

# *Prediction and Analysis of Allergenic Epitopes of Tree-Nuts and its Cross-Reactivity*

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**Abstract**—With a whopping 10-25% of the world's population being affected by it, allergies have become one of the top 10 reasons for visit to primary care physicians. Among this, tree-nut allergies are one of the most common allergies causing food substances. In the contemporary times various computational tools have emerged in order to facilitate time and cost-effective study of food allergens. This does not only aid in fabrication of a cure but also in its prevention as by analyzing for cross-reactivity among different allergens, patients can be advised against a number of possible other food substances which are likely to trigger the same response by their immune system. In the present study, the tool being utilized is EpiPro1.0 which has been developed by the authors in order to carry out accurate and efficient epitope prediction of an allergenic sequence (FASTA format). The tool also utilizes a novel algorithm in order to find the consensus of the results obtained through a number of different web-servers. In the present study, 20 different allergenic sequences from 6 major allergy causing tree-nuts, namely Almonds, Black Walnut, Brazil Nut, Cashew Nut, English Walnut and Hazel Nut, have been analyzed and 326 possible allergy causing epitopes have been predicted. Since, patients suffering from one tree-nut allergy tend to show sensitivity towards other tree-nuts as well, their cross-reactivity has also been studied in order to make accurate predictions regarding possible allergic reactions.

**Keywords**—Allergens, B-cell epitopes, consensus, cross-reactivity

## I. INTRODUCTION

Even in the contemporary age of technological development, allergies still continue to pose a daunting challenge for the medical society [1,2]. This has provided for a number of open-source computational tools to be developed in order to carry out time and cost-efficient predictions and analysis. The primary step in allergy analysis is to obtain B-cell epitopes of the allergenic sequence, which appear as amino-acid subsets. Chemically these allergens are proteins (chain of amino-acids) and it is due to certain subsets of these amino-acids which renders a protein its allergenic properties [3].

Obtaining these epitopic sequences from its parent protein is a daunting task in itself. Experimental methods for carrying out epitope prediction are often very costly and time inefficient. In addition, they also struggle in terms of accuracy of their results[4]. Hence, number of computational tools are being developed in order to perform epitope prediction. Researchers have emphasized that if a consensus can be obtained of the results predicted through different web-servers it would have a significant positive impact over the accuracy of the so obtained result [5]. This served as the motivation for developing EpiPro1.0[6] (Epi(tope) Pro(gnosis)1.0), a novel tool developed by the author in order to make up for the various drawbacks and carry out simple, efficient and a more accurate epitope prediction and analysis. EpiPro1.0 is an

opensource software available at (<https://github.com/amogh7/EpiPro1.0>) which has been developed on python2.7 and html5. It provides as an umbrella in order to incorporate a number of epitope prediction web-servers based over different algorithms (random forest algorithm, recurrent neural networks, etc) and facilitates a bio-informatician to carry out 'one-click' epitope prediction through each of the individual web-servers without having to go through the understanding of their different interfaces. In addition, EpiPro1.0 also provides the user with a novel algorithm in order to get the consensus from the results obtained through different web-servers. While obtaining the consensus is the dominant advantage provided by the tool, leaving it out still renders a massive increase in efficiency, by almost ~1650% in comparison to the current methodologies in place.

In the present study, analysis has been carried out over tree-nut allergens. These are one of the most prominent food allergies, in terms of both the number of people affected and the severity of the allergic reaction it induces. In addition to being highly unpredictable, even very small amounts of tree nuts are deemed potent enough to induce an allergic reaction. Furthermore, the high probability of its patient going into anaphylactic shock demands a patient, allergic to tree-nuts, to carry epinephrine auto-injector at all times[7]. Hence, an extensive analysis of tree-nut allergens shall be of immense aid to the medical society.

In the present study, authors have moved one step further to develop EpiPro1.1 which also enables the user in order to analyze the results of different allergens to be compared for cross-reactivity. As patients allergic to one type of tree-nut often show high levels of sensitivity to a number of other tree-nuts, extensive analysis of cross-reactivity between different tree-nuts is of major importance. In the present study, EpiPro1.1 has been utilized in order to carry this out and a major number of hits have been detected.

The present paper incorporates the study of six different tree-nuts, namely Almonds(*Prunus dulcis*), Black Walnut(*Jutland Nigar*), Brazil Nut(*Bertholletia excelsa*), Cashew Nut(*Anacardium occidentale*), English Walnut(*Jutland regia*) and Hazelnut(*Corylus*). A total of twenty allergenic sequences belonging to one of the six mentioned tree nuts were analysed, namely : Almonds - 'Pru du 3', 'Pru du 4', 'Pru du 5' and 'Pru du 6'; Black Walnut - 'Jug n 1' and 'Jug n 2'; Brazil Nut - 'Ber e 1' and 'Ber e 2'; Cashew Nut - 'Ana o 1', 'Ana o 2' and 'Ana o 3'; English Walnut - 'Jug r 1', 'Jug r 2', 'Jug r 3' and 'Jug r 4'; Hazelnut - 'Cor a 1', 'Cor a 8', 'Cor a 9', 'Cor a 11', and 'Cor a 14'.

## II. STATE OF ART

In the modern age, researchers are equipped with a number of computational tools to facilitate epitope prediction. These

tools, being based over different algorithms often show discrepancy amongst their results. A number of studies have suggested that a consensus of the results obtained from multiple such tools shall significantly bolster the accuracy. However, to the best of the knowledge of the authors, no such tool could be found in literature which would render the facility of obtaining the consensus. In their previous study authors have developed a tool to predict the epitopes using various web-servers. A novel algorithm has also been developed, which would provide EpiPro1.0 to obtain the consensus from the results of a number of different web- servers (six in the present case).

III. MATERIALS AND METHOD

The allergenic protein sequences(FASTA format) were obtained from National Centre of Biotechnology Information([www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov))[8].

A total of six web-servers were used through EpiPro1.0 in the present study, namely: AAP[9], FBCPred[10], BcePred[11], BCPred[12], BepiPred2.0[13] and ABCPred[14].

IV. RESULT AND DISCUSSION

The various allergenic sequences of the six tree-nuts were analyzed and their possible epitopes were predicted using the consensus result of the six different web-servers (as mentioned afore). The length of the predicted epitopic sequences is also of importance (the longer the sequence, the more likely it is to be epitopic) and EpiPro1.0 allows the user to obtain consensus predictions of desired lengths [6]. Here, the length of the sequences considered in the result is equal to or greater than 5. Table I. summarizes the result.

TABLE I. PREDICTED EPITOPIC SEQUENCES

Tree-Nut	Allergen	Predicted Sequences
Almond	Pru du 3	PKAMAA
		TPCINYVAN
		NYVANGGALN
		IPYKISPST
		VNGIPYTANAG
		ALNPSCCTG
	Pru du 4	GAVIRGKKG
		YDEPLTPGQCN
		DQPGTL
	Pru du 5	PLTPGQCN
		AEPKKEEKVEEKED
	Pru du 6	PGAGAGAAAPAAEPAK
		ETFEDSQ
		QQFRPSRQEGGQG
		FQGEDQQ
		FNPQQQGRQQ
		NLQGQDDNR
		QREREKQREQE
		EKQREQEQQGGGQD
		SAGGRGDQERQEEQQ
		PFSRSAGGRGDQERQQ
		QEEQSQRE
		GGRGDQERQEEQSQ
		DFVSPF
		DFYNPQG
		QVVENENG
		ISFRTDE
		YNRQES
		LSATSPPR
		GGGGQDNGVE
		RTDENGFTN
		AETFEDSQPQ

		PPRGR
		RPSRQEGGQGG
		NLQGQDDNRN
		SWNPSDPQFQ
		QQQQQQQQGNGNN
		FYNPQGG
		QLNQLEARE
		ENGDP
		PQDEFNPQQQGR
		QQQGRQQ
		GVTESWNPS
		QQQQQQQF
		DDNRNEIVR
		QNKEWQLNQL
		FGQNKEWQL
Cashew-Nut	Ana o l	RQYDEQQK
		EKKGREREHEEEEE
		EKYYKEKKG
		RQCERQEGGQQ
		DEDEDEAEED
		HNYKREDD
		ENKRES
		YIANNDEN
		VFHGGGENP
		KLFEKQDQ
		MSRRGEG
		WPFTEESTGS
		LFKKDPSQS
		ANITK
		ATVAS
KVMEKEA		
KRESIN		
HGPGGENPESFYRA		
AERIDYPPL		
GGMSVPFYNSRATK		
EHEEEEEWGTGG		
HLSSKSSHP		
SQCMRQCE		
SQSNKYGQ		
DEDEDEAEED		
EAEEDENP		
CMRQCERQEGGQ		
KERGQHNYKREDD		
RRGEGPKIWP		
PYVFEDEFT		
EEEDENPYVFEDE		
SSSKSSHPSYKK		
KVQRQYDEQQKEQ		
GHFEVFHGP		
INVRQ		
EGPKIWPTEESTGS		
RCQERYKKERGQ		
QERYKKERGQHNY		
VKECEK		
PEWRKEKEGR		
YVFEDEFT		
KVMEKEAKELA		
ESFYRA		
VPFYNSRATK		
RGEGPKIWPTEES		
PQQGRQQQS		
CYNEGN		
NQLDRTP		
DVSNSQNQ		
QQQQHQSRGR		
RGSEEESEDEKR		
ESEDEKRRWGQRD		
SQSERGSESEES		
PSRSQSERGSES		
LRVIRPSRSQSERGS		
ISFKTND		
SREDA		
TTLTSGES		
TMRLKENIN		
MTGISYPGCP		

	Ana o 2	CPETYQ	
		VEAWDP	
		EGNSPVVTVT	
		LEPDNRVEYEAGTVE	
		PARADIYTPEV	
		NNQQT	
		RKIKFNNQ	
		PARADIYTP	
		DVFQQQQHQ	
		QQQQHQSRGRNL	
		AGRTS	
		ALEPDNR	
		QEWQQQDECQ	
		DGEVREGQM	
	GEGMTG		
	AMTSPLAG		
	QTTLTSG		
	GESSH		
	QRDNGIEETI		
	NPKDVFQQQQQ		
	Ana o 3	VEVEEDSGREQ	
		VKQEVQRGGRYNQRQES	
		LQQEQIKGEEVRELYE	
		IVEVEEDSGRE	
	Brazil-Nut	Ber e 1	QMEESPYQTMRRGMPE
			EGMDESC
			TVVEEENQEECREQMQRQQ
	Ber e 2	QQEEMQPRGEMRR	
QGSREQEEER			
SQFQGSREQ			
CYNDGD			
NIQRSQKQRG			
ETARKVRGE			
VVVKQA			
AQEPQYRLEAEA			
PAEADFYNPRAG			
FQSMS			
GSREQEEERGRF			
EVWDYTDQQF			
IQNIDNPAE			
DNPAEADFYNPR			
NAPKL			
IREELQ			
VRGEDDQRG			
QKQRGERYGLRGG			
LRGIPVGV			
MVVVPQNFVVV			
YEQEELYECRIQ			
LTAQEPQYR			
LWRLNANSVYV			
REELEQQEGGGYNG			
TSPLRGIPV			
Black-Walnut		Jug n 1	IDNPRRRGE
	QQRSRGGYDEDNQ		
RGEEMEEMVQ			
Jug n 2	EGCQEIQIRQQ		
	CQIQEQSPERQ		
	RQYKEQQGRERGP		
	KEQQGRERGPEASPE		
	ESKGREEEQ		
	ERGPEASPRRESKG		
	SQSIRSRHESEE		
	YFHSQSIRSRHES		
	NQDSN		
	TPRDRL		
	FFDQQEQR		
	RFFDQQE		
	VIIRAS		
	LKSER		
	PWGRSSGGPISLKSE		
	SSQSFEDQGRREQEEEST		
	HVSSQ		
	FGINGENNQ		
	NQLEREA		

		TERQSRRGQG	
		VPTERQSRRGQ	
		RCERQ	
		QIQEQSPERQRC	
		KSERPSYSNQ	
		AGQRPWGRRS	
		QEEEEESTG	
		EREAKEL	
		SRHESEEG	
		SQMESY	
		PGQVREYYAAGAKSPD	
		EEEEQRHNPYYFHS	
		PYYFHSQ	
		PAGATEYVINQDS	
	ERQSRRGQGR		
	DQEQREG		
	AGAKSPDQS		
	EEIEEIFESQM		
	VPHYNSKATV		
	SFNMPREE		
	NNPGQVR		
	GQRPWGRRSSGGPIS		
	SYSNQFGQ		
	English-Walnut	Jug r 1	DIDNPRRRGEG
			RQSRSGGYDEDNQ
			VRRQQ
			IDNPRRRGEGCRE
			QSRSGGYDEDNQRQHF
RRRGEGCREQIRQQ			
RGEEMEEMVQ			
Jug r 2		PNECGIS	
		YDEDNQROHFR	
		NECGISSQRCEIR	
		SSQSYEGQGRREQE	
		LKSESPYSNQ	
		GGPISLKSESP	
		CQIQEQSPERQRC	
Jug r 3	GREEEQQRHN		
	DDEENPRDPREQYRQ		
	SQMESY		
	SRHESEEGEV		
	NNPGQFREYYAAGAKS		
	VPAGA		
	ERQSRRGQGR		
	DQEQREG		
	PERQRC		
	GAKSPDQ		
	YAAGAKSPD		
	LDANPNTSM		
	EEIEEIFESQM		
	REAKEL		
VPHYNSKATV			
Jug r 4	PRDPEQRYEQCQQ		
	SFNMPREE		
	SESPYSNQIFG		
	PYYFHSQSIR		
	LRGTVP		
	GGRQQ		
	ETFEEQSRQSQGGQ		
	YNDGS		
	NQLDQN		
	EQHRRQ		
	QQRQRPGEHQQQ		
	ETARRLOSENDHR		
	REEQEREERKERER		
	RESEERRQSRGG		
SERRQSRGGRRDD			
SREEQEREERKERERE			
KERERERESE			
QIPREDA			
NDGSNP			
HVVYA			
LLDTNNA			
VIESWDPNNQQF			

		AGVIESWDPNNQ
		IEAEAGVIE
		EHGQQQRGLGNN
		PETFEESSQRQS
		ERRQSRRGGRDDNG
		KTNENAMVSP
		QRPGEHGQQQRG
		GNPDEFRPQQGQQ
		GCPETF
		HRRSIVR
		ENDHRRSI
		RRLQSENDHRRS
		NDGSNPVVA
		IPREDARRLK
		STVNSHTLPVL
		IPREDARRLKFN
		RGGRDDNG
		QRGLGNNVF
		PQQQQEYEQHR
Hazelnut	Cor a 1	GPVGDKV
		KGGKEKV
		SPFKYVKERVE
		RVEEVD
		GPGTI
		VENVEGNGGPGT
	Cor a 8	RAVNDASRTTSD
		ARASLT
		GVNIPYKISPSTN
	Cor a 9	VGLRRQQ
		EDPQQQSQQ
		GQRQGGQSQRSEQ
		QQQSQQGQRQGGQSQ
		CYNDGD
		DEHQRRQQQFGQRR
		GEQGEQEQQEGG
		DTARRLQSNQDK
		LQSNQDKRR
		RESEQERERQRR
		RPERSRQEWER
		RQGGGRD
		WERQERERESEQR
		EWERQE
		LQVVRPERSRQEW
		QVVDDNG
		SREEA
		EQGEQEQQEGGNNV
		QISPL
		GGRGRDV
		KTNDNA
		YNRQE
		NDGDSPVVTVS
		PGCPETFE
		PETFEDPQQQS
		NTVNS
		RGDLQREGLY
		SSSERKRRSE
		IEAEACQIE
		REEARRLKYNRQE
		SSERKRRSESEGR
		NPDDEHQRRQGGQQ
		QSNQDKRRNIVKVE
		NTVNSNTLPV
		QQGEGNNVFSG
		IEAEACQIESWDHN
		AQISP
	Cor a 11	PELKKCKHK
		QQEEGNSSEESYGKEQEN
		QICEKA
		EHFESR
		LENFTKRS
		YMINRDEN
		VKASREK
		KGSIV
		EQSKGS

		KVFGEQSK
		SQHEEGP
		LLHKHPSQS
		PSREV
		FFFPGNKQQEE
		GPYYNSRAT
		GAGGEDPESFYRAF
		APGHFEAF
		ERQFDEQRRDG
		VAPAGHPVAVIAS
		PPRIWPFGGESS
		HEEGPPR
		VREEKRESFN
		PNKQQEEGRRGGRA
		NRDENEKL
		VNEFERDAKE
		EAFYGAGGEDPE
		KHPSQSNQ
		KVRREQLE
		EDPELKK
		NEFERDAKEL
		RDERQF
		RREQLEKV
		GNSSEESYGKEQEN
		KRESFNV
		PSQSNQFG
	Cor a 14	DIVNQGGRRGESC
		GSYDGSNQQ
		QQGEMRGEEM
		ITTVDVDE
		EDIVNQGGRR
		YDGSNQQQQELEG

The number of epitopic sequences predicted can aid to pinpoint what induces the allergenic properties to the various tree-nut allergenic proteins under study.

In addition, with the tendency of patients suffering from allergy due to one tree-nut, often showing sensitivity to other forms of tree-nut as well, a novel methodology was developed in EpiPro1.1 in order to study for cross-reactivity between different allergens. The obtained result is illustrated in Table II.

The result depicts the high probability of cross-reactivity shown by tree-nut allergens. With Hazelnut and Cashew-nut showing similarities in epitopic sequences among five and four other tree-nut species under consideration respectively, it shows if someone who is allergenic to one of any of these species, might also show sensitivity against the other species. Also, as the number of sequences in common increases, the higher is the probability for a person to show sensitivity against the other species. Also, as the number of sequences in common increases, the higher is the probability for a person to show sensitivity to multiple tree-nuts. Hence, from the result we can observe, someone showing sensitivity to hazelnut has a high probability to show sensitivity against Black-nut as well, and vice and versa.

#### V. CONCLUSION

20 different allergenic sequences from over 6 different tree-nuts were analyzed using EpiPro1.1, and a total of 362 epitopic amino-acid sequences were identified through a consensus over 6 different web-servers. Cross-reactivity study showed Almonds to have cross-reactivity against Brazil-Nut, Cashew-Nut and Hazelnut; Black-Nut to show cross-reactivity against Brazil-Nut, Cashew-Nut and Hazelnut; Brazil-Nut to show cross-reactivity against Almonds, Black-Nut and Hazelnut; Cashew-Nut

to show cross-reactivity against English- Nut, Hazelnut,

TABLE II CROSS-REACTIVITY

Tree-Nut	Cross-Reactive Sequence	
<b>Almonds</b>		
Brazil-Nut	DFYNP	
Cashew-Nut	RQEGGQ	
	QQGRQQ	
Hazelnut	QQQQQ	
	IPYKISPST	
	EQEQQG	
	YNRQE	
	ETFED	
	QQQQQ	
<b>Black-Nut</b>		
Brazil-Nut	REQEEE	
Cashew-Nut	EESTG	
	EAKEL	
Hazelnut	RGEEM	
	SNQFG	
	IDNPRRRGE	
	QQSRSGGYDEDNQ	
	RGEEMEEMVQ	
	EQIQRQQ	
	CQIQEQSPERQ	
	GREEEQ	
	SRHESEE	
	YFHSQSIR	
	DQEQQR	
	GGPISLKSE	
	QGRREQE	
	ERQSRRGQG	
	QIQEQSPERQRC	
	PSYSNQ	
	REAKEL	
	SRHESEEG	
	SQMESY	
	REYYAAGAKS	
	YAAGAKSPD	
	EEEQQRHN	
	PYYFHSQ	
	ERQSRRGQGR	
	DQEQQREG	
	GAKSPDQ	
	EEIEEIFESQM	
	VPHYNSKATV	
	SFNMPREE	
	NNPGQ	
	SYSNQFG	
		GGPIS
	<b>Brazil-Nut</b>	
Hazelnut	CYNDGD	
<b>Cashew-Nut</b>		
English-Nut	RRGEG	
	EAKEL	
Hazelnut	PESFYRA	
	YNSRAT	
	PGCPE	
	SPVVTV	
	QQQQQ	
<b>English-Nut</b>		
Hazelnut	RGEEM	
	SNQFG	
	QSQQGQ	
	TARRLQS	
	EQERE	
	ERESE	
	IESWD	
	IEAEA	
	PETFE NPDDE	
	GCPETF	
	ARRLK	
	GNNVF	

Almonds and Black-Nut; Cashew-Nut to show cross-

reactivity against English-Nut, Hazelnut, Almonds and Black-Nut and Hazelnut to show cross-reactivity against all 5 other tree-nuts species under study. With 20 different allergenic sequences, the task to predict the consensus among the huge number of possible epitopic sequences obtained through various different web-servers and further analyzing it for cross-reactivity would have been practically impossible and heavily prone to human error. EpiPro1.1 does not only make it simple and time efficient, but also significantly bolsters the accuracy of the obtained result.

REFERENCES

- [1] D. Chandrika, International Journal of Otorhinolaryngology and Head and Neck Surgery, 3(1): Jan 2017, pp.1-6.
- [2] [https://www.foodsmatter.com/allergy\\_intolerance/miscellaneous/articles/food\\_allergy\\_india.html](https://www.foodsmatter.com/allergy_intolerance/miscellaneous/articles/food_allergy_india.html).
- [3] A. Johri, Neelabh, M. Srivastava, "A computational study of B-cell epitopes of wheat allergens and identification of its IgE binding residues," Proceedings of the 12th INDIACom; INDIACom-2018; IEEE Conference ID: 42835, pp. 1095-1099, 2018.
- [4] J. V. Ponomarenko, M. H. V. V. Regenmortel, "B-cell epitope prediction," In: Gu J, Bourne PE, editors. Structural bioinformatics, second ed. John Wiley & Sons, Inc, pp. 849-879, 2009.
- [5] <http://ailab.ist.psu.edu/bcpred/>.
- [6] A. Johri, M. Srivastava, unpublished.
- [7] <https://www.foodallergy.org/common-allergens/tree-nut>.
- [8] [www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov).
- [9] Y. E. Manzalawy, D. Dobbs and V. Honavar, "Predicting linear B-cell epitopes using string kernels," Journal of molecular recognition, vol 21, pp 243-255, Jul 2008.
- [10] Y. E. Manzalawy, D. Dobbs and V. Honavar, "Predicting flexible length linear B-cell epitopes," In Computational systems bioinformatics, vol 7, pp. 121-131, NIH Public Access, 2008.
- [11] S. Saha and G. P. S. Raghava, "BcePred: Prediction of Continuous B-Cell Epitopes in Antigenic Sequences Using Physico-chemical Properties," In G. Nicosia, V. Cutello, P. J. Bentley and J. Timis (Eds.) ICARIS 2004, LNCS 3239, pp. 197-204, Springer, 2004.
- [12] J. Chen, H. Liu, J. Yang and K. C. Chou, "Prediction of linear B-cell epitopes using amino acid pair antigenicity scale," Amino acids, vol. 33, pp. 423-428, September 2007.
- [13] M. C. Jespersen, B. Peters, M. Nielsen and P. Marcatili, "BepiPred-2.0: improving sequence-based B-cell epitope prediction using conformational epitopes," Nucleic Acids Res, 2017 (Web Server issue).
- [14] S. Saha and G. P. S. Raghava, "Prediction of continuous B cell epitopes in an antigen using recurrent neural network," Proteins: Structure, Function, and Bioinformatics, vol 65, pp. 40-48, Oct 2006.