

# **Corrigendum: Genome Reduction for Niche Association in Campylobacter Hepaticus, A Cause of Spotty Liver Disease in Poultry**

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### A corrigendum on

## Genome Reduction for Niche Association in *Campylobacter Hepaticus*, A Cause of Spotty Liver Disease in Poultry

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In the original article, there was a mistake in **Table 3** as published. **Table 3** had additional genes inserted for isolates S11-0036, S11-0038, S11-0069, and S12-0071. Isolate S12-002 should not be included in **Table 3**.

Additionally, there was an incorrect sentence. Incorrect sentence describing the number of RNA coding sequences and the GC content. A correction has been made to Results, *C. hepaticus* Isolates Have Reduced Genomes, Paragraph Number One and appears below.

The *C. hepaticus* isolates had a lower number (average of 44) of RNA coding sequences and a lower GC content (average of 28.4%) in comparison to the *C. jejuni* reference genomes (average of 52.4 and 30.5%, respectively).

Similarly, there was an incorrect sentence. Incorrect sentence describing the genes related to pathogenicity of *C. hepaticus*. A correction has been made to Results, genes related to the Pathogenicity of *C. hepaticus*, Paragraph Number One and appears below.

The UK *C. hepaticus* isolates contained relatively few genes linked to pathogenesis: 5 were identified in the genomes of S11-0036, S11-0069, S11-0071 and (from farms 2, and 4); 6 in S11-0038 (farm 2); 15 in S10-0209, S12-1018, S11-5013, and S11-010, (farm 1); and 7 in isolate S12-0322 (farm 5; **Table 3**). The *cpp* and *cmgB3/4* genes, both components of the pTet plasmid (Batchelor et al., 2004), and a complete pTet plasmid (Batchelor et al., 2004) sequences were identified in isolates S11-010, and S12-0322 (**Table 3**).

Finally, in incorrect spelling of metabolism was used, we omitted "the" and misspelled "rich." A correction has been made to Discussion, Paragraph Number Four and appears below.

### OPEN ACCESS

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Petrovska L, Tang Y, Jansen van Rensburg MJ, Cawthraw S, Nunez J, Sheppard SK, Ellis RJ, Whatmore AM, Crawshaw TR and Irvine RM (2017) Corrigendum: Genome Reduction for Niche Association in Campylobacter Hepaticus, A Cause of Spotty Liver Disease in Poultry. Front. Cell. Infect. Microbiol. 7:480. doi: 10.3389/fcimb.2017.00480 TABLE 3 | Presence of pathogenicity-related genes in C. hepaticus.

Protein (name)	Protein ID	S11-0036	S11-0038	S11-0069	S11-0071	S10-0209	S12-1018	S11-5013	S11-010	S12-0322
		F2	F2	F4	F4	F1	F1	F1	F1	F5
MCP	EAQ73158									
TrkA	ABS44147									
CHP1	EAQ72353									
CHP2	EAQ72298									
HP1	EAQ71971									
HAD-superfamily phosphatase, subfamily IIIC	EAQ72583									
Putative 3-oxoacyl- synthase	ABS43995									
Methyltransferase	CAL35414									
DNA adenine methylase	AAW34814									
HP2	EAQ72552									
HP3	HP3									-
Putative DNA-binding protein	AAW34848									
Putative acyl carrier protein	CAL35413									
Putative acyl carrier protein	AAW35934									
CHP3	EAQ71755									
Putative SAM domain containing methyltransferase	CAL35414									
CHP4	EAQ72353									
cpp14	AAR29498.1									
cpp17	AAR29501.									
cpp22	AAR29505.									
cpp18	AAR29502.									
cpp47	AAR29530.									
cpp45	AAR29528.									
cpp29	AAR29512.									
cpp13	AAR29497.1									
pTet	AY714214.									
cmgB3/4	AAR29514.1									

Purple, present; blank, absent; orange, plasmid pTet (pCC31, AY394560.1) related proteins, dark blue, proteins not present in C. jejuni 11168. Farms 1, 2, 4, and 5 are indicated (F1, F2, F4, and F5).

Furthermore, Stahl and co-workers found that the ability to metabolize L-fucose *in vivo* provided *C. jejuni* with competitive advantage during colonization of the piglet infection model. Similar was not observed in the chick commensal model (Stahl et al., 2011), suggesting potential niche specific advantage for colonization in the L-fucose rich environment in the pig small intestine and cecum.

The authors apologize for these errors and state that this does not change the scientific conclusions of the article in any way. **Conflict of Interest Statement:** The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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