antibiotics

MDPI

Supplementary Material

Rumi and Pasteurized Kareish Cheeses Are a source of β-Lactam-Resistant *Salmonella* in the Nile Delta Region of Egypt: Insights into Their Incidence, AMR Pattern, Genotypic Determinants of Virulence and β-Lactam Resistance

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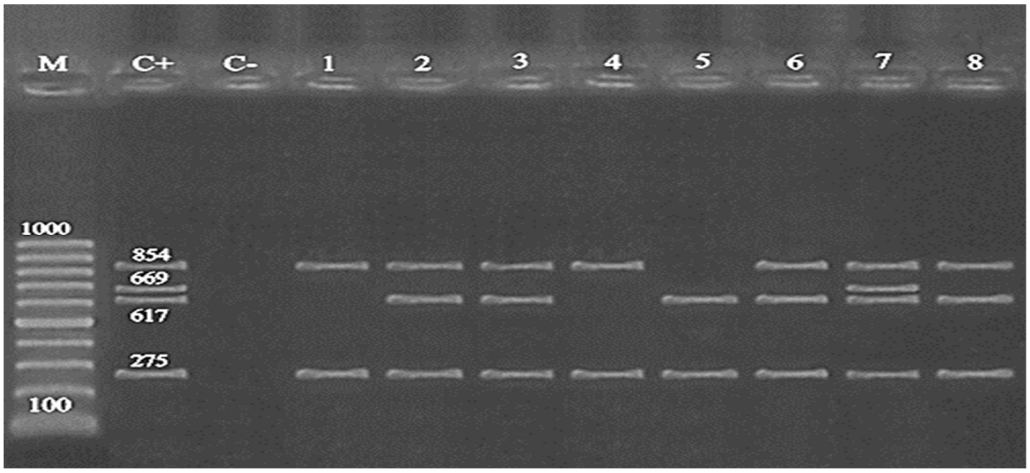

Figure S1. A representative gel photo showing the results of M-PCR amplified *invA* (275 bp), *stn* (617 bp), *spvC* (669 bp), and *hilA* (854 bp) virulence genes of *Salmonella* strains (n=44). Lanes: M; DNA ladder (100 bp). C+; positive control, C-; no template control, 1; *S*. Anatum, 2; *S*. Enteritidis, 3; *S*. Infantis, 4; *S*. Rissen, 5; *S*. Shubra, 6; *S*. Tsevie, 7; *S*. Typhimurium, 8; *S*.Virchow.

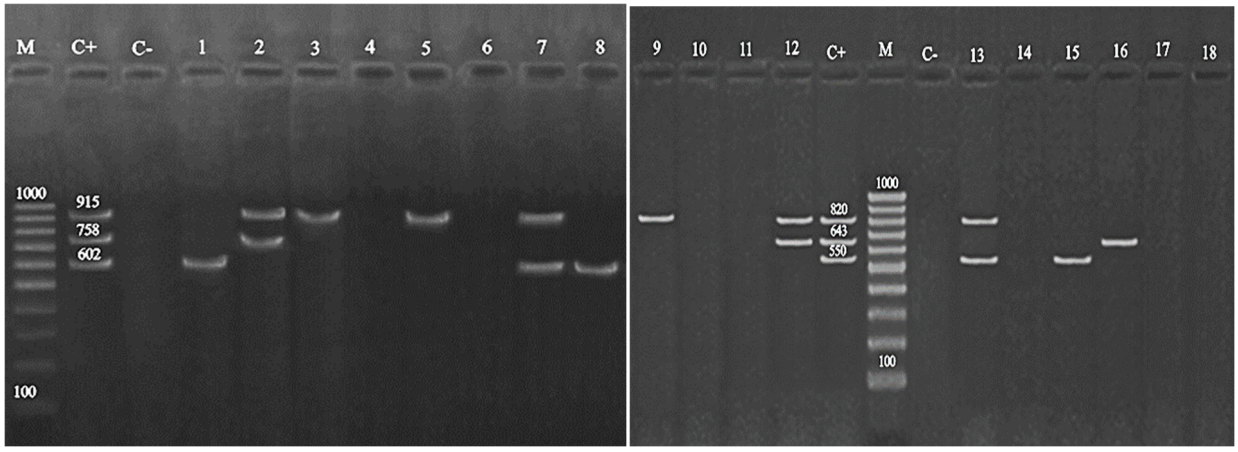

Figure S2. Representative gel images showing the M-PCR amplified *bla*$_{CMY-1}$ (915 bp), *bla*$_{CMY-2}$ (758 bp), *bla*$_{OXA-2}$ (602 bp), *bla*$_{OXA-1}$ (820 bp), *bla*$_{TEM-1}$ (643 bp) and *bla*$_{CTX-M}$ (550bp) β-lactams resistance genes of *Salmonella* strains (n=44). Lanes: M; DNA ladder (100 bp), C+; positive control, C-; no template control, 1,10; *S.* Shubra, 2,12; *S.* Enteritidis, 3,9; *S.*Virchow, 4,11; *S.* Tsevie, 5,14,15; *S.* Infantis, 6,17; *S.* Rissen, 7,13,16; *S.* Typhimurium, 8,18; *S.* Anatum.

Table S1. The susceptibility degree of *Salmonella* isolates (n=44) to the tested antibiotics.

Classification	Antibiotics	Sensitive (%)	Intermediate (%)	Resistance (%)
Penicillins	AMP	0/44 (0.0)	13/44 (29.55)	31/44 (70.45)
	AMX	0/44 (0.0)	13/44 (29.55)	31/44 (70.45)
	AMC	4/44 (9.09)	10/44 (22.73)	30/44 (68.18)
Cephalosporins	CAZ	6/44 (13.64)	3/44 (6.82)	35/44 (79.55)
	CEP	4/44 (9.09)	3/44 (6.82)	37/44 (84.09)
	CEF	4/44 (9.09)	4/44 (9.09)	36/44 (81.82)
	CTZ	5/44 (11.36)	2/44 (4.55)	37/44 (84.09)
	CFP	9/44 (20.45)	3/44 (6.82)	32/44 (72.73)
Carbapenems	IPM	19/44 (43.18)	14/44 (31.82)	11/44 (25)
	MPM	18/44 (40.91)	24/44 (54.55)	2/44 (4.55)
Monobactams	ATM	16/44 (36.36)	11/44 (25.0)	17/44 (38.64)
Glycopeptides	VAN	15/44 (34.09)	18/44 (40.91)	11/44 (25)
Aminoglycosides	GM	0/44 (0.00)	32/44 (72.73)	12/44 (27.27)
	AMI	15/44 (34.09)	19/44 (43.18)	10/44 (22.73)
	NEO	16/44 (36.36)	19/44 (43.18)	9/44 (20.45)
Tetracyclines	TET	4/44 (9.09)	5/44 (11.36)	35/44 (79.55)
Macrolides	ERY	0/44 (0)	4/44 (9.09)	40/44 (90.91)
Lincosamides	CLI	0/44 (0)	4/44 (9.09)	40/44 (90.91)
Quinolones	NAL	6/44 (13.64)	18/44 (40.91)	20/44 (45.45)
Fluorquinolones	CIP	11/44 (25)	17/44 (38.64)	16/44 (36.36)
Sulfonamides	SMX	3/44 (6.82)	15/44 (34.09)	26/44 (59.09)
	TMP-SMX	4/44 (9.09)	15/44 (34.09)	25/44 (56.82)
Polymyxins	COL	25/44 (56.82)	11/44 (25)	8/44 (18.18)

Ampicillin: AMP; Amoxicillin: AMX; Amoxycillin-Clavulanic acid: AMC; Cefazolin: CAZ; Cephalothin: CEP; Cefoxitin: CEF; Ceftazidime: CTZ; Cefepime: CFP; Imipenem: IPM; Meropenem: MPM; Aztreonam: ATM; Vancomycin: VAN; Gentamicin: GM; Amikacin: AMI; Neomycin: NEO; Tetracycline: TET; Erythromycin: ERY; Clindamycin: CLI; Nalidixic acid: NAL; Ciprofloxacin: CIP; Sulfamethoxazole: SMX; Trimethoprim/ Sulfamethoxazole: TMP-SMX; Colistin: COL.

Table S2. The investigated virulence, NS-/ES-/AmpC- BLR genes, sequences (5′–3′) of forward (F) and reverse (R) primer sets, and amplicon size (bp) for each primer pair.

Factors	Target genes		The nucleotide Sequence (5′ > 3′)	Annealing temp.	Amplicon size (bp)	Reference
Virulence	*invA*	F	TATCGCCACGTTCGGCAA	53°C	275	[1]
		R	TCGCACCGTCAAAGGAACC			
	stn	F	TTGTGTCGCTATCACTGGCAACC	59°C	617	[2]
		R	ATTCGTAACCCGCTCTCGTCC			
	spvC	F	CGGAAATACCATCAAATA	42 °C	669	[3]
		R	CCCAAACCCATACTTACTCTG			
	hilA	F	CGGAAGCTTATTTGCGCCATGCTGAGGTAG	65°C	854	[4]
		R	GCATGGATCCCCGCCGGCGAGATTGTG			
NS β-lactamases	bla_{OXA-1}	F	ATGAAAAACACAATACATATCAACTTCGC	62°C	820	[5]
		R	GTGTGTTTAGAATGGTGATCGCATT			
	bla_{OXA-2}	F	ACGATAGTTGTGGCAGACGAAC	62°C	602	
		R	ATYCTGTTTGGCGTATCRATATTC			
ES β-lactamases	bla_{TEM-1}	F	CAG CGG TAA GAT CCT TGA GA	55 °C	643	[6]
		R	ACT CCC CGT CGT GTA GAT AA			
	bla_{CTX-M}	F	GTTACAATGTGTGAGAAGCAG	60°C	550	[7]
		R	CCGTTTCCGCTATTACAAAC			
AmpC β-lactamases	bla_{CMY-1}	F	GTGGTGGATGCCAGCATCC	60°C	915	[5]
		R	GGTCGAGCCGGTCTTGTTGAA			
	bla_{CMY-2}	F	GCACTTAGCCACCTATACGGCAG	60°C	758	
		R	GCTTTTCAAGAATGCGCCAGG			

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