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

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A corrigendum on

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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, S11-0038, S11-0069, 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.
### TABLE 3 | Presence of pathogenicity-related genes in C. hepaticus.

| Protein (name) | Protein ID |
|---------------|-----------|
| MCP           | EAQ73158  |
| TrkA          | ABS44147  |
| Chp1          | EAQ72353  |
| Chp2          | EAQ72298  |
| Hp1           | EAQ71971  |
| HAD-supersfamily 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         | AAR29501.1 |
| Cpp22         | AAR29505.1 |
| Cpp18         | AAR29502.1 |
| Cpp47         | AAR29528.1 |
| Cpp45         | AAR29512.1 |
| Cpp13         | AAR29497.1 |
| Ptet          | AY714214.1 |
| cmgB3/4       | AAR29514.1 |

Purple, present; blank, absent; orange, plasmid pTet 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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