

June 20-21, 2018
Rome, Italy

Bernard E Bihain, J Plant Physiol Pathol 2018, Volume 6
DOI: 10.4172/2329-955X-C1-013

RNA FRAMESHIFTS CAUSE PLANT PROTEIN ALLERGENICITY

Bernard E Bihain

Genclis, France

Background: In all cells, a significant percentage of RNA sequences may diverge from the DNA template. Unlike editing, RNA-DNA Divergences (RDD) caused by transcription infidelity lead to base substitutions within and across base families and this RNA are translated. Here we report on a novel Trait Identification event causing single-base omission (RDD gap) in three different legumes with different allergenicity.

Methodology: Because of the degeneracy of the genetic code, RNA with frameshifts translates into protein variants with cationic peptide at the carboxy-terminal end that may thereby modify their immunogenicity. RNA sequences from peanut, soybean and green bean were aligned to their respective DNA templates and gap rates were calculated as the proportion of gap per RNA read.

Findings: RDD gap rate was highest in peanut, intermediate in soybean and lowest in green bean. Allergens from peanut and soybean differ from non-allergenic proteins of the same species by a greater diversity of gap in allergens. The same increased gap density was also observed in sesame allergens. Three recombinants Ara h 2 translated from frameshifted RNA but not the protein translated from RNA with canonical sequence induced specific IgE production without adjuvant and clinical allergy in mice. Analysis of RDD gap pattern of peanut proteins that were not described as peanut allergens led to identification of two novel peanut proteins with a gap profile consistent with

allergenicity. The recombinant form of these two novel peanut allergens candidate show specific reactivity toward IgE present in sera of peanut allergic patients but not of subjects without peanut allergy.

Conclusion & Significance: Specific DNA sequences in legumes and at least one grain allows transcriptional slippage. Translation of frameshifted RNA produce low abundance diversified variants causing IgE production. Genomic editing and production conditions minimizing RDD gap occurrence may significantly reduce the allergenicity of these important protein sources.

Biography

Bernard E Bihain created GENCLIS in 2004. After receiving his Doctorate in Medicine from the Free University of Brussels in 1984, he began a surgery internship followed by a Postdoctoral fellow at Columbia University in 1988. Thereafter, he took a position in 1990 as Assistant Professor of Physiology at the University of Louisiana. He was awarded the position of INSERM Research Director in 1992 and became Professor and Chairman of the Department of Biochemistry, University of Rennes, where INSERM Unit 391 was created in 1994. He then undertook the Direction of the Department of Functional Genomics of the genomic company Genset. He has actively contributed to the emergence of genomic technologies. His pragmatism, stemming from his experience as a surgeon, powers the translational activities of GENCLIS. He has authored over 50 publications in peer-reviewed journals, and his studies are cited in more than 5000 scientific articles.

bbihain@genclis.com

