and/or the dust that was generated while they were moved. He was involved in feeding crickets to reptiles, and hence, was exposed to them daily without gloves or other protective clothing. Whether he himself ate any cricket is not clearly known yet. A skin prick test with the standard battery of biologically standardized aeroallergens showed positive results for mites (*Dermatophagoides pteronyssinus* and *Dermatophagoides farinae*), moulds (*Alternaria alternata*), and *Olea europea* pollen, and negative results for other pollens (grasses, *Parietaria judaica*, *Platanus acerifolia* and *Cupressus arizonica*), and animal epithelia (cat and dog). He did not present symptoms after handling other insects, such as grasshoppers, mealworms and cockroaches. The second patient was a 50-year-old woman with oral pruritus, oral itching, and oropharyngeal and lingual oedema following cricket ingestion. She could, however, handle them in kitchen without any problem. She also showed similar symptoms

with grasshopper and sIgE-positive for shrimp; however, an oral provocation test showed that she could safely eat them peeled. She ate scorpions, worms and tarantulas without any symptom. A skin prick test for *D. pteronyssinus* and *D. farinae* was positive, and so was a prick-by-prick test with shrimp head; however, the latter with shrimp body was negative.

After obtaining written informed consent to participate in the study, both patients were diagnosed using prick-by-prick with four cricket species, including *Gryllus assimilis*, *Gryllus bimaculatus*, *Grylloides sigillatus* and *Acheta domesticus*. All four were species bred by patient 1, *A. domesticus* and *G. bimaculatus* being the species most frequently used in human food.⁶

Allergens were extracted from the four cricket species. Briefly, crickets were homogenized and extracted in PBS (phosphate-buffered saline) 0.01 M. After dialysis, the extracts were filtered, frozen and freeze-dried. Further analyses were performed after dissolving the extract in water. Protein profiles were analysed by SDS-PAGE under reducing conditions. Bands separated by electrophoresis were analysed using ImageQuant TL software (GE Healthcare, Uppsala, Sweden) (Figure S1). The molecular distribution of proteins was similar across the four cricket species, with bands ranging from 13 to 275 kDa (Figure 1, SDS).

Levels of sIgE for crickets were determined using ImmunoCAP (Thermo Fisher Scientific, Uppsala, Sweden) in both patients. Since no commercial uniCAP is available for these allergens, the four extracts were labelled with Biotin Protein Labelling Kit (Roche Diagnostics, Mannheim, Germany) and used in streptavidin uniCAPs (Thermo Fisher Scientific) according to the manufacturer's instructions. Both patients were sIgE-positive for the four cricket extracts. Patient 1 showed 1.4 kU/L for *G. assimilis*, 1.6 kU/L for *G. bimaculatus* and *G. sigillatus*, and 2.40 kU/L for *A. domesticus*. Patient 2 had 0.6 kU/L for *G. assimilis*, *G. bimaculatus*, and *A. domesticus*, and 0.8 kU/L for *G. sigillatus*.

Allergenic profile of the patients was investigated by immunoblotting. A total of 20 µg of protein from each cricket species was separated by SDS-PAGE, transferred to a Trans-Blot® Turbo™ Transfer Pack (Bio-Rad, Hercules, CA, USA), and incubated overnight with each serum, diluted 1:5. After incubation with anti-human-IgE-PO (SouthernBiotech, Birmingham, AL, USA), the reaction was developed with Clarity™ Western ECL Substrate (Bio-Rad) and visualized by chemiluminescence. In patient 1, the IgE recognized an

approximately 75-kDa band in all extracts and two extra bands (150 and 250 kDa) in *A. domesticus* extract (Figure 1, P1). In patient 2, the IgE recognized two bands of approximately 75 kDa and 95 kDa in *G. assimilis*, three bands (approximately 70 kDa, 75 kDa and 95 kDa) in *G. sigillatus* extract, and the same 5 bands in the range of 75–250 kDa in the *G. bimaculata* and *A. domesticus* extracts (Figure 1, P2).

A common band of 75 kDa was identified by immunoblotting in both patients. To improve the resolution of this 75-kDa band, separation was performed in 8% acrylamide SDS-PAGE. Two bands were observed (Figure S2), and both were sequenced by LC-MS/MS (Liquid Chromatography Tandem Mass Spectrometry) for identification. Details of the method are included in the Supporting Information, and the identified proteins are listed in Table S1. Analysis revealed the protein as hexamerin-like protein 2 (HLP2). Forty-two of the identified peptides showed homology with HLP2 from the cricket *Teleogryllus commodus* and covered 38% of the sequence (Figure 2). This is the first report of the capacity of this protein to bind IgE from patients diagnosed with cricket allergy. Although hexamerin 1B precursor had previously been reported as a cricket allergen of approximately 60 kDa,⁵ it was identified in a patient diagnosed with prawn allergy by cross-reactivity. Hexamerins are ubiquitous in insects and are composed of six subunits.⁷ Both hexamerin allergens showed

36.5% identity (Figure S3). This fact corroborated that HLP2 and hexamerin 1B are different allergens, although both belong to the haemocyanin family. Other allergens from the haemocyanin family had previously been identified in cockroaches (Per a 3 and Bla g 3)^{8,9} and shrimp.¹⁰ Per a 3 consists of an allergen of approximately 72 kDa with a 40.8% identity with HLP2 (Figure S4), thereby supporting the idea that cricket HLP2 is a new allergen.

A limitation of this study was the extraction method, since not all allergens would have the same solubility in PBS 0.01 M. Allergens that are less soluble may also be involved in the sensitization of patients. However, in view of the results, both patients could have been sensitized to the same allergen, although IgE from patient 2 recognized other allergens in the four cricket species as well and that from patient 1 recognized other allergens of *A. domesticus*. However, in both patients, HLP2 was the band recognized by IgE with a higher intensity. Patient 1, as an insect breeder suffering from occupational allergy, also handled other insect species, mainly cockroaches; however, he did not present symptoms in that process. In this patient, the sensitization route was respiratory and/or cutaneous. From a practical point of view, we may conclude that new jobs, which involve contact with natural products, should include methods to prevent workers' sensitization, including personal protective equipment or other control methods. Patient 2, on the other hand, was able to consume other insects without any symptoms. She did not eat shrimp; however, she tolerated headless peeled shrimp after an oral food challenge. Crustaceans have haemocyanin, especially in the hepatopancreas that is located in the head; therefore, patients usually can tolerate them if they are peeled, as in the case of patient 2. In case of crickets, the whole body is eaten; therefore, haemocyanin is ingested by default, producing the symptoms as in patient 2. In this patient, sensitization was induced by ingestion. In this case, suspicion of shrimp sensitization should have been analysed in more detail before the introduction of new food in the diet.

In summary, HLP2 was identified and characterized as a cricket allergen. In the two patients studied, the new allergen was involved in occupational and food allergies, respectively. Further studies would be recommended to confirm its relationship with allergic symptoms, cross-reactivity with other insects, and prevalence in allergic patients.¹⁰

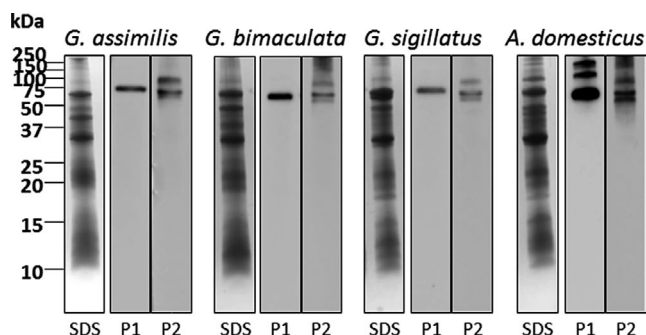


FIGURE 1 Protein and allergenic profile of the four cricket species. Each panel shows the SDS-PAGE (SDS) and allergenic profile (immunoblot) of patient 1 (P1) and patient 2 (P2). Twenty micrograms of each cricket species extract (indicated above each panel) were run in the SDS. The same quantity of extract was used in the immunoblot; serum of each patient was diluted 1:5

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V L A L V A A F A A A S V I P E R T R K V A D K E L L K K Q R D I L R L L I R V H Q P S Y V A E V L E V A Q S F N P E E H L E L Y K D Q E A
V K L L A L Y R A G E L L P R H K P F S V V Y K R H V K Q A V L I F D V L Y N A V D Y Q T F Y K T A A Y L R D R V N E G Q F I Y A L S V A
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D V H S K P L S G Y A P Q L T Y H N G I P F P S R P E G I V N D V D I I D I E V V R N L E R R L Q D A I D L G V A F D E S I N K V V L A D
N D G L E I L G N L I H G N K D S L N R Q Y Y G S L Y L G L R A L F G H V V D P Y H K Y N V A P G V L E H F E T A L R D P A Y Y R I V A R V
V E L F R H Y K S L L K T Y T R E E L T F P G V K I E A V D V D K L V T Y V D D F V F D L N S A V E P N V E V A Q K L D I R V R Q P R L N
H K P F S V R V S V D S D K A A R V A V R F Y L G P K Y N Y L G R P L S V E E R R Q Y L V E I D R F P Y D R E Y P P R S R P L P P T H P A L
H L G Q A H R I T I P H Q S H P R T L H L P L S H L A V H L T Q A H L T T I P H Q F H P R S R P L P L I P C N T P R S S P S Q H Q P S S I S
H A L E P S P T L I P C G T P R
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FIGURE 2 Amino acid sequence of hexamerin-like protein 2 from the cricket *Teleogryllus commodus* (CBI database accession number AU015577.1). Regions highlighted in red correspond to peptides identified by LC-MS/MS, having a sequence coverage of 38%

CONFLICTS OF INTEREST

MAL, AGR and JC are employees of LETI Pharma, S.L.U.

AUTHOR CONTRIBUTIONS

MDM and JCC contributed to the design of the work, acquisition and interpretation of data, revising the manuscript critically, final approval and agrees to be accountable for all aspects of the work. MALM contributed to the analysis and interpretation of data, drafting the manuscript, final approval and agrees to be accountable for all aspects of the work. AGR contributed to the acquisition, analysis and interpretation of data, revising the manuscript critically, final approval and agrees to be accountable for all aspects of the work. CM, RF and MA contributed to the acquisition of data, revising the manuscript critically, final approval and agrees to be accountable for all aspects of the work. JC contributed to the design of the work, interpretation of data, drafting and revising the manuscript critically, final approval and agrees to be accountable for all aspects of the work.

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DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available from the corresponding author upon reasonable request.

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SUPPORTING INFORMATION

Additional supporting information may be found online in the Supporting Information section.

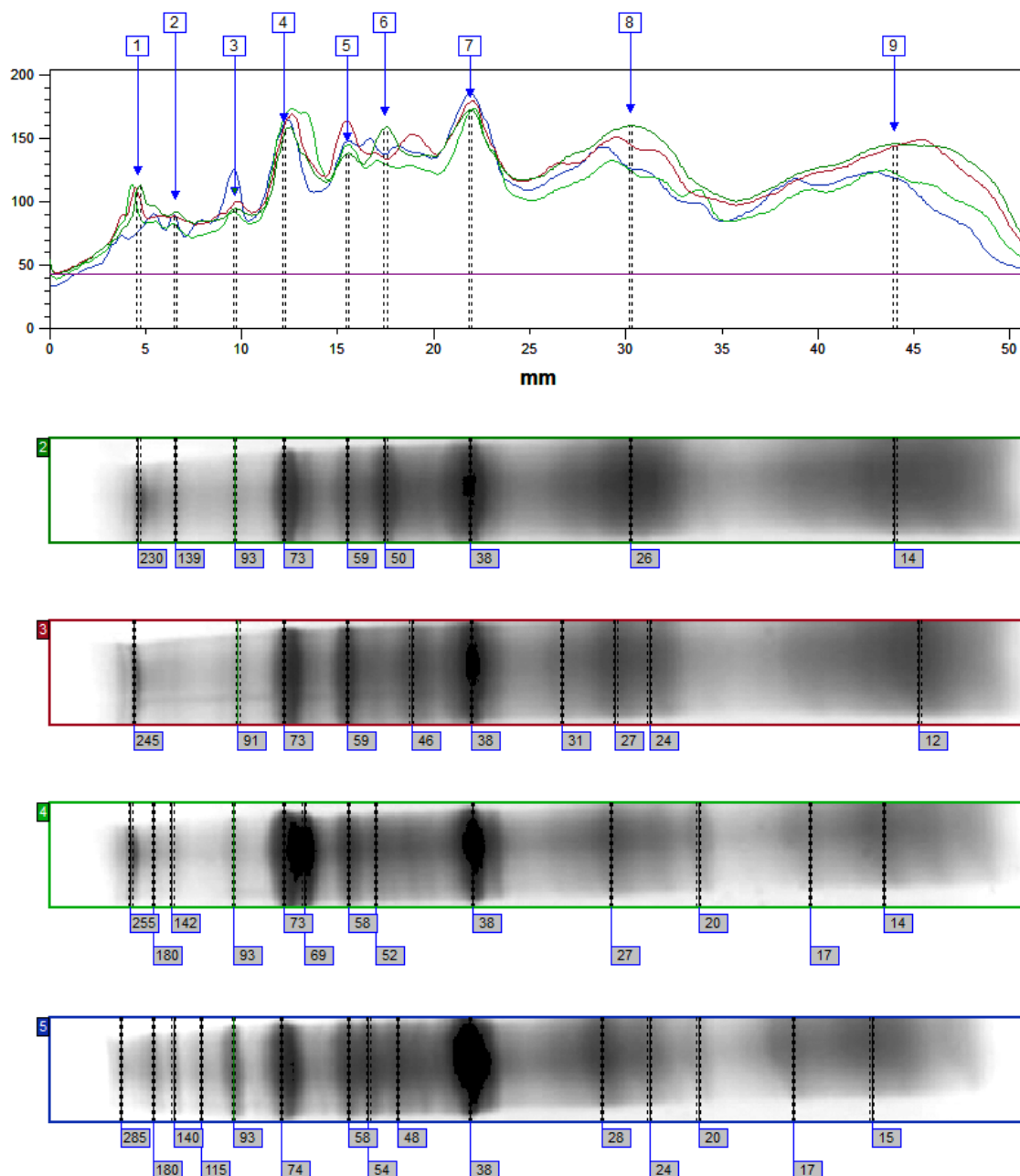
Supporting Information

Materials and Methods LC-MS/MS sequencing

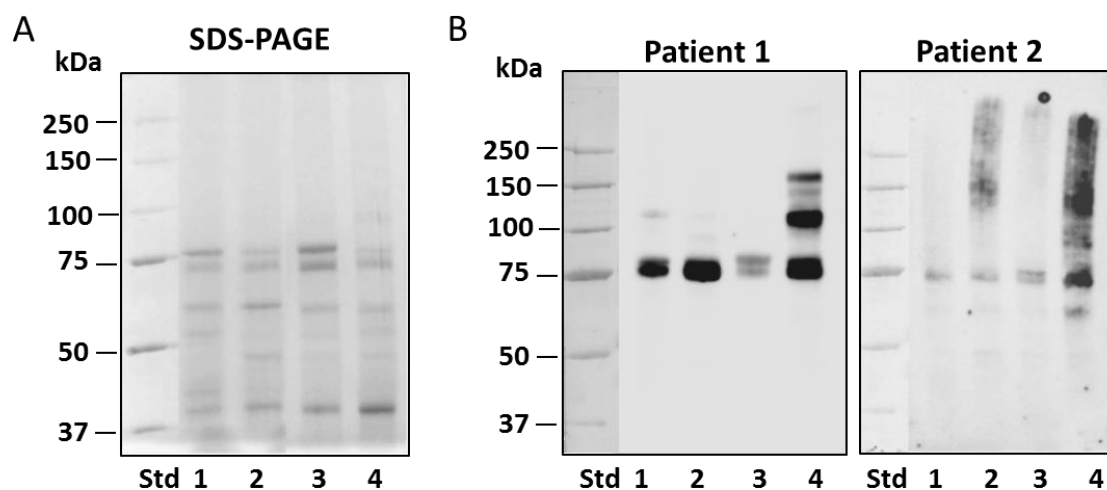
Identification of proteins by LC/MS-MS was performed in two different proteomic services: Centro Nacional de Biotecnología (CNB) and Proteomics Unit of Universidad Complutense (UCM), both located in Madrid (Spain).

After trypsin digestion the peptides were analyzed in a 5600 TripleTOF (Sciex, Framingham, MA, USA) mass spectrometer (CNB) or in an EASY-nLC 1000 System coupled to the Q-Exactive HF (ThermoFisher Scientific, Waltham, MA, USA) mass spectrometer through the Nano-Easy spray source (UCM). In both services the DDA (data dependent acquisition) mode was used.

The MS/MS data were analyzed with Peaks v7.5 (Bioinformatics Solutions, Waterloo, Canada) to identify the peptides against NCBI DataBase with taxonomic restriction to Orthoptera (CNB, 36000 sequences) or Ensifera (UCM, 16964 sequences).



Supporting Information, Figure 1: Protein profile of the four cricket species. Analysis of the bands and matching of the protein profile (SDS-PAGE) of the four species. Line 2 (green) - *G. assimilis*, line 3 (red) - *G. bimaculatus*, line 4 (light green) - *G. sigillatus* and line 5 (dark blue) - *A. domesticus*. Numbers in each line correspond to the calculated MW using Image Quant TL Software (Cytiva, Marlborough, MA, USA) for the different protein bands with Precision Plus MW standard (Bio-Rad).



Supporting Information, Figure 2: Protein and allergenic profile in 8% acrylamide. A: Ten micrograms of protein of each extract were separated in SDS-PAGE with 8% acrylamide. B: Immunoblot of the two patients for the four cricket species. Std. – Molecular weight standard Precision Plus (Bio-Rad), 1- *G. assimilis*, 2- *G. bimaculatus*, 3- *G. sigillatus* and 4- *A. domesticus*, sera were diluted 1:5.

HEX1B	MRFLVLAALAGLCAVSAVS--VENDTYKYSQEKQKEIFRLFKYINQPSFYPDFIEVAQSY	58
HLP2	----VLALVAAFAAASVIPERTRKVADKELLKKQORDILRLLRVHQPSYVAEVLEVAQSF	56
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HEX1B	NFYDFKADYIKPEVVVEFYRFYYYGKILQGEIFSVFYKEHLRQAIALFKLFYYANTWET	118
HLP2	NPEEHLELYKDQEA VKKLLALYRAGELLPRHKPF SVVYKRHV KQAVLIFDVL YNAV DYQT	116
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HEX1B	FYKTAVWARNNVNEGMYL YSL SVALIHRPDTYYALPPIYEVYPYFYFNSEVIQEAQYYK	178
HLP2	FYKTAAYLRDRVNEGQFIYALSVAVLHRQDTHDVLPPPYEVYPEFFVNSEI IHEATEEY	176
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HEX1B	QMYSSQSGAHYNGRTIYANYSG---YYLNLYPEQSMAYFTEDVGVNSFYYYYNLYYPYW	234
HLP2	LQ-GKQLPI-TINAAYYTNSAWYYTYPQVSNPEQLLN YFTEDIGLSTFHTYFN YEYPVW	234
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HEX1B	MSGEEFN LKY-DNRGELFYMYQQILARYYLERLSNGFGEIDYFNWEVP--FENGYYPTM	291
HLP2	FSASKYGVGVAPRRGEIFYYYLLQLFNRYQLERLSNGLPPVYPIDYDVH SKPLSGYAPQL	294
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HEX1B	CYPNGLQFPARPSYRLYEYFYNYGQHYGYNKYAYSYTFVKDYERRIRDAIDSGYVFTRS	351
HLP2	TYHNGIPFPRPEGIVVND-----VDIIDIEVVRNLERRLQDAIDLGVAFDES	342
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HEX1B	GQKVDLFSRDGINILGNLIEGNPDSPYYKYYGAYQVFARHLLGYSFQPLTYHKTYPSALE	411
HLP2	INKVV LADNDGLEILGNLIHG NKDSLNRQYYGSLYLGLRALFGHVVDPYHKYNVAPGVLE	402
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HEX1B	HFETSMRDPAFYQLYKKLINYFYRFKSQYYKYYTEQDLVFEGVEVKNVFDRLVTYFDYY	471
HLP2	HFETALRDPAYYRIVARVVELFRHYKSL-LKTYTREELTFPGVKIEAVDV DKLVTYVDDF	461
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HEX1B	YSDISSAVYVTPEEFVQDSFKVQVAQPRLNYPFTYKIYVDSSIDTEAVVKVFLGPKYDE	531
HLP2	VFDLNSAVEVPNV-EVAQKLDIRVRQPRLNHKPF SVRVSVSDSKAARVAVRFYLGPKYNY	520
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HEX1B	YGRYINLTENWMNFVQFDHFVYKLGSGQN VITRNS-----REIYNYMHDRTSY	579
HLP2	LGRPLSVEERRQYLVEIDRFYPDREYPPRSRPLPPTH PALHLGQAHRITIPHQSHPRTLH	580
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HEX1B	YQLYQKAMGVFDEKQGEYKYTQFWFGFPQRYMLPKGT YGGFPYQFYVYVT--KYVPYKA	637
HLP2	LPLSHLAVHL-----TQAHLTTIPHQFHPRSRPLPLIPCNT	616
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HEX1B	QKDGVP--VGMGSQYVDGYPMGYPFDRPVYGYMYAIPNGYFYETKIFHRDSDVFNYS	695
HLP2	PRSSPSQHQPSSISHALEPSPTLIPCGTPR-----	646
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HEX1B	QQDYYYGKRYNFANQRYQSKKH DYK YLSGSKDYVRPQYETQGRYPEQYYAQGSNYAQEQY	755
HLP2	-----	646
HEX1B	YPSRSYERQDYHYH	769
HLP2	-----	646

Supporting Information, Figure 3: Sequence alignment of hexamerin proteins identified as allergens in crickets (Clustal Omega, EMBL-EBI, Cambridgeshire, UK). HEX1B corresponds to Hexamerin 1B precursor from the beetle *Tribolium castaneum* (accession number gi:283046829) that was used to identify the allergen in *G. bimaculatus* (Srinroch *et al.*, 2015) and HLP2 corresponds to hexamerin-like protein 2 from the cricket *Teleogryllus commodus* used to identify the cricket allergen in this study (accession number AU015577.1). Percentage of identity between both sequences is 36.5%. * The amino acids are identical in both proteins; : Conserved substitution of the amino acids; . Semi-conserved substitution of the amino acids.

Per a 3	MKTALVFAAVVAFVAARFPDHKDYQLADKQFLAKQRDVLRLFHRVHQHNILNDQVEVGI	60
HLP2	-----VLALVAAFAAASV-IPERTRKVADKELLKKQRDILRLLIRVHQPSYVAEVLEVAQ	54
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Per a 3	PMTSKQTSATT-VPPSGEAVHGVQLQEGHARPRGEPFSVNYEKHREQAIMLYDILLYFANDY	119
HLP2	SFNPEEHLELYKDQEA VKKLLALYRAGELLPRHKPFSVVKRHKVQAVLIFDVLYNAV DY	114
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Per a 3	DTFYKTACWARDRVNEGFMFYSFSIAVFHRDDMQGVMLPPPYEVYPYLFVDHDIHMAQK	179
HLP2	QTFYKTAAYLRDRVNEGQFIYALSVAVLHRQDTHDVVLP PPYEVYPEFFVNSEIIEATE	174
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Per a 3	YWMKNAGSGEHH-----SHVIPVNFTLRTQDHLLAYFTSDVNLNAFNNTYRYYPSPW	231
HLP2	EYLQGKQLPITINAAYYTNSSAWYYTYPQVSNPEQLLNYFTEDIGLSTFHTYFNIEYPVW	234
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Per a 3	YNTTLYGHNI-DRRGEQFYTYKQIYARYFLERLSNDLPDVYPFYYSKPV--KSAYNP NL	288
HLP2	FSASKYGVGVAPRRGEIFYYYLLQLFNRYQLERLSNGLPPVYPIDYDVH SKPLSGYAPQL	294
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Per a 3	RYHNGEEMPVRPSNMYVTNFDLYYIADIKNYEKRVEDAIDFGYAFDEHMKPHSLYHDVHG	348
HLP2	TYHNGIPFPSRPEGIVNDVDIIDIEVVRNLERRLQDAIDLGVAFDESINKV-VLADNDG	353
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Per a 3	MEYLADMIEGNMDSPNFYFYGSIYHMYHSMIGHIVDPYHKMGLAPS-LEHPETVLRDPVF	407
HLP2	LEILGNLIHGKDSLNRQYYGSLYLGLRALFGHVVDPYHKYNVAPGVLEHFETALRDPAY	413
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Per a 3	YQLWKRVDHLFQKYKNRLPRYTHDELA FEGVKVENVDVGKLYTYFEQYDMSLDMAVYVNN	467
HLP2	YRIVARVVELFRHYKSLLKTYTREELTFPGVKIEAVDVKLVTVVD DFDLNSAVEVPN	473
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Per a 3	VDQISNVDVQL-AVRLNHKPFITYNIEVSSDKAQDVYVAVFLGPKYDYL GREYDLNDRRHY	526
HLP2	VEVAQKLDIRVRQPRLNHKPFSVRVSVSDKAARVAVRFYLGPKYNYLGRPLSVEERRQY	533
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Per a 3	FVEMDRFPYHVGAGKTVIERNSH-----DSNIIAPERDSYRTFYKKVQEAYEGKSQ-	577
HLP2	LVEIDRFYPDREYPPRSRPLPPTH PALHLGQAHRTIPHQSHPRTLHLPLSHLAVHLTQA	593
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Per a 3	YYVDKGHN YCGYPEN-LLIPKGGKGGQAYTFYVIVTPYVKQDEHDFEPYNYKAFSYCGVG	636
HLP2	HLTTIPHQFHPRSRPLPLIPCNTPRSSPSQ---HQP--SSISHALEPS--PTLIPCGTP	645
	: . *~: . *** .. . * .. .* :** :~ **.	
Per a 3	SERKYPDNKPLGYPFDRKIYSNDFYTPNMYFKDVII FHKKYDEGVQGH	685
HLP2	R-----	646

Supporting Information, Figure 4: Sequence alignment of the cockroach allergen Per a 3 (Q25641) and HLP2 from the cricket *Teleogryllus commodus* (AUO15577.1.). Both proteins belong to the hemocyanin family of allergens. Percentage Identity between both sequences is 40.8%. * The amino acids are identical in both proteins; : Conserved substitution of the amino acids; . Semi-conserved substitution of the amino acids.

Supporting Information Table 1: Results for the band identification by LC-MS/MS. The two bands separate with a 8% acrylamide SDS-PAGE were sequence independently.

Band	Accession	Description	Score	Coverage [%]	Peptides	MW [kDa]
<i>G. assimilis</i> upper	AUO15577.1	hexamerin-like protein 2, partial (<i>Teleogryllus commodus</i>)	408.86	40	42	74.4
	ADK64952.1	heat shock protein 90 (<i>Gryllus firmus</i>)	234.97	17	11	83.5
<i>G. assimilis</i> lower	AUO15577.1	hexamerin-like protein 2, partial (<i>Teleogryllus commodus</i>)	245.6	21	17	74.4
	ADK64952.1	heat shock protein 90 (<i>Gryllus firmus</i>)	266.23	19	13	83.5
<i>G. bimallula</i> upper	AUO15577.1	hexamerin-like protein 2, partial (<i>Teleogryllus commodus</i>)	317.95	35	34	74.4
	ADK64952.1	heat shock protein 90 (<i>Gryllus firmus</i>)	197.33	16	11	83.5
	AUO15580.1	hexamerin-like protein 1 (<i>Gryllotalpa</i> sp. XZ-2017)	106.90	4	4	80.5
<i>G. bimallula</i> lower	AUO15577.1	hexamerin-like protein 2, partial (<i>Teleogryllus commodus</i>)	304.47	27	19	74.4
	ADK64952.1	heat shock protein 90 (<i>Gryllus firmus</i>)	235.12	20	14	83.5
	ACY44282.1	translational elongation factor-2, partial (<i>Acheta domesticus</i>)	104.10	4	3	81.4
<i>G. sigilatus</i> upper	AUO15577.1	hexamerin-like protein 2, partial (<i>Teleogryllus commodus</i>)	284.77	24	22	74.4
	ADK64952.1	heat shock protein 90 (<i>Gryllus firmus</i>)	181.46	8	5	83.5
<i>G. sigilatus</i> lower	AUO15577.1	hexamerin-like protein 2, partial (<i>Teleogryllus commodus</i>)	330.63	27	24	74.4
	ADK64952.1	heat shock protein 90 (<i>Gryllus firmus</i>)	203.84	14	10	83.5
	AAQ62963.2	transferrin (<i>Romalea microptera</i>)	110.33	4	3	80.1
<i>A. domestica</i> upper	AUO15577.1	hexamerin-like protein 2, partial (<i>Teleogryllus commodus</i>)	363.36	35	32	74.4
	AUO15580.1	hexamerin-like protein 1 (<i>Gryllotalpa</i> sp. XZ-2017)	184.22	9	6	80.5
	AFP54305.1	heat shock protein 70c (<i>Paratlanticus ussuriensis</i>)	173.15	8	4	70.1
	ADK64952.1	heat shock protein 90 (<i>Gryllus firmus</i>)	142.49	5	4	83.5
<i>A. domestica</i> lower	AUO15577.1	hexamerin-like protein 2, partial (<i>Teleogryllus commodus</i>)	305.37	28	23	74.4
	ADK64952.1	heat shock protein 90 (<i>Gryllus firmus</i>)	200.51	11	8	83.5
	AFP54305.1	heat shock protein 70c (<i>Paratlanticus ussuriensis</i>)	164.03	6	4	70.1