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C-source metabolic profilings of foodborne Shiga-toxin producing *E. coli* match serogroup differentiations and highlight functional adaptations

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ABSTRACT

The tropism of pathogenic STEC for foodstuffs and cattle reservoir is related to functional specializations. An investigation of C-source utilization patterns among and between STEC serogroups was performed using omnilog phenotypic microarrays (OM). OM functional groupings were compared with STEC phylogroups, seropathotypes, EFSA's molecular risk assessment groups and serogroups. OM INT reduction activities of 37 STEC strains growing on 190 C-substrates were compared. Each strain had its own specific C-utilization profile but 23% of the substrates was used by all strains, 47% by none, and 30% was variably metabolized. Galactose, mannose, *N*-acetyl-glucosamine (GlcNAc), and *N*-acetyl neuraminic acid (Neu5Ac) found in the mucus layer of the bovine small intestine were metabolized by all strains. The 56 most informative substrates divided the C-utilization patterns (CP) into three clusters with: (A) harboring all O157 and O145 strains; (B) all O26 strains, and (C) strains of the other serogroups. Significant correlations between INT reduction values of pair of strains per CP group supported these differentiations. CP of group A and B strains were respectively defective in the use of galactonic acid-γ-lactone and rhamnose. Most CP group C strains grew with L-lyxose. Adjusted Wallace coefficients analyses of the datasets indicated high probabilities for the prediction of the use of glycolic acid, β-hydroxybutyric acid, L-lyxose and D-galactonic acid-γ-lactone and 5-keto-D-gluconic acid by a serogroup. The use of a C-substrate could be predicted from the classification of a strain into a phylogroup or seropathotype. Significantly lower numbers of C-substrates were used by seropathotype A strains like O157 ones. Improvements of STEC identification keys were proposed using the most discriminant C-substrates found in this study.

1. Introduction

Shiga toxin-producing *Escherichia coli* (STEC) strains are major worldwide foodborne pathogens, causing severe and sometimes lethal human infections, such as hemolytic uremic syndrome (HUS) cases, especially among young children (Croxen et al., 2013; Kaper et al., 2004). They are notably responsible of outbreaks and sporadic cases of acute illnesses (reaching each year 2,801,000 cases), and cause annually 3890 HUS cases and 230 deaths (Majowicz et al., 2016). The key virulence trait of STEC is the synthesis of Shiga toxins (Stx) but additional virulence factors boosting their pathogenicity have been described (Karmali, 2009). Most typical pathogenic strains harbor a LEE (locus of enterocyte effacement) involved in the intimate adherence to the host-cell membrane (Franzin et al., 2015). Recent outbreaks, such as the one involving STEC O104:H4 strains lacking the LEE, led to the observation of additional virulence properties (Beutin and Fach, 2014; Navarro-Garcia, 2014). STEC virulence thus appears multi-factorial, and several factors remain to be identified (Karmali et al., 2010).

More than 380 STEC serotypes have been reported in humans so far but only ten of them have been consistently associated with severe cases and foodborne outbreaks (Caprioli et al., 2005; Mathusa et al., 2010). To improve the assessment of clinical and public health risks associated with STEC, Karmali et al. (2003) proposed a seropathotype classification (using a gradient from seropathotype A – high risk- to seropathotypes D and E – minimal risk). This classification considers the prevalence of STEC serotypes and their association with human outbreaks, including the severity of the clinical outcomes (Karmali et al., 2003). Serotypes O157:H7 and O157:NM have been classified in the seropathotype A, those of serotypes O26:H11; O103:H2; O111:NM; O121:H19 and O145:NM into seropathotype B, and those of O91:H21 and O113:H21 into seropathotype C. Recently, a new scheme for STEC categorization according to potential risk for human health was

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Table 1
Serotype, seropathotype, molecular risk assessment and phylogenetic groups, and origin of the 37 O157 and non-O157 *E. coli* strains used in this study.

Serogroup	Strain	Serotype	Pathotype	STEC seropathotype[a]	STEC molecular risk assessment group[b]	Phylogenetic group[c]	Origin	References
O157	620	O157:H7	STEC	A	I	D	Host independent origin (Food-bovine meat)	King et al., 2014
	RD9	O157:H7	STEC	A	I	D	Host independent origin (Food-bovine meat)	King et al., 2009
	540	O157:H7	STEC	A	I	D	Host independent origin (Food-bovine meat)	Kerangart et al., 2016
	FCH6	O157:H7	STEC	A	I	D	Host independent origin (Food-raw goat's milk cheese)	Espié et al., 2006
	EDL 933	O157:H7	STEC	A	I	D	Host gut (Human)	Perna et al., 2001
	Sakaï	O157:H7	STEC	A	I	D	Host gut (Human)	Hayashi, 2001
	m622	O157:H7	STEC	A	I	D	Host independent origin (Food-raw milk cheese)	Franz et al., 2011
	m638	O157:H7	STEC	A	I	D	Host gut (Human)	Franz et al., 2011
O26	21765	O26:H11	STEC	B	I	B1	Host independent origin (Food-raw cow milk cheese)	Espié et al., 2006
	2245/98	O26:H11	STEC	B	I	B1	Host gut (Human)	Zimmerhackl et al., 2010
	64/36	O26:H11	AEEC	ND	ND	B1	Host independent origin (Food-raw ewe milk)	Neto et al., 2012
	3073/00	O26:H11	STEC	B	I	B1	Host gut (Human)	Zimmerhackl et al., 2010
	37.40	O26:H11	STEC	B	I	B1	Host independent origin (Food-bovine meat)	Neto et al., 2012
	279/8	O26:H11	STEC	B	I	B1	Host independent origin (Food-raw cow milk cheese)	Kerangart et al., 2016
	11368	O26:H11	STEC	B	I	B1	Host gut (Human)	Ogura et al., 2009
	MB 2659 (PH10)	O26:H11	STEC	B	I	B1	Host gut (Human)	Possé et al., 2007
O103	PMK5	O103:H2	STEC	B	I	B1	Host gut (Human)	Mariani-Kurkdjian et al., 1993
	262.03.18.1	O103:H-	*E. coli*	ND	ND	B1	Host independent origin (Food-bovine meat)	This study
	MB 2652 (PH3)	O103:H2	STEC	B	I	B1	Host gut (Human)	Possé et al., 2007
	MB 2653 (PH4)	O103:H2	STEC	B	I	B1	Host gut (Human)	Possé et al., 2007
O111	CL37	O111:H8	STEC	B	I	ND	Host gut (Human)	Zhang et al., 2002
	J43	O111:H8	STEC	B	I	ND	Host gut (Bovine)	Bibbal et al., 2015
	622-4	O111:H8	STEC	B	I	ND	Host independent origin (Food-raw cow milk cheese)	Kerangart et al., 2016
O145	2513-21	O145:H28	STEC	B	I	D	Host independent origin (Food-raw cow milk cheese)	Kerangart et al., 2016
	991	O145:H28	STEC	B	I	D	Host independent origin (Food-bovine meat)	Kerangart et al., 2016
	MB 2817 (PH88)	O145:H28	STEC	B	I	D	Host gut (Human)	Possé et al., 2007

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