



# The PATHOGENesis of Food Allergy

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Keywords: archaea, bacteria, skin, atopic dermatitis, cross-reactivity, egg allergy, IgE sensitization

## **SUMMARY**

The current paper suggests that egg allergy may arise due to microbial proteins that are homologous to egg allergens. These microbial proteins elicit an allergic response and lead to the development of specific microbial IgE molecules. These molecules cross-react with egg allergens and result in egg allergy. Some examples of microbial proteins that share similar sequences as egg allergens are presented in this paper.

Food allergy has a negative impact on the quality of life and nutrition. In addition, it can lead to life-threatening reactions. The pathogenesis of food allergy is still not fully understood. Many young children develop food allergy with no known prior ingestion of the food allergen in question. The strong connection between food allergy and atopic dermatitis has been well-documented. While the prevalence of food allergy in the general pediatric population is 4–5%, the prevalence of food allergy in atopic dermatitis is at least 20% (1). This connection between food allergy and atopic dermatitis has led to the suggestion that the skin may be the site of food IgE sensitization, leading to food allergy. The dual-allergen-exposure hypothesis suggests that food allergens are sensitized via eczema, whereas early gastro-intestinal exposure leads to tolerance (2). This hypothesis is supported by multiple basic studies that provide evidence for IgE sensitization via the skin [reviewed in (3)]. In addition, it has been shown that environmental level of peanut allergens is increased in children who developed peanut allergy (4). The early introduction of peanut has led to the prevention of peanut allergy (5). Likewise, early introduction of egg has also met with some success, although the results were not as consistent (3). It has been suggested that improvement in eczema, in addition to early introduction of egg, is needed for successful prevention of egg allergy (6). This suggestion further highlights the importance of skin in the pathogenesis of food allergy. A hypothesis is proposed here that the interaction between the neonatal skin and microbial proteins is important for the development of IgE sensitization and egg allergy.

The current hypothesis predicts the presence of microbial proteins that are homologous to egg allergens. Table 1 shows the microbial proteins that share homology with the IgE-binding domains of Gal d 1 (ovomucoid) (7). Four out of the 6 microbial proteins share > 60 % identity with a clinically-relevant IgE-binding region of Gal d 1 (FNPVCGTDGVTYDN) (8). Significant homology was also found between microbial proteins and Gal d 2 (ovalbumin), but no homology was found in the IgE-binding domains of Gal d 2 (9) (data not shown). To further confirm the correlation between microbial proteins and Gal d 1, prospective studies may be carried out to look for these microbial pathogens in atopy-prone neonates and correlate with neonates who eventually develop allergy to Gal d 1. These microbial pathogens can also be inoculated in animal models to show the development of specific IgE that cross-react with Gal d 1. Atopy-prone neonates who are born to parent with atopic dermatitis, asthma or allergic rhinitis have inherent skin barrier defects that predispose them to develop atopic dermatitis. Microbial pathogens are capable of evading these barrier defects to interact with the cutaneous immune system in these children. The processing of microbial proteins by antigen-presenting cells and subsequent presentation of antigenic peptides to T helper type 2 cells leads to the production of IL-4 and IL-13, which induce B cells to express specific IgE molecules. Bacterial allergy has been described more than half a century ago (10). It is

## **OPEN ACCESS**

### Edited by:

George N. Konstantinou, 424 General Military Hospital, Greece

#### Reviewed by:

Anastasios Panagiotis Konstantinopoulos, Independent Researcher, Athens, Greece

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#### Specialty section:

This article was submitted to Pediatric Immunology, a section of the journal Frontiers in Pediatrics

Received: 24 July 2019 Accepted: 04 November 2019 Published: 21 November 2019

#### Citation:

Ong PY (2019) The PATHOGENesis of Food Allergy. Front. Pediatr. 7:484. doi: 10.3389/fped.2019.00484

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Microbe		Microbial protein*			NCBI/GenE ref. sequen		Homologous egg allergen*			
Sphingobacteriales (bacteroidetes)			T9SS type A sorting domain- containing protein			WP_088748939.1			Gal d 1	
Microbe		200 NPVAPCPA				230 IFVPGVCGEPT	'IFQ <mark>PCLDPNA</mark> '	250 VNTNPC		
Gal d 1	MNCSSYANT 100	: TSEDGKVMVLCNR 110	. :::: : A <mark>FNPVCGTDO</mark> 120		: :: <mark>Ahkveqgasvd</mark> i 140	: : . KRHDGGC-RKE 150	: . LAA <mark>VSVDCSE</mark> 160	: <mark>YPKPDC</mark> 170		
Microbe		270 CNGVTYVNSCYAT				310 EIGVPFVPNTI	320 YIWSPATGLS	CDNCPD		
Gal d 1		SDNKTYGNKCNFC								
Bacteroidetes bacterium (bacteroidetes)			T9SS C-terminal target domain-containing protein			RMG76445.1			Gal d 1	
Microbe	CYDRONIV	NGGYTTVDPLTO		420	CTTYDS&C	430	440	450	N <b></b>	
	:	:	: :	:::: :	:.:: . :	:				
Gal d 1	CKETVPMN 90	ICSSYANTTSEDO 100	GKVMVLC-N 110	RA <mark>FNPVCGTD</mark> 120	GVTYDNECLL 130	CAHKVEQGAS 140	SVDKRHDGGC 150	RKELAA <mark>VSV</mark> 160	DCSE	
								500		
Microbe		470 VYDPVCGCNDI		480 MAEAAGVV · ·		500 SSIWCDNATI	510 PIQCGDFLPY	520 EKTTGLVNK	ISNY	
	-PDTLCPY : :		::::	MAEAAGVV	<mark>SYTP-GPC</mark> SG : :				ISNY	
Microbe Gal d 1 Methanophag archaeon (Arc	-PDTLCPY : : YPKPDCTA 170 gales	VYDPVCGCNDI :.:: : EDRPLCGSDNKT 180 Kazal-type so	YGNKCNFC	MAEAAGVV : NAVVESNGTL 200	<mark>SYTP-GPC</mark> SG • • : : TLSHFGKC	SSIWCDNATI			ISNY	
Gal d 1 Methanophag archaeon (Arc	-PDTLCPY : : YPKPDCTA 170 gales chaea)	VYDPVCGCNDII :.:: : EDRPLCGSDNKT 180 Kazal-type s domain-cont 70 PAD	E::::: TYGNKCNFC: 190 erine protease ir aining protein 80 KTYANKCTA	MAEAAGVV : : NAVVESNGTL 200	SYTP-GPCSG : : ILSHFGKC 210 RCV64500. 90 VNAWTVGECS	SSIWCDNATI	PIQCGDFLPY 110 CTEEEKQAEV	EKTTGLVNK Gald 1 120 CTQEYDPVC		
Gal d 1 Methanophag archaeon (Arc Microbe	-RQADMCT : :: <u>YPKPDCTA</u> 170 -KQADMCT : .:.	VYDPVCGCNDII :.:: : EDRPLCGSDNKT 180 Kazal-type s domain-cont 70 YAD	E::::: TYGNKCNFC: 190 erine protease ir caining protein 80 KTYANKCTA ::::::	MAEAAGVV :	SYTP-GPCSG ILSHFGKC 210 RCV64500. 90 VNAWTVGECS : :	SSIWCDNATI 100 TA <mark>VWVN(</mark> .:::	110 TEEEKQAEV	Gald 1 120 CTQEYDPVC :::::::::	GDDG :.:. GSDN	
Gal d 1 Methanophag archaeon (Arc Microbe Gal d 1	-RQADMCT : :: yPKPDCTA 170 gales chaea) -KQADMCT : .:. GKVMVLCN 110 130 ITYGNKCT	VYDPVCGCNDII :.:: : EDRPLCGSDNKT 180 Kazal-type s domain-cont 70 PAD YNPVCGDNGP .::: . : IRA FNPVCGTDGN 120 140 PACSSGN	E: E: E FYGNKCNFC 190 erine protease ir caining protein 80 KTYANKCTA E: E: E TYDNECLL 130 15 /NAWTAGEC	MAEAAGVV : NAVVESNGTL 200 ahibitor CSSGE : CAHKVEQGAS 140 0 16	SYTP-GPCSG . : : ILSHFGKC 210 RCV64500. 90 VNAWTVGECS : : : VDKRHDGGCR 150 0 17	SSIWCDNATI 100 TA <mark>VWVN(</mark> .:: :. KELAA <mark>VSVD(</mark> 160 0 18	110 TEEEKQAEV :.:: CSEYPKPD 170 30 1	Gald 1 120 CTQEYDPVC :: : : : : CTAEDRPLC 18 90	GDDG :.:. GSDN 0 200	
Gal d 1 Methanophag archaeon (Arc Microbe Gal d 1 Microbe	-RQADMCT : :: yPKPDCTA 170 cales chaea) -KQADMCT : :: GKVMVLCN 110 130 ITYGNKCT :::::	VYDPVCGCNDII :.:: : EDRPLCGSDNKT 180 Kazal-type s domain-cont 70 PAD YNPVCGDNGP .::: . : IRA FNPVCGTDGN 120 140 PACSSGN	E: E: E: FYGNKCNFC: 190 erine protease in aning protein 80 KTYANKCTA E: E: E TYDNECLL: 130 15 NAWTAGEC E: E:	MAEAAGVV : NAVVESNGTL 200 ahibitor CSSGE : CAHKVEQGAS 140 0 16	SYTP-GPCSG . : : ILSHFGKC 210 RCV64500. 90 VNAWTVGECS : : : VDKRHDGGCR 150 0 17	SSIWCDNATI 100 TA <mark>VWVN(</mark> .:: :. KELAA <mark>VSVD(</mark> 160 0 18	110 TEEEKQAEV :.:: CSEYPKPD 170 30 1	Gald 1 120 CTQEYDPVC :: : : : : CTAEDRPLC 18 90	GDDG :.:. GSDN 0 200	
Gal d 1 Methanophag archaeon (Arc Microbe Gal d 1 Microbe Gal d 1 Candidatus N	-PDTLCPY : : YPKPDCTA 170 gales shaea) -KQADMCT : .:. GKVMVLCN 110 130 ITYGNKCT ::::: KTYGNKCN	VYDPVCGCNDII :.:: EDRPLCGSDNKT 180 Kazal-type si domain-cont 70 PAD YNPVCGDNGF .:::: IRA FNPVCGTDGV 120 140 PACSSGNV : IFCNAVVESNGTI	E: E: E: FYGNKCNFC: 190 erine protease in aning protein 80 KTYANKCTA E: E: E TYDNECLL: 130 15 NAWTAGEC E: E:	MAEAAGVV : NAVVESNGTL 200 hibitor CSSGE  CAHKVEQGAS 140 0 16 PINDSSEKIA	SYTP-GPCSG . : : ILSHFGKC 210 RCV64500. 90 VNAWTVGECS : : : VDKRHDGGCR 150 0 17	SSIWCDNATI 100 TA <mark>VWVNG</mark> .::: KELAA <mark>VSVDG</mark> 160 0 18 NAGPTPFNL	110 TEEEKQAEV :.:: CSEYPKPD 170 30 1	Gald 1 120 CTQEYDPVC :: : : : : CTAEDRPLC 18 90	GDDG :.:. GSDN 0 200	
Gal d 1 Methanophag archaeon (Arc Microbe Gal d 1 Microbe Gal d 1 Candidatus N sp. NM25 (Arc	-PDTLCPY : : YPKPDCTA 170 gales chaea) -KQADMCT : .:. GKVMVLCN 110 130 ITYGNKCT :::::. KTYGNKCN itrosopumilus chaea) 290	VYDPVCGCNDII :.:: : EDRPLCGSDNKT 180 Kazal-type s domain-cont 70 PAD YNPVCGDNGH .:::: . : IRA FNPVCGTDGV 120 140 PAC SSGNV : . : IFCNAVVESNGTI DUF4377 do 300 3	E: E: E FYGNKCNFC: 190 erine protease in aning protein 80 <b>KTYANKCTA</b> E: E: E <b>JTYDNECLL</b> 130 15 <b>/NAWTAGEC</b> E: E: E <b>JTLSHFGKC</b> main-containing 10	MAEAAGVV : NAVVESNGTL 200 ahibitor CSSGE : CAHKVEQGAS 140 0 16 PINDSSEKIA 9 protein 320	SYTP-GPCSG : : TLSHFGKC 210 RCV64500. 90 VNAWTVGECS . : : VDKRHDGGCR 150 0 17 REFIENSDWY WP_109876 330	SSIWCDNATI 100 TA <mark>VWVN( .::::</mark> KELAA <mark>VSVD(</mark> 160 0 18 NAGPTPFNLT 664.1 340	PIQCGDFLPY 110 TEEEKQAEV : CSEYPKPD 170 30 1 FFVGLKPGPC 350	Gald 1 Gald 1 120 CTQEYDPVC :: : : :: CTAEDRPLC 18 90 TSCWTFTYE Gald 1 0 36	GDDG :.:. GSDN 0 200 YQVV 0	
Gal d 1 Methanophag archaeon (Arc Microbe Gal d 1 Microbe Gal d 1 Candidatus N sp. NM25 (Arc	-PDTLCPY : : YPKPDCTA 170 gales chaea) -KQADMCT : .:. GKVMVLCN 110 130 ITYGNKCT :::::. KTYGNKCN itrosopumilus chaea) 290	VYDPVCGCNDII :.:: EDRPLCGSDNKT 180 Kazal-type s domain-cont 70 PADYNPVCGDNGF .::: IRAFNPVCGTDGV 120 140 PACSSGNV : IFCNAVVESNGTI DUF4377 do	E: : : : PYGNKCNFC 190 erine protease ir aning protein 80 CTYANKCTA : : : : /TYDNECLL 130 15 /NAWTAGEC . : : : JLSHFGKC omain-containing 10 EYAPVCGVI	MAEAAGVV : NAVVESNGTL 200 ahibitor CSSGE : CAHKVEQGAS 140 0 16 PINDSSEKIA 9 protein 320	SYTP-GPCSG . : : TLSHFGKC 210 RCV64500. 90 VNAWTVGECS : : : VDKRHDGGCR 150 0 17 REFIENSDWY WP_109876 330 MISSNHV	SSIWCDNAT 100 TAVWVN( .::: KELAAVSVD( 160 0 18 NAGPTPFNL 664.1	PIQCGDFLPY 110 TEEEKQAEV : CSEYPKPD 170 30 1 FFVGLKPGPC 350	Gald 1 Gald 1 120 CTQEYDPVC :: : : :: CTAEDRPLC 18 90 TSCWTFTYE Gald 1 0 36	GDDG :.:. GSDN 0 200 YQVV 0	
Gal d 1 Methanophag archaeon (Arc Microbe Gal d 1 Microbe Gal d 1 Candidatus N sp. NM25 (Arc Z Microbe	-PDTLCPY : : YPKPDCTA 170 gales chaea) -KQADMCT : .: GKVMVLCN 110 130 ITYGNKCT :::::: KTYGNKCT itrosopumilus chaea) 290 AKSLKDRG : .	VYDPVCGCNDII :.:: EDRPLCGSDNKT 180 Kazal-type s domain-cont 70 PADYNPVCGDNGF .:::::: IRAFNPVCGTDGV 120 140 PACSSGNV : IFCNAVVESNGTI DUF4377 dc 300 3 WQTKYPNFACTL	E: : : : PYGNKCNFC 190 erine protease ir aning protein 80 (TYANKCTA : : : : 7TYDNECLL 130 15 /NAWTAGEC . : : : JTLSHFGKC omain-containing 10 EYAPVCGVI : : : : :	MAEAAGVV 	SYTP-GPCSG : : TLSHFGKC 210 RCV64500. 90 VNAWTVGECS : : : VDKRHDGGCR 150 0 17 REFIENSDWY WP_109876 330 MISSNHX	SSIWCDNAT 100 TAVWVN( :::: KELAAVSVD( 160 0 18 NAGPTPFNL 664.1 340 VAT-KHVGEC ::::	PIQCGDFLPY 110 TEEEKQAEV : CSEYPKPD 170 30 1 FFVGLKPGPC 350	Gald 1 Gald 1 120 CTQEYDPVC :: : : :: CTAEDRPLC 18 90 TSCWTFTYE Gald 1 0 36	GDDG :.:. GSDN 0 200 YQVV 0	

TABLE 1 | Microbial proteins that share similar sequences as the IgE-binding domains of Gal d 1.

#### TABLE 1 | Continued

Microbe	Microbial pro	otein*	NCBI/GenBa ref. sequence		Homologous egg allergen* Gal d 1		
Nitrosopumilus maritimus S (Archaea)	CM1 Proteinase inh	ibitor I1 Kazal	ABX12911.1				
290	300 31	0 320	330	340			
Microbe KNLEQRG	WQIPLPVFACTLEY	APVCGVDGKTYGNK	CAIASSHVT	IKHVGEC TNDIP			
				: :.:			
	<mark>-EYPKPDCTAED</mark> 170	RPLCGSDNKTYGNK 180 19	CNFCNAVVESNGTLT 0	LSHFGKC 210			
160	170	100 19	0 200	210			
Nitrosopumilus (Archaea)	MBL fold meta	allo-hydrolase	WP_0149626	656.1	Gal d 1		
2	50 260	270	280	290	300	310	
Microbe EKQPYLR		VICAESLQL	LFKSHDGS-PACVSN	NDAKKKLQERGW	QTSIPLLACT		
	··· ··· ··· ··		. : ::: :		: :.	. :::::	
Gal d 1LR 50	60		ISKEHDGECKETVPN 80 90	100	DGKVMVL-CN 110	120	
50	60	70	80 90	100	TIO	120	
320	330	340	350 3	360 37	0 38	0	
Microbe GKTYGNS	CMINSNHVAT		DTKGIFEKTLDYTT	2PAVVDEEKGYF	VTEIADDVYW	LVGNGYQTMF	
MICTODE GRIGNS							
: :: :	1	• • • •					
: :: :			AVSVDCSEYPKPDC	TAEDRPLCGSDN	KTYGNKCNFC	NAVVESNGTL	

\*The protein sequences of bacteria/archaea and egg allergen, ovomucoid (Gal d 1), were first screened in microbial protein BLAST database of National Center for Biotechnology Information (NCBI) (https://blast.ncbi.nlm.nih.gov/Blast.cgi). Homology was searched using an 80-amino-acid sliding window alignment with a default threshold for at least 35% identical amino acids (www.allermatch.org) (Wageningen University and Research) (UnitProt allergen database). Identity was based on Full Fasta 36 (http://www.allergenonline.org/databasefasta.shtml) (University of Nebraska-Lincoln).

also known that specific IgE to staphylococcal toxins can develop in young children with atopic dermatitis (11). Bacteria such as bacteroides can be acquired during birth or they can be part of neonates' microbiome (12). The skin also contains a wide array of microbial pathogens that can participate in the development of allergy (13). More recent data suggests that many microbial organisms (e.g., proteobacteria and archaea) previously thought to exist only in the environment such as soil, fresh or marine waters are now found to be part of the human skin microbiome (14, 15). Proteobacteria and bacteroides are also known to be present in atopic dermatitis lesions (16). The current proposal is conceptual that microbial proteins can be a sensitizing source in the development of food allergy in predisposed children. Preliminary data also suggests the presence of homologous proteins between microbes and other food

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allergens including peanut and cow's milk (unpublished data). Whether these microbial pathogens have a direct interaction with neonates, leading to the development of specific IgE, remains to be proven. It is possible that the prevention of egg allergy requires a different approach by targeting microbial pathogens.

## **AUTHOR CONTRIBUTIONS**

PO conceived the idea, generated the data, and wrote the paper.

## ACKNOWLEDGMENTS

The current hypothesis is developed from the project Prediction of eczema, infections and allergy sponsored by The Albert and Bettie Sacchi Foundation.

- Bough HA, Liu AH, Sicherer S, Makinson K, Douiri A, Brown SJ, et al. Atopic dermatitis increases the effect of exposure to peanut protein antigen in dust on peanut sensitization and likely peanut allergy. *J Allergy Clin Immunol.* (2015) 135:164–70. doi: 10.1016/j.jaci.2014.10.007
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**Conflict of Interest:** The author declares that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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