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Author Correction: Characterisation of N-linked protein glycosylation in the bacterial pathogen *Campylobacter hepaticus*

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Correction to: *Scientific Reports* <https://doi.org/10.1038/s41598-022-26532-0>, published online 05 January 2023

The original version of this Article contained an error in the legend of Figure 2.

“(A) SDS-PAGE of *C. hepaticus* HV10T, *C. jejuni* 354, *C. coli* 52/2 and *C. upsaliensis* 54/7 whole cell lysates (WCL) containing 25 µg of protein. (B) SBA lectin blot binding profiles to N-glycans present in WCL of *C. hepaticus* HV10T, *C. jejuni* 354, *C. coli* 52/2, *C. upsaliensis* 54/7 containing 25 µg of protein. (C) SDS-PAGE of *C. lari* 54/6, *C. fetus* 54/3 alongside negative controls, *S. Typhimurium* PT44. The equivalent amount of protein from WCL of the different *Campylobacter* species were also digested with proteinase K (P.K). Whole cell lysates were separated by 8–16% SDS-PAGE and either developed with SimplyBlue™ SafeStain or transferred to PVDF membranes for blotting. (D) SBA lectin blot binding profiles to N-glycans present in WCL of *C. lari* 54/6, *C. fetus* 54/3, *C. coli* 52/2, *E. coli* JM109 and *S. Typhimurium* PT44 containing 25 µg of protein.”

now reads:

“(A) SDS-PAGE of *C. hepaticus* HV10T, *C. jejuni* 354, *C. coli* 52/2 and *C. upsaliensis* 54/7 whole cell lysates (WCL) containing 25 µg of protein. (B) SBA lectin blot binding profiles to N-glycans present in WCL of *C. hepaticus* HV10T, *C. jejuni* 354, *C. coli* 52/2, *C. upsaliensis* 54/7 containing 25 µg of protein. (C) SDS-PAGE of *C. lari* 54/6, *C. fetus* 54/3 alongside negative control, *S. Typhimurium* PT44. The equivalent amount of protein from WCL of the different *Campylobacter* species were also digested with proteinase K (P.K). Whole cell lysates were separated by 8–16% SDS-PAGE and either developed with SimplyBlue™ SafeStain or transferred to PVDF membranes for blotting. (D) SBA lectin blot binding profiles to N-glycans present in WCL of *C. lari* 54/6, *C. fetus* 54/3 and *S. Typhimurium* PT44 containing 25 µg of protein.”

Additionally, the original version of this Article contained errors in the legend of Figure 5.

“Ion-trap CID-MS spectra of two *C. hepaticus* HV10T glycopeptides. Spectra represent fragmented ions produced from the N-glycan. (A) *C. hepaticus* HV10T glycopeptide 23IQGTIAQIYDNNK36 with a delta mass of 1405.56 Da. (B) *C. hepaticus* HV10T glycopeptide 266AALAEGEANATIISAK282 with a delta mass of 1405.56 Da. Above is the heptasaccharide structure linked to the peptide drawn using the symbol nomenclature for glycans SNFG. The MS/MS spectra display fragmented ions generated from the glycan with the structure HexNAc-HexHAc-[Hex]-HexNAc-HexHAc-HexNAc-diNAcBac.”

now reads:

“Ion-trap CID-MS spectra of two *C. hepaticus* HV10^T glycopeptides. Spectra represent fragmented ions produced from the N-glycan. (A) *C. hepaticus* HV10^T glycopeptide ²⁶⁶AALAEGEANATIISAK²⁸² with a delta mass of 1405.56 Da. (B) *C. hepaticus* HV10^T glycopeptide ²³IQGTIAQIYDNNK³⁶ with a delta mass of 1405.56 Da. Above is the heptasaccharide structure linked to the peptide drawn using the symbol nomenclature for glycans SNFG. The MS/MS spectra display fragmented ions generated from the glycan with the structure HexNAc-HexHAc-[Hex]-HexNAc-HexHAc-HexNAc-diNAcBac.”

The original Article has been corrected.

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