

The following supplement accompanies the article

Polymorphic repetitive loci of the amphibian pathogen *Batrachochytrium dendrobatidis*

Stephen Garland^{1,*}, Timothy Y. James², David Blair³, Lee Berger¹, Lee F. Skerratt¹

¹**Amphibian Disease Ecology Group, and the School of Public Health, Tropical Medicine and Rehabilitation Sciences,
James Cook University, Townsville, Queensland 4811, Australia**

²**Department of Ecology and Evolutionary Biology, University of Michigan, Ann Arbor, Michigan 48108-1048, USA**

³**School of Marine and Tropical Biology, James Cook University, Townsville, Queensland 4811, Australia**

*Email: sgarland@bses.com.au

Disease of Aquatic Organisms 97: 1–9 (2011)

Supplement. Additional figures

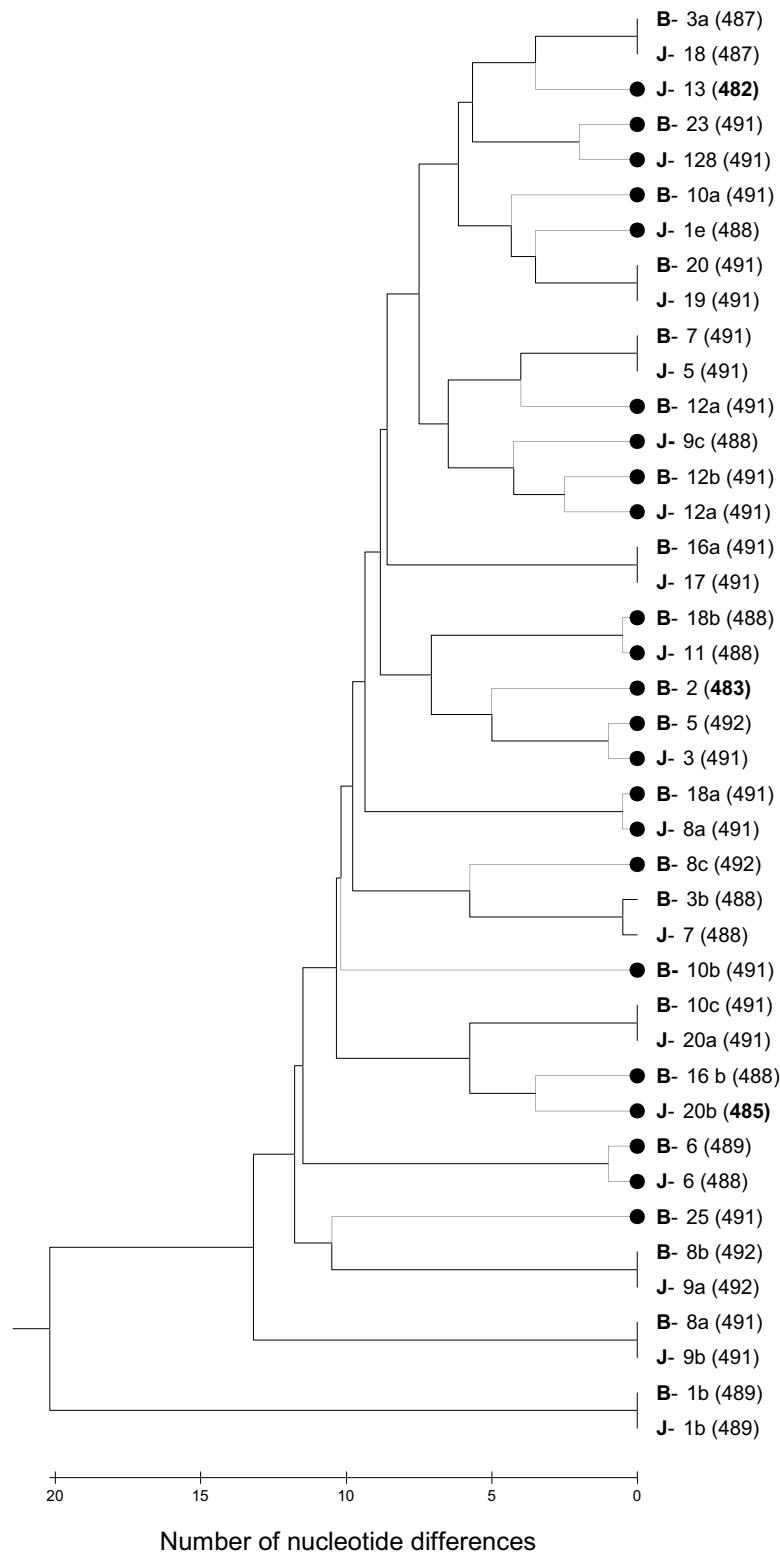


Fig. S1. UPGMA dendrogram based on the number of nucleotide differences with pair-wise deletion of indels for marker system MS5 fragments. JEL423 paralogs are represented by **B** (Broad Institute genome sequence), then the SuperContig number and letter subscript if more than one per SuperContig, followed by the fragment size (bp) in brackets; unique size variants in bold. The nucleotide positions and strand designation (+ or -) for each paralog are: 1b (3787468-3787956+), 2 (2259135-2259617-), 3a (1642898-1643384+), 3b (3613-4100+), 5 (6545-7036+), 6 (1414637-1415125+), 7 (240420-240910+), 8a (900888-901378+), 8b (847677-848168-), 8c (11692-12183+), 10a (1004659-1005149-), 10b (9658-10148+), 10c (27923-28413+), 12a (886377-886867-), 12b (646146-646631-), 16a (472693-473183-), 16b (7865-8352+), 18a (41903-42393+), 18b (13039-13526+), 20 (10292-10782+), 23 (12646-13136+), 25 (7207-7697-). JAM81 paralogs are represented by **J** (JGI genome sequence), then Scaffold number and subscript if more than one per scaffold, followed by the fragment size (bp) in brackets. The nucleotide positions and strand designation (+ or -) for each paralog are: 1b (3758385-3758873+), 3 (8760-9250+), 5 (397040-397530+), 6 (143998-144485-), 7 (13725-14212+), 8a (61759-62249+), 9a (237757-238248+), 9b (183807-184297-), 9c (1062096-1062583-), 11 (20111-20598+), 12a (501899-502389-), 12b (9558-10048+), 13 (6638-7119+), 17 (48083-48573+), 18 (375047-375533+), 19 (25089-25579+), 20a (240970-241460-), 20b (259214-259698-), 128 (3091-3581+). (●) Paralogs or alleles unique to one strain.

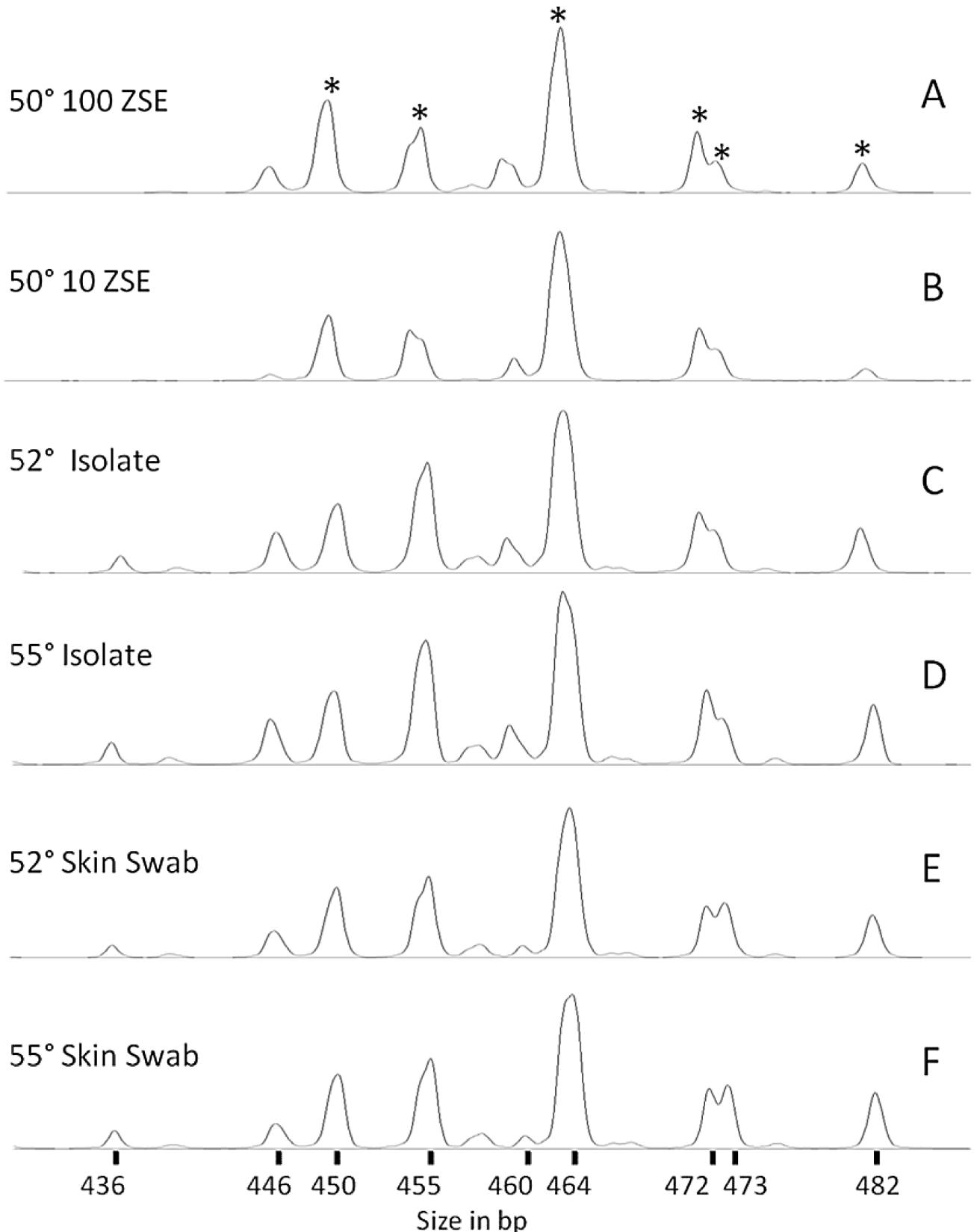


Fig. S2. Marker system MS4. (A,B) The effect of different template concentrations at an annealing temperature of 50°C. (A) 100 zoospore equivalents (ZSE) and (B) 10 ZSE. * in (A) indicates consistently amplified size variants for all sample/PCR-condition combinations. (C) to (F) show representative results from fragment analysis of using 2 annealing temperatures across 8 Australian isolates and one skin swab from infected frogs. (C) & (D) show a representative result obtained for an extract obtained from a culture at an annealing temperature of 52°C (C) and 55°C (D). (E) & (F) show the results obtained from an extract obtained from a skin swab at an annealing temperature of 52°C (E) and 55°C (F).

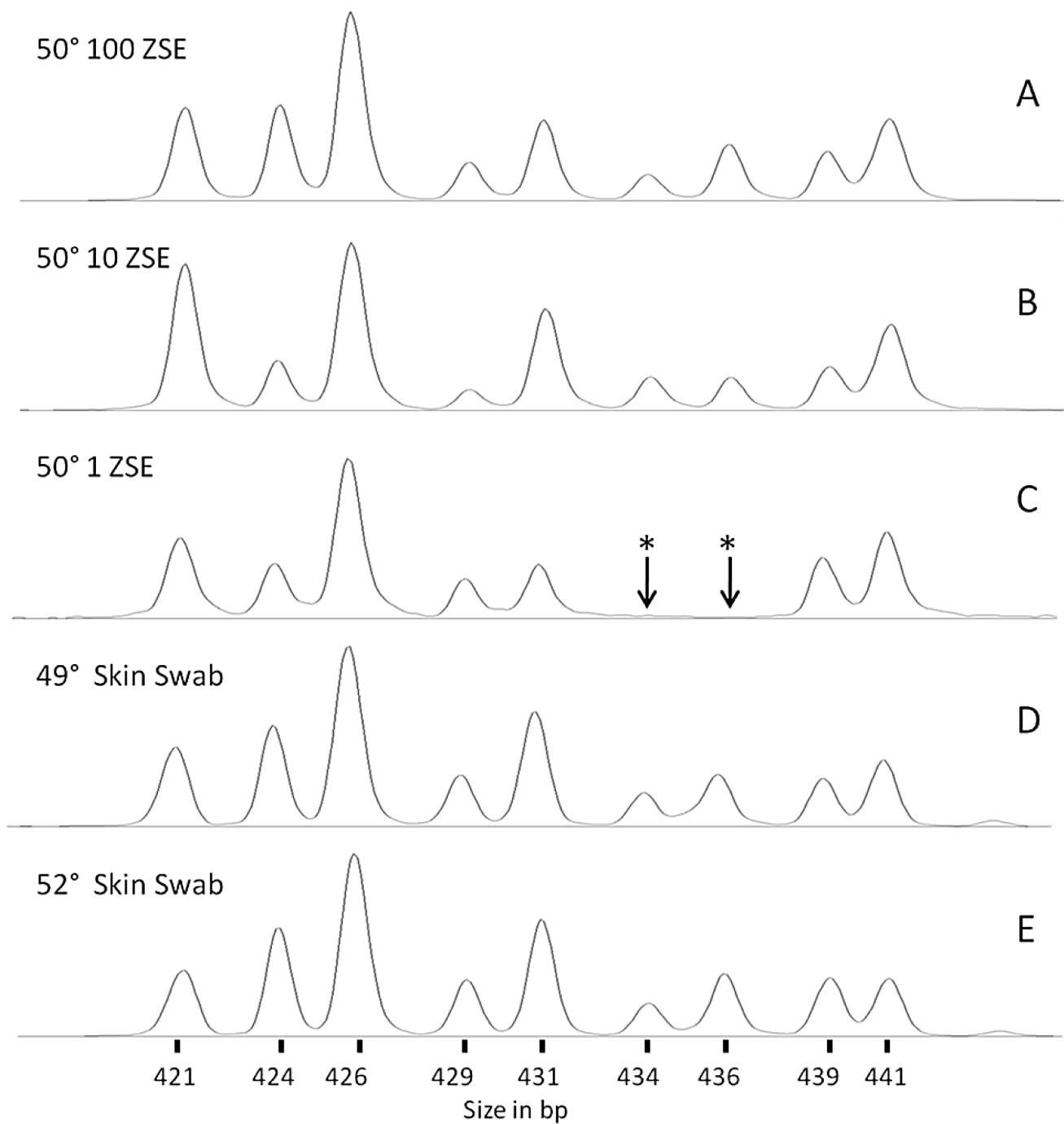


Fig. S3. Marker system MS6. (A to C) The effect of different template concentrations at an annealing temperature of 50°C. (A) 100 zoospore equivalents (ZSE), (B) 10 ZSE and (C) 1 ZSE. The grey arrows marked with * in (C) indicate the failure of the 434 and 436 bp size variants to amplify at 1 ZSE (C). (D) & (E) show representative results from fragment analysis of using 2 annealing temperatures across 8 Australian isolates and 2 skin swabs from infected frogs. The result for a skin swab at an annealing temperature of 49°C (D) and 52°C (E) are representative for all other sample/PCR-condition combinations.

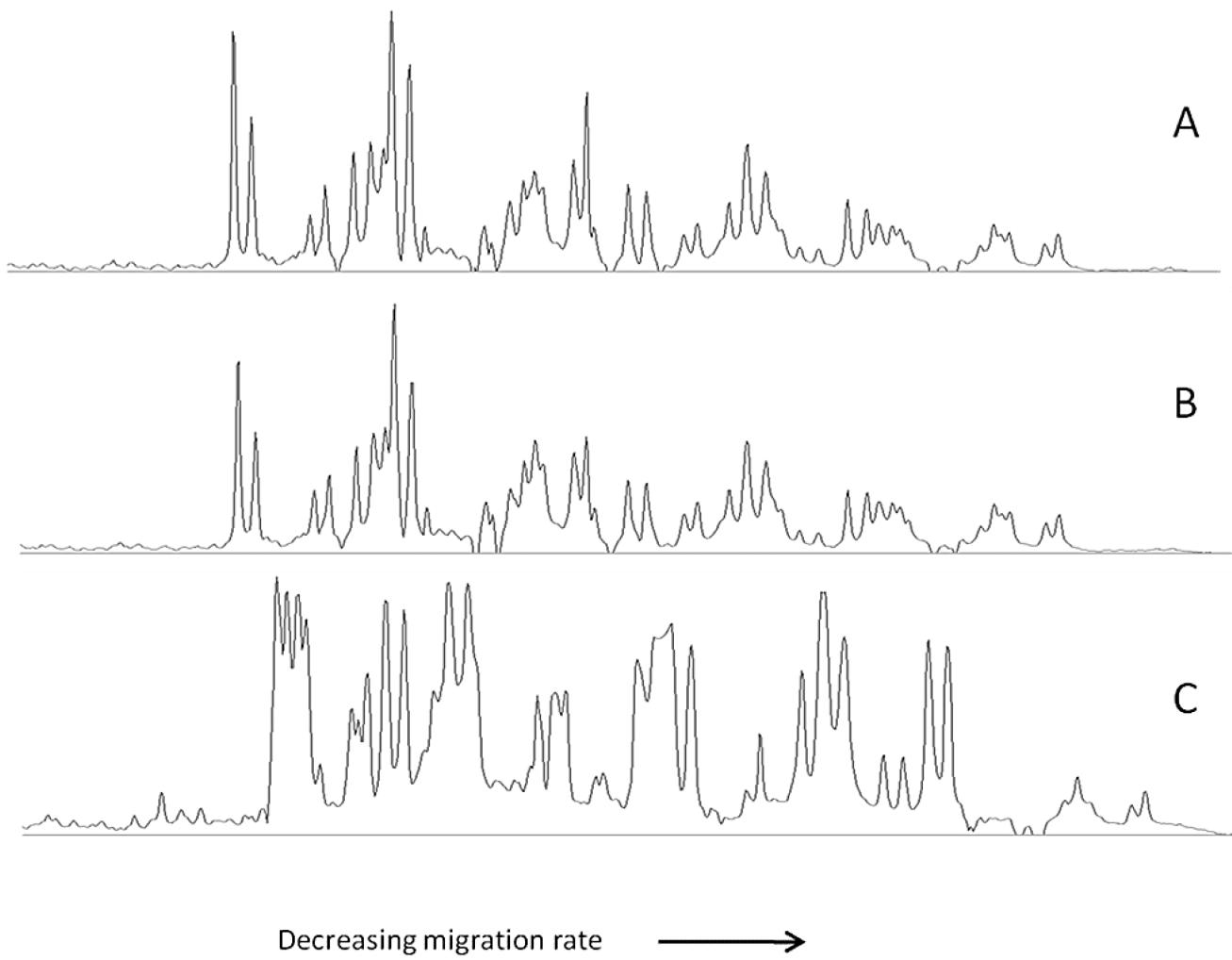


Fig. S4. Intra- and inter-run variability of capillary electrophoresis-single strand conformation polymorphism (CE-SSCP) analysis of marker system MS1 at 25°C, non-denaturing matrix, isolate Rockhampton-Lcaerulea-99-LB-1. Electrophoregrams are for the 6-FAM labelled strand only. (A) & (B) Same PCR batch and electrophoresis run (November 2009) but different PCR amplification and electrophoretic injection. Notice the excellent reproducibility. (C) Different PCR batch and electrophoresis run (September 2009) to (A) & (B) Notice the different band migration patterns between (C) and both (A) & (B).

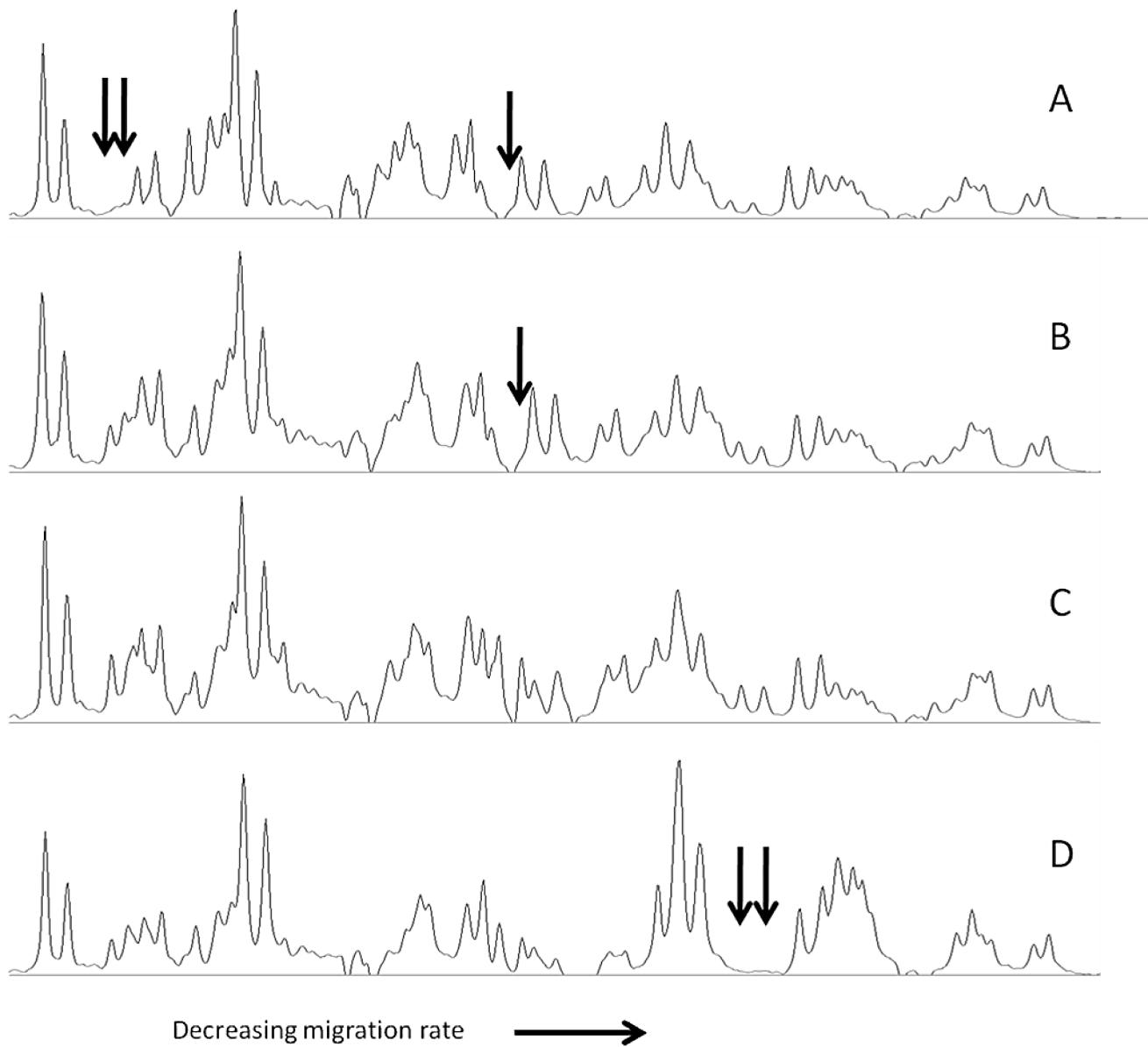


Fig. S5. Inter-strain polymorphisms as demonstrated by capillary electrophoresis-single strand conformation polymorphism (CE-SSCP) analysis of marker system MS1 at 25°C, non-denaturing matrix, November 2009. Electrophoregrams are for the 6-FAM labelled strand only. Vertical arrows indicate missing peaks. (A) Rockhampton-lcaerulea-99-LB-1, (B) Mt Misery-Lrheocola-05-LB-1, (C) Melbourne-Llesueuri-00-LB-1 and also represents the same pattern as Tully-L rheocola-06-LB-1, (D) Townsville-Lcaerulea-05-LB-1.