

Cry8-01 MSPNNQNEYEIIDATPSTSVSNDSTKYPYANEPTNALQNMNYKDYLRMSEGYDNKYFANPEVFAAPG-GITTTGITIVTKLLGWLGLPFAGETGMALNFILGLLWPTSGNPWAEMLMILVEELINQKIEEAVRNKALADLANSGRALQSYLNAFEDWQKNPNIFRSKELVRRERFANAHESLRTEMSSFAIRGFEIPILLATYA 200
Cry8-02 MSPNNQNEYEIIDATPSTSVSNDTTRYPFANEPTNALQNMNYKDYLRMSEGYDSEYAGSPEAFTSGQDAVKAAIGVVQGILGKLGVPFVGPIVSLYSALIDVLWPGGKSQWEIFMEQVEALINKKIAEYARNKAI AELEGLGNKYIYLTALEEWQKNPSSSTRVLRDVQNRFEILDSLFTQYMPSPRVAGYEVPLLTVYA 200



Cry8-01 QAANLHLFLIKDVQIYGKEWGYTQADIDLFYREQVEFTKEYTEHCININYNDGLNQLKGSNAKQWIAFNRRREMTLTVLDVVALLFSNYDVMYP IKTTTELRTIYTDPLGYTKGSSSTPPWYNYGSSFSYIESVAIPAPSLVKWLSQIEIYSKSAKATP-QSADYWAGHTITYHYGGONGQAVANYGORTNPVAVDRY 400
Cry8-02 QAANLHLLLLKDA SNFGEEWGLTGSEVNTYIDRQMSLTAEYS DHCVKWYNTGLDQLKGSNAKQWVAYNRRREMTLTVLDVVALLFSYSDTETYP IETTAQLTREVYMDPLG--AVDVS NIGSWYDKAP SFS SAIESAAIRPPHLFDFITGLIVYTQLRNLTS DRYIRFWAGHTIGYKKVNTPETNVQMYGTNQNLQDTSTF 400



Cry8-01 NFEQADIYRVSS-----SVASSTTSGVKLLTTKAIFDGINTRKGLVSYRYE-KSSNFFNELKDTITELPVQLSSPPTYGD AEQYSHRLSYVSNAPTEYSSGGHLILGLIPVLGWTHTSLTQTNQIHSDSITQIPAVKVS NLESGTSVVANPGFTGCOLLKRT---STGRMGT LKLT VAGILSREMTIRIRYAATDFKL 600
Cry8-02 DFKGYNIYKTL SKDAVLFDISQSGYTYTFFGMPEVEFFLVNQVNNTSKLVYKPVSKDIIQKTRDSELELPATSDP IIS---NAYSHRLNHTFIYSSSTN-----TYVPVFSWAHWSADLENTIYPEKITQIPAVKANYTGPSTTVINSRGLYGGNIVHTSNANATEAILGINCRFNFTSNQKYIVRIRYAADRSGTL 600



Cry8-01 QVIYKGILQSSSYNSNKT MNKGENLTYGKFKFAN--FTLPISLLIPSDL SIDVQNLSGGEVYIDRIEFIPVGATYEA EQDLEN AKKAVNALFTNTKDGLRPGVTDYEVNQ AANLVECLSDDLYPNEKRL LFDVREAKRLSEARNLLQDPDFQ EINGENGWTASTGIEVIEGDAVFKGRYLHLPGAREIDTETYPTLYQ 800
Cry8-02 KLS-AGTSSRTIDFNATMTPGTSLEYNSFKYAMSN TFFEVSTNQILNLLIFVSENFPG-NLYIDKXEFIPVD EYEA EQDLEN AKKAVNALFTNTKDGLRPGVTDYEVNQ AANLVECLSDDLYPNEKRL LFDVREAKRLSEARNLLQDPDFQ EINGENGWTASTGIEVVEGDALFKGRYLRLPGARQIDTETYPTLYQ 800



Cry8-01 KVEEGVLKPYTRYRLRGFVGSSQGLEIYTIRHQ TNRI VKNVPDDLDPVPPVNDGRINRCSEQKYVNSRLEVE-----NRSGEAHEFSIPIDTGEIDYNENAGI WVGFKITDPEGYATLG NLELVEEGPLSGDALERLQREEQQWKIQMTKRREETDRKYMI AKQAVDRLYADYQDQQLNPNVEITDITAAQNVIQSI 1000
Cry8-02 KIDEGV LKPYTRYRLRGFVGRSQGLEIYTIRHQ TNRI VKNVPDNLDPASPGNAGDGINRCSEQKYVNSRLEGEKGLPNGSRSAE AHEFS LPI D IGEIDYNENAGI WVGFKITDPEGYATLG NLELVEEGPLLGD TLERVKREEQQWKIQMTKRREETDRKYMI AKQAVDRLYADYQDQQLNPNVEITDITAAQNVIQSI 1000



Cry8-01 PYVYNDAFPGLPGMNYTKFTELTDRLQQAWSLYDQRNAIPNGDFRNELSNWNTTAGVNVQQLNGTSVLVIPNWD AQVSQQFTVQPNQRYVLRVTARKEGVGN GYVSIRDGQNQTETLTFSASDYDTNGVYNIQASNTNGYNTNGVYNDQTYITKTAEFIPHTNQVWIEMSETEGTFYIESVELIVDVE 1189
Cry8-02 PYVYNDAFPGLPGMNYTKFTELTDRLQQAWSLYDQRNAIPNGDFRNELSNWNTTAGVNVQQLNGTSVLVIPNWD AQVSQQFTVQPNQRYVLRVTARKEGVGN GYVSIRDGQNQTETLTFSASDYDTNGVYNIQASNTNGYNTNGVYNDQTYITKTAEFIPHTNQVWIEMSETEGTFYIESVELIVDVE 1189

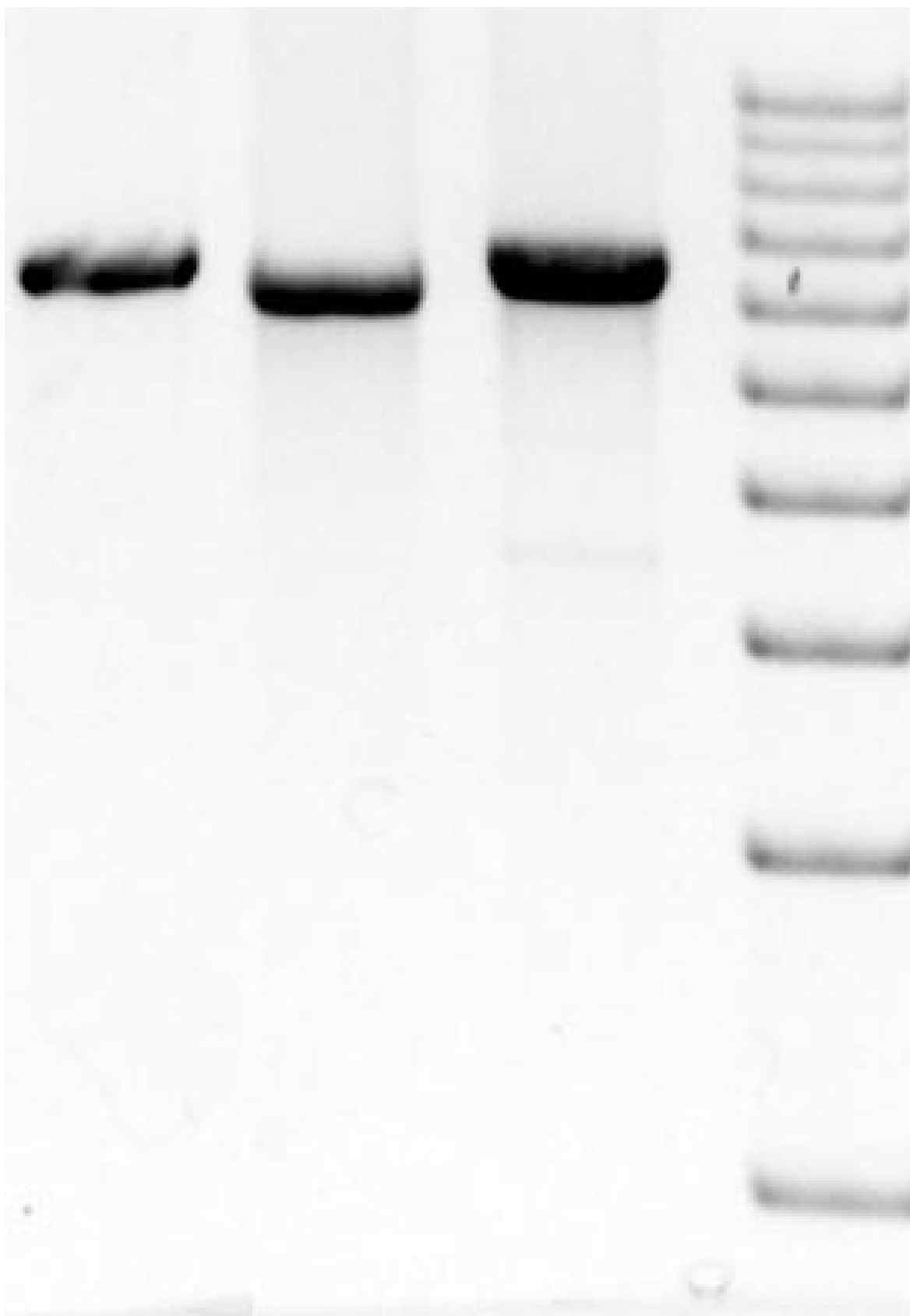


1

2

3

4



9162 bp

8144 bp

Supplemental Fig. 1: Protein sequence alignment of Cry8Kb3 and Cry8Pa3 from *Bacillus thuringiensis* INTA Fr7-4. The histogram below the alignment indicates the degree of similarity. The regions between brackets correspond to each of the three domains of the proteins in sequential order.

Supplemental Fig. 2: Agarose 0.6% gel electrophoresis of PCR products using primers: C801-F1 and C802-R1 (lane 1); C801-F2 and C802-R1 (lane 2); C801-F1 and C802-R2 (lane 3); 1-Kb molecular marker (Promega) (lane 4). The amplifications involve part of the *cry8Kb3* and *cry8Pa3* genes with their intergenic region, demonstrating that they are coded in the same strand separated by a 5.6 kb-distance.