



Figure 1S. Results of the rep-PCR analysis. The two VEB-6-positive *P. mirabilis* isolates found in poultry meat (#16 and #17) in Bern (Switzerland) are indistinguishable to each other and possess a 94% genetic identity with the VEB-6-positive strain (VB1248) found in a French patient. The CMY-2-positive isolates found in humans in Bern (n=4; i.e., 4810.05, 4810.40, 4812.18, and 5106.42) do not show any genetic relation with those detected in meat.

Table 1S:**Primers used for the characterization of the class 1 integron**

Number	Primer	Nucleotide sequence (5'-3')	Positions	Designed/Reference
1	S026-outR	CAACCTGAAGGGCAACAG	-812(-794)	(1)
2	IRi	TGTCGTTTTTCAGAAGACGG	1-19	(1)
3	Int1-F	GGGTCAAGGATCTGGATTTCG	736-756	(2)
4	Int1-R	ACATGCGTGTAAATCATCGTCG	273-294	(2)
5	5-CS	GGCATCCAAGCAGCAAGC	1256-1273	(3)
6	5-CSINV	GCTCCATAACATCAAACATCG	1290-1310	(3)
7	tnpRTn3-R	TGGAGCGGGCAATACTGA	1727-1744	(1)
8	AACA4-R	TGTTTCGCTCGAATGCCTG	2538-2555	(1)
9	aadB-F	CGATCGATGCACGGCTA	2728-2744	(1)
10	AADB-B	CGCATATCGCGACCTGAAAGC	3147-3167	(3)
11	dhfrA1-R	CTTGAACGTGTTACGACCGC	3419-3438	This study
12	QACEΔ1-B	CAAGCTTTTGCCCATGAAGC	4649-4668; 8927-8946; 14075-14094	(3)
13	Sul-F	GACGGTGTTTCGGCATTCT	4765-4782; 9043-9060; 14191-14208	(1)
14	Sul1-B	GCAAGGCGGAAACCCGCGCC	5221-5240; 9499-9518; 14647-14666	(3)
15	Sul1-newR	GTGATTGCGCTTCGCAGATC	5513-5532; 9791-9910; 14939-14958	This study
16	tetATn1721-outR	CATGATGGCGTAGTCGAC	5877-5894	(1)
17	tetAintR	CTCCGGCAAAAAGGAAACAGC	6154-6173	This study
18	5' of VEB	CAACCACAACGCAAACCCCTT	7158-7177	This study
19	VEB-OUT2	GGAATTACTATTTGAATAAATAA	7549-7571	(4)
20	VEBINV1	CAGTTTGAGCATTTGAATACAC	8378-8394	(3)
21	VEBINV2	AGCGTATTTGTTGCAGAGTCC	7627-7647	(3)
22	VEB-OUT1	AATATCCTTTTTACGATTTTCAT	8426-8448	(4)
23	3' of VEB	TTATGACAACGGCGGAAGGG	8789-8808	This study
24	orf513-F	ATGGTTTCATGCGGGTT	10490-10506	(1)
25	orf513-R	CTGAGGGTGTGAGCGAG	10948-10964	(1)
26	3' of Orf513	AACAGAAAACAGCCAAGGCG	11711-11730	This study
27	qnrA1-outF	CCTTTGCCGATCTGGATG	12712-12729	(1)
28	qnrA1-newR	CTTCGAGGTTGACCCGTCTG	12740-12759	This study
29	qnrA1-R	CTAATCCGGCAGCACTAT	12813-12830	(1)
30	PM4-F	CAAGCGCTCTTTGGCAATCA	13009-13028	This study
31	orfPM4-outR	TAAGTGCTTCCCAGAGCGTG	13168-13187	This study
32	PM5-F	CTGCAAACACGAGCACAG	13578-13597	This study
33	orf5-R	GATTTTCGAGTTCTAGGCG	15633-15650	(1)
34	orf6-mF	CTTCCATCATCAACCCTG	15767-15784	(1)
35	tnpA6100-F	CGATCAGCTATCGCGACCTT	16233-16255	This study
36	tnpA6100-F2	CGCGGTTTCAAATCGATCCC	16715-16734	This study
37	tnpA6100-R2	GCCAGCTCCTGACAGTTCAA	17056-17075	This study
38	IRt	TGTCATTTTCAGAAGACGA	17112-17129	(1)
39	S044-R	TTCTCCCTGATCTTCATC	17620-17637	(1)

Primers used for the characterization of the class 2 integron

Number	Primer	Nucleotide sequence (5'-3')	Positions	Designed/Reference
1	Int2-F	CACGGATATGCGACAAAAAGGT	484-505	(2)
2	Int2_F_SSE	TGCACCATACAGCAGCGTAA	142-161	This study
3	Int2_seq1_F	TAAGCAGACAGCTCCTTGGC	1774-1793	This study
4	125`CS	TTTTTGTGCTGCCATATCCGTG	495-505	(5)
5	23`CS	TGGGCTGAGAGAGTGGT	+253--269	(5)
6	dfrA1	AGCTGTTCACCTTTGGC	941-957	(5)
7	hep74	CGGGATCCCGGACGGCATGCACGATTGTGA	723-738	(6)
8	hep51	GATGCCATCGCAAGTACGAG	2913-2932	(6)
9	hep51-RC	CTCGTACTTGCGATGGCATC	2913-2932	This study
10	satR	TCATCTGTGCTCCCGAG	1937-1954	(5)
11	aadAF	ATGAGGGAAGCGGTGATCGCC	2019-2039	(2)
12	aadA1	TCGATGACGCCAACTAC	2064-2080	(5)
13	Aada1_IntF	ACGTTGTCCCGCATTTGGTA	2583-2602	This study
14	ybfA_F	GTGAGACAACCAGATGGGCA	3832-3851	This study
15	ybfB_R	TGCCCATCTGGTTGTCTCAC	3832-3851	This study
16	ybeB-Fout	TTTCGCTTGCCCTGACAGAT	3328-3347	This study
17	ybgA_R	CAATGAGTTCTTGAGCGCGG	4523-4542	This study

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