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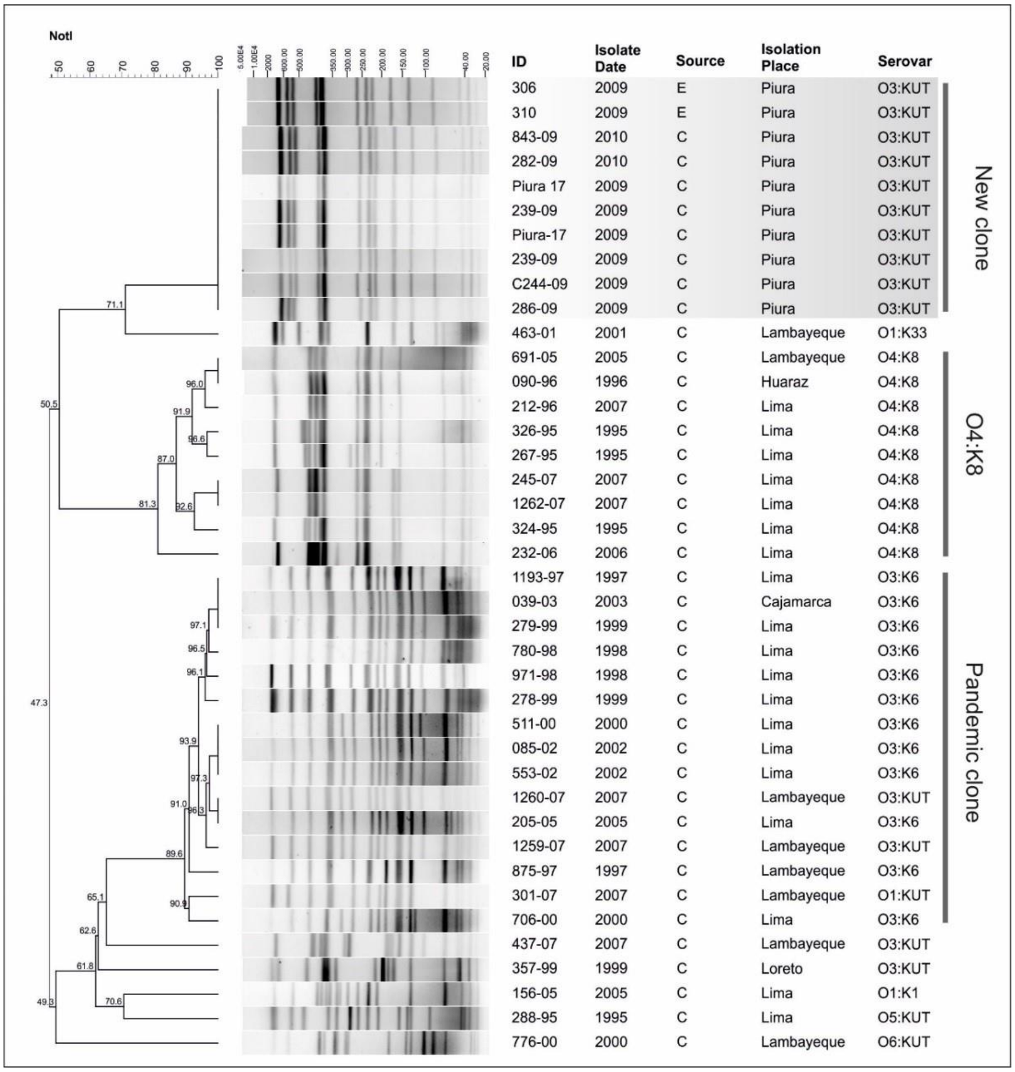
Outbreak of *Vibrio parahaemolyticus* Sequence Type 120, Peru, 2009

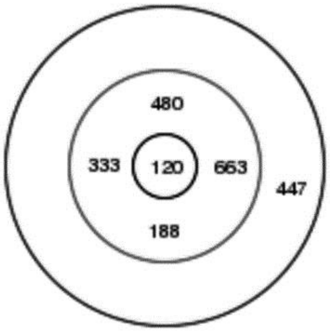
Technical Appendix



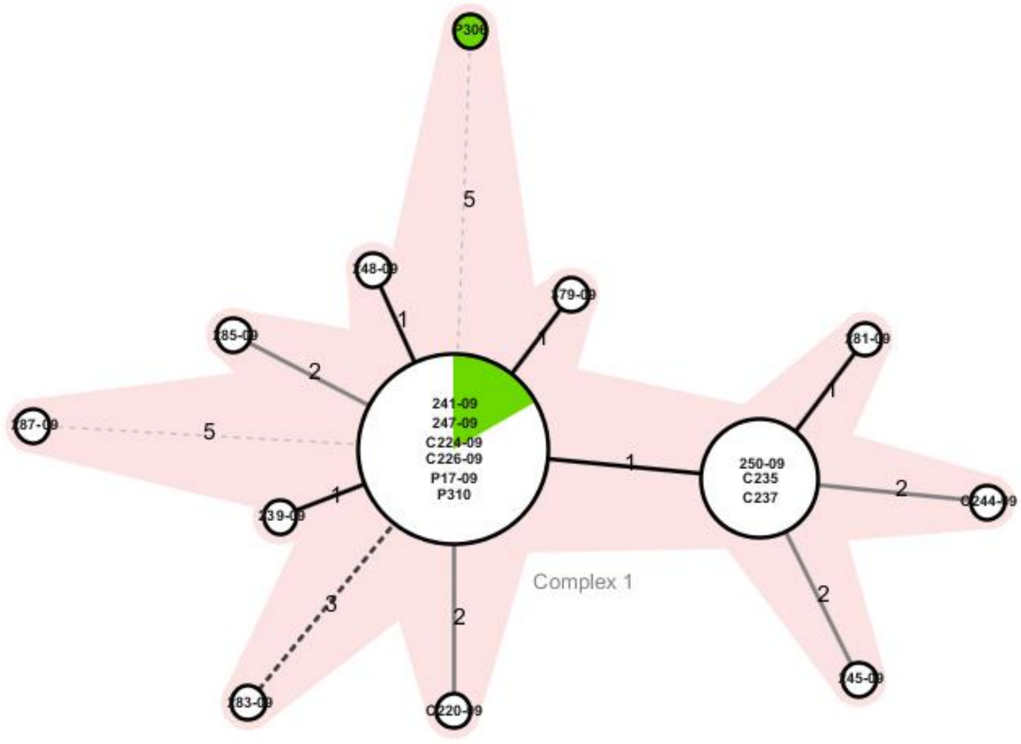
ID	Isolate Date	Source	Isolation Place	Serovar
306	2009	E	Piura	O3:KUT
310	2009	E	Piura	O3:KUT
843-09	2010	C	Piura	O3:KUT
282-09	2010	C	Piura	O3:KUT
Piura 17	2009	C	Piura	O3:KUT
239-09	2009	C	Piura	O3:KUT
Piura-17	2009	C	Piura	O3:KUT
239-09	2009	C	Piura	O3:KUT
C244-09	2009	C	Piura	O3:KUT
286-09	2009	C	Piura	O3:KUT
463-01	2001	C	Lambayeque	O1:K33
691-05	2005	C	Lambayeque	O4:K8
090-96	1996	C	Huaraz	O4:K8
212-96	2007	C	Lima	O4:K8
326-95	1995	C	Lima	O4:K8
267-95	1995	C	Lima	O4:K8
245-07	2007	C	Lima	O4:K8
1262-07	2007	C	Lima	O4:K8
324-95	1995	C	Lima	O4:K8
232-06	2006	C	Lima	O4:K8
1193-97	1997	C	Lima	O3:K6
039-03	2003	C	Cajamarca	O3:K6
279-99	1999	C	Lima	O3:K6
780-98	1998	C	Lima	O3:K6
971-98	1998	C	Lima	O3:K6
278-99	1999	C	Lima	O3:K6
511-00	2000	C	Lima	O3:K6
085-02	2002	C	Lima	O3:K6
553-02	2002	C	Lima	O3:K6
1260-07	2007	C	Lambayeque	O3:KUT
205-05	2005	C	Lima	O3:K6
1259-07	2007	C	Lambayeque	O3:KUT
875-97	1997	C	Lambayeque	O3:K6
301-07	2007	C	Lambayeque	O1:KUT
706-00	2000	C	Lima	O3:K6
437-07	2007	C	Lambayeque	O3:KUT
357-99	1999	C	Loreto	O3:KUT
156-05	2005	C	Lima	O1:K1
288-95	1995	C	Lima	O5:KUT
776-00	2000	C	Lambayeque	O6:KUT

Technical Appendix Figure 1. Representative *Not*I restriction patterns and clustering analysis of *V. parahaemolyticus* strains. Origin, isolation years, pulse-field gel electrophoresis type designations, and O:K serotypes are indicated in the right. Dendrogram generated by using Bionumeric software. Numbers at the dendrogram roots show the similarity value (similarity percentage) among the identified clusters. Numerals at the top of the figure indicate molecular weights (in kbp). Eur, European clone; New, new O3:K6 clone; Old, O3:K6 strains isolated before 1995.

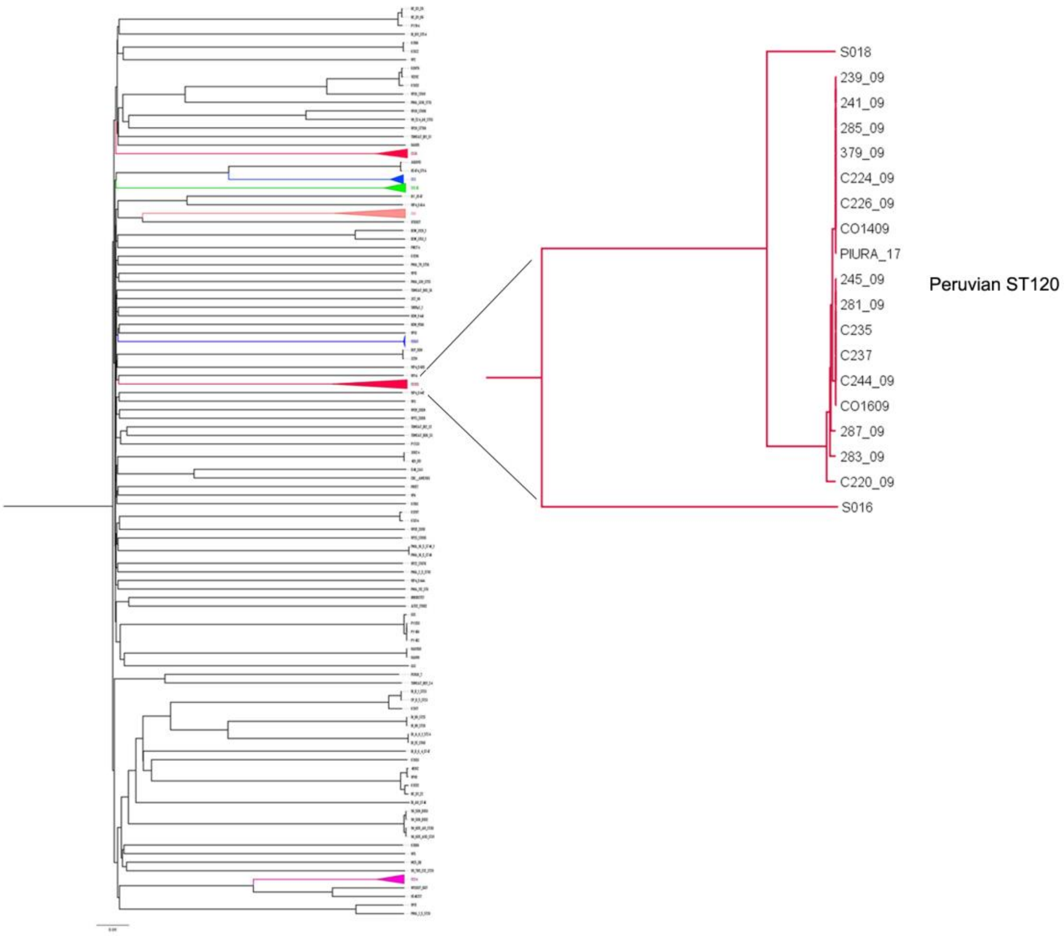
ST	dnaE	gyrB	recA	dtdS	pntA	pyrC	tnaA	clonal complex	Country (# strains Vp MLST)
120	60	108	86	98	18	45	51	120	China (6)
188	60	108	86	99	18	45	51	120	China (1)
333	60	108	31	98	18	45	51	120	China (1)
447	60	108	86	13	18	62	51	120	China (1)
480	60	4	86	98	18	45	51	120	China (2)
663	60	108	86	98	29	45	51	120	-



Technical Appendix Figure 2. eBURST analysis showing clonal complex 120. Table shows sequence type members of this clonal complex found in the *Vibrio parahaemolyticus* multilocus sequence typing database and the number of strains with those sequence types.



Technical Appendix Figure 3. Minimum spanning tree of the Peruvian strains of *Vibrio parahaemolyticus* showing the amount of single-nucleotide polymorphisms differing among them, the clonality of the strains, and the fact that the seafood's sequence type 120 strains were undistinguishable from clinical sequence type 120 strains. Seafood's isolates shown in green. Numbers above the connected lines are single-nucleotide polymorphisms. Lines are not drawn at scale.



Technical Appendix Figure 4. Neighbor-joining tree showing the high diversity of *Vibrio parahaemolyticus* strains isolated globally and the placement of the Peruvian strains within strains belonging to sequence type 120 from China (1,683 loci were shared among the 236 genomes available at GenBank).