Table S1 Strains of *Arcobacter* spp. used in the study.

SPECIES	STRAIN	SOURCE
A. bivalviorum		
n=3	F4[T,a,b], F118-2[a,b], F118-4[a,b]	Mussels
A. butzleri		
n=21	LMG 10828[T,a,b], LMG 11118[b]	Human faeces
	F42, F46[a,b], F49, F51	Pork
	F15, F22, F23, F24, F25	Turkey
	F47, F52	Chicken
	F50[b], F53	Beef
	F1, F2, F29, F30, F98-1	Mussels
	T62	Soil
A. cibarius		
n=8	CECT 7203[T,a,b]	Chicken
	NC81[b], NC88[b]	Piggery effluent
	H742, H743[b], H745, H746[b], H748	Poultry carcasses
A. cloacae		
n=2	SW28-13[T,a,b]	Sewage
	F26[a,b]	Mussels
A. cryaerophilus		
n=19	LMG 9904[T,a,b], LMG 9871[a]	Bovine abortion foetus
	LMG 9865[a,b], LMG 10241[b], LMG 6622, LMG 10229[a,b]	Porcine abortion
	LMG 9065[a], LMG 7537[a], LMG 9863[a,b]	Ovine abortion foetus
	LMG 10829[a]	Human blood
	LMG 9861[a,b]	Bovine abortion foetus
	FE4[a,b], FE5[a,b], FE6[a,b], FE9[a,b], FE11[a], FE13[a], FE17[a]	Chicken faeces
	FE14[b],	Ovine faeces
A. defluvii	CECT 7697[T,a,b], SW28-7[a,b], SW28-8, SW28-9, SW28-10, SW30-2[a,b],	
n=11	SW30-7, SW30-8	Sewage
	CC42[b]	Pig faeces
	CH8-2, SAN599-9[b]	Mussels
A. ellisii		
n=3	F79-6[T,a,b], F79-2[a,b], F79-7[a,b]	Mussels
A. halophilus		
n=1	LA31B[T,a,b]	Hypersaline lagoon
A. marinus		
n=1	CECT 7727[T,a,b]	Seawater/starfish

A. molluscorum		
n=3	CECT 7696[T,a,b], F91[a,b], F101-1[a,b]	Mussels
A. mytili		
n=3	CECT 7386[T,a,b], CECT 7385[a,b]	Mussels
	T234[b]	Brackish water
A. nitrofigilis		Roots of *Spartina*
n=5	CECT 7204[T,a,b], LMG 7547[b]	*alterniflora*
	F39[b], F40[¶], F72[b]	Mussels
A. skirrowii		
n=5	LMG 6621[T,a,b]	Lamb faeces
	LMG 9911	Porcine abortion
	Houf 989[a,b], Houf 994[b]	Cow faeces
	S7[b]	Sludge
A. suis		
n=1	F41[T,a,b]	Pork
A. thereius		Porcine abortion
n=5	LMG 24486[T,a,b], LMG 24487[a,b]	foetus
	SW24[b]	Sewage
	F61-1[b]	Pork
	F93-4[b]	Clams
A. trophiarum		
n=3	LMG 25534[T,a,b], LMG 25535[a,b]	Pig faeces
	CECT 7650[a,b]	Chicken cloaca
A. venerupis		
n=1	F67-11[T,a,b]	Clams

ATCC: American Type Culture Collection. LMG: Belgian Co-ordinated Collection of Microorganisms. CECT: Colección Española de Cultivos Tipo.
[a]Strains from which the 16S rRNA gene was sequenced for verification of identity [19].
[b]Strains from which the *rpoB* gene was sequenced for verification of identity [19].

Table S2 Targeted genes and PCR conditions of the compared methods.

Author	Targeted species (expected amplicon)	Targeted gene: Position (nt)[a]	Primers (pmol)	Concentrations[b,c]	Conditions
Houf *et al*. [14]	*A. butzleri* (400) *A. cryaerophilus* (230) *A. skirrowii* (640)	16S rRNA: 959 – 1357 23S rRNA: 1720 – 1964 16S rRNA: 705 - 1357	ARCO (50) BUTZ (50) CRY1 (50) CRY2 (50) SKIR (25)	$MgCl_2$ 1.3 mmol l^{-1} *Taq* DNA polymerase 1.5 U	Initial denaturation 94°C, 2 min and final extension 72°C, 5 min 32 Cycles of: Denaturation 94°C, 45 s; Annealing 61°C, 45 s; Chain extension 72°C, 30 s
Kabeya *et al*. [15]	*A. butzleri* (692) *A. cryaerophilus* 1A (728) *A. cryaerophilus* 1B (152) *A. skirrowii* (448)	23S rRNA: 1174 - 1865 23S rRNA: 1135 – 1865 23S rRNA: 1713 – 1865 23S rRNA: 1423 - 1865	N.c.1A (25) ARCO-U (25) N.butz (2.5) N.c.1B (2.5) N.ski (2.5)	MgCl2 1.5 mmol l-1 Taq DNA polymerase 2.5 U	Initial denaturation 94°C, 3 min and final extension 72°C, 5 min 30 Cycles of: Denaturation 94°C, 30 s; Annealing 62°C, 60 s; Chain extension 72°C, 60 s
Figueras *et al*. [18]	Species specific patterns for species[d]	16S rRNA: 47 - 1073	CAH 1am (25) CAH 1b (25)	MgCl2 1.5 mmol l-1 Taq DNA polymerase 2.5 U	Initial denaturation 94°C, 2 min, final extension 72°C, 10 min 30 Cycles of: Denaturation 94°C, 30 s; Annealing 52°C, 30 s; Chain extension 72°C, 90 s
Pentimalli *et al*. [16]	*A. butzleri* (203) *A. cryaerophilus* (212) *A. skirrowii* (257) *A. cibarius* (145)	16S rRNA: 803 – 1006 *gyrA*: 2337 – 2549 *gyrA*: 1366 – 1622 *gyrA*: 2364 - 2778	16S Arcobutz (30) Gyr Arcocry (30) Gyr Arcoski (30) Gyr Arcocib (50) All F and R	MgCl2 2.0 mmol l-1 Taq DNA polymerase 2.0 U	Initial denaturation 94°C, 2 min and final extension 72°C, 7 min 40 Cycles of: Denaturation 94°C, 60 s; Annealing 55°C, 60 s; Chain extension 72°C, 60 s
Douidah *et al*. [9]	*A. butzleri* (2061) *A. cryaerophilus* (395) *A. skirrowii* (198) *A. cibarius* (1125) *A. thereius* (1590)	23S rRNA: 646 - 2707 *gyrA*: 2255 – 2640 23S rRNA: 646 – 844 23S rRNA: 646 - 1771 23S rRNA: 646 - 2236	ButR (50) SkiR (50) TheR (50) CibR (50) ArcoF (50) GyrasF (50) GyrasR (50)	MgCl2 1.5 mmol l-1 Taq DNA polymerase 1.5 U	Initial denaturation 94°C, 2 min and final extension 72°C, 10 min 30 Cycles of: Denaturation 94°C, 45 s; Annealing 58°C, 45 s; Chain extension 72°C, 2 min
De Smet *et al*. [17]	*A. trophiarum* (382)	*hsp60*: 686 - 1068	hsp60F and R (50)	MgCl2 1.4 mmol l-1 Taq DNA polymerase 2.0 U	94°C, 3 min, final extension 72°C, 5 min 30 Cycles of: Denaturation 94°C, 45 s; Annealing 58°C, 45 s; Chain extension 72°C, 30 s
Figueras *et al*. [19]	Species specific patterns for the different species[d]	16S rRNA: 47 - 1073	CAH 1am (25) CAH 1b (25)	MgCl2 1.5 mmol l-1 Taq DNA polymerase 2.5 U	Initial denaturation 94°C, 2 min, final extension 72°C, 10 min 30 Cycles of: Denaturation 94°C, 30 s; Annealing 52°C, 30 s; Chain extension 72°C, 90 s

[a] Positions of 16S rRNA gene are based on *Escherichia coli*, and those of the 23S rRNA and *gyrA* genes on sequences present in the genome of *A. butzleri* RM4018.

[b] All PCRs included dATP, dCTP, dGTP, and dTTP (Applied Biosystems(TM)) at a concentration of 200 µM each, 5 µl 10X Invitrogen(TM) buffer, and Milli-Q water in a final volume of 50 µl. The Taq DNA polymerase was supplied by Invitrogen(TM).

[c] For the m-PCR of Kabeya *et al*. (15) 50 µg of DNA was used, and 100 µg for the other methods.

[d] Digestion of the 16S rRNA obtained amplicon (1026 bp) with the different endonucleases *Mse*I [18], *Mse*I, *Mnl*I, or *Bfa*I [19] generated species specific RFLP patterns for the 17 tested species of the genus.

Table S3 Literature review of 171 studies (2000-2012)[a] that identified 4223 strains of *Arcobacter* using the five compared PCR methods.

Number of Identified strains (%) of the different species in relation with the method used

Species	No (%)	Houf *et al*. [14]	Kabeya *et al*. [15]	Figueras *et al*. [18]	Douidah et al. [9] De Smet et al. [17][b]
A. butzleri	2690 (63.7%)	1763 (64.5%)	241 (79%)	445 (72.2%)	241 (42.5%)
A. cryaerophilus	1152 (27.3%)	850 (31.1%)	45 (14.8%)	112 (18.2%	145 (25.6%)
A. skirrowii	209 (4.9%)	87 (3.2%)	19 (6.2%)	33 (5.4%)	70 (12.3%)
Other *Arcobacter* spp.	172 (4.1%)	35 (1.3%)[c]	---	26 (4.2%)[c]	111 (19.6%)[d]
Total	4223	2735 (64.8%)	305 (7.2%)	616 (14.6%)	567 (13.4%)

[a]Of the 171 references found using the ISI Web of Knowledge (last access on July 30th 2012), Houf *et al.* [14] was cited in 123 studies; Kabeya *et al*. [15] in 21; Douidah *et al*. [9]/De Smet *et al*. [17] in 11; and Figueras *et al*. [18] in 16. Pentimalli *et al*. [16] was cited three times, but used only for background information.
[b]The method designed by De Smet *et al.* [17] only detects or identifies *A. trophiarum*, and was intended to complement the m-PCR of Douidah *et al.* [9]. Therefore, they are grouped together as a single method.
[c]The remaining 14 *Arcobacter* spp. were detected using other molecular identification methods such as 16S rRNA or *rpoB* gene sequencing and/or 16S rRNA-RFLP [17,18] used in parallel [5,6,7,23,24,25,26].
[d]These strains included 100 *A. thereius*, 10 *A. trophiarum*, and 1 *A. cibarius* (0.2%, 1/567) that were identified by De Smet *et al*. [27,28] using this combination of methods.