



Article

Toxic determination of Cry11 mutated proteins obtained using rational design and its computational analysis

Suarez-Barrera M.O^{1,3}, Herrera-Pineda Diego¹, Rondón-Villarreal P¹, Pinzón-Reyes EH^{1,4}, Ochoa Rodrigo⁵, Visser L¹, and Rueda N.J^{1*}

¹ Facultad de Ciencias Médicas y de la Salud, Instituto de Investigación Masira, Universidad de Santander

² Department of Pathology and Medical Biology, University of Groningen, University Medical Center Groningen, Groningen, The Netherlands

³ Max Planck Tandem Group in Nanobioengineering, Institute of Chemistry, Faculty of Natural and Exact sciences, University of Antioquia.

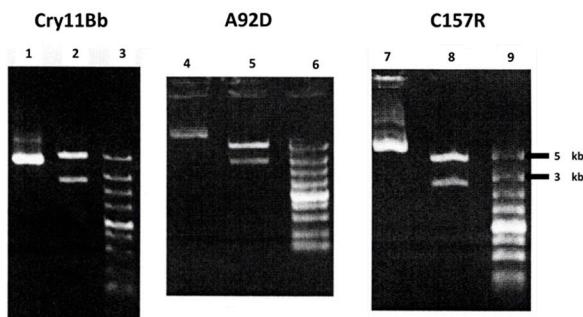
⁴ Centro de Bioinformática, Simulación y Modelado (CBSM), School of Bioinformatic, Universidad de Talca, Talca, Chile

⁵ Biophysics of Tropical Diseases, Max Planck Tandem Group, University of Antioquia, 050010 Medellin, Colombia

* Correspondence: Juliana.forero@udes.edu.co

Supplementary materials

A Cry11Bb and Variants digestions



B Cry11Aa and Variants Digestion

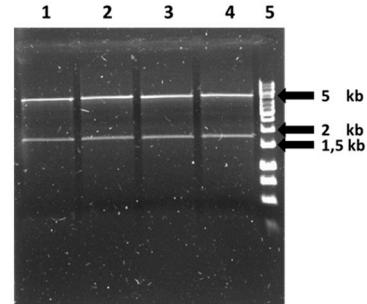


Figure S1. Restriction enzyme assay HindIII/ SacI for every native and variant gene obtained. 1) 553; 2) 556; 3) 553-556; 4) Cry11Aa; 5) Weight marker.

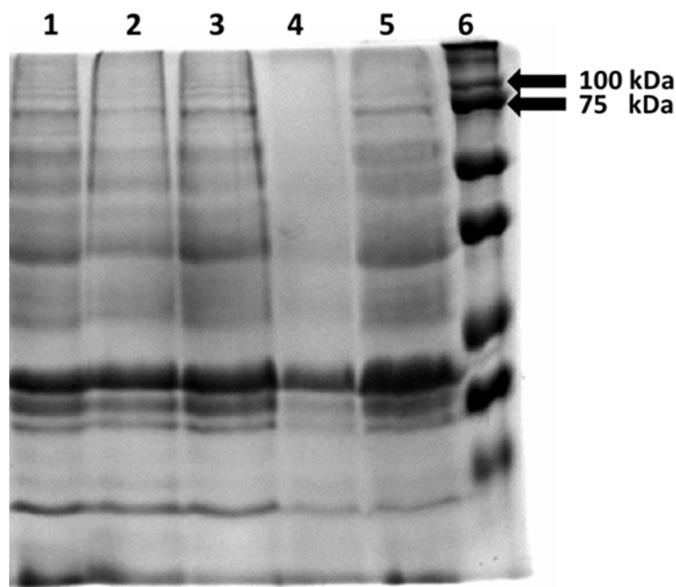


Figure S2. A. SDS-PAGE Cry11Aa – 72 kDa. Lane 1. Variant 553; Lane 2. variant 556; Lane 3. Double mutant 553-556; Lane 4. Negative Control BMB171; Lane 5. Positive Control Cry11Aa; Lane 6. Weight marker.

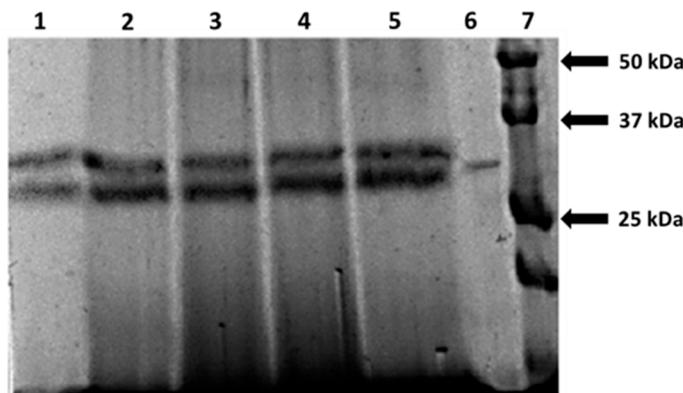


Figure S2. B. SDS-PAGE Cry11Aa active toxin (32- 34 kDa). Lane 1. Cry11Aa; Lane 2. Variant 8Aa; Lane 3. Variant 553; Lane 4. Variant 556; Lane 5. Variant 553-556; Lane 6. Negative control BMB171; 7) Weight marker.

Table S1. Oligos designed to obtain the variants 8Cry11Aa-553, 8Cry11Aa-556 and 8Cry11Aa-553/556.

Position	ID	Sequence
553	3C8F	5'-AGAAGAGTGGTATTTCGCAGTGGTTGTA-3'
	3C8R	5'-TACAAACCACTGCGATAAATACCACTCTTCT-3'
556	6C8F	5'-GGTATTCTCGCAGTTGTTGTAGAAAAGA-3'
	6C8R	5'-TCTTTTACTACAAACAACGAGAAATACC-3'
553-556	36C8F	5'-AGAAGAGTGGTATTTCGCAGTTGTTGTAG- TAAAAGA-3'
	36C8R	5'-TCTTTTACTACAAACAACGAGAAATACCAC- TCTTCT-3'