Correction to: Genetic and Phenotypic Characteristics of a Multi-strain Probiotic for Broilers

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The authors would like to correct the errors in the publication of the original article. The correct details are given below.

- Abstract: “*Bacillus amyloliquefaciens* DPN123 produced phytase, amylase, surfactin and iturin A1.” should read “*Bacillus amyloliquefaciens* DPN123 produced phytase, amylase, surfactin and bacillomycin D from the iturin group”.
- Page 9: “The detected high-resolution Mr values (< 10 ppm) of the possible surfactin analogues in the 50% fraction corresponded to that of the C13, C14, C15 and C16 surfactin analogues (Srf1-5) (Fig. 4a; Table S4).” has to be “The detected high-resolution Mr values (ppm < 10) of the possible surfactin analogues in the 50% fraction corresponded to that of the C13, C14 and C15 surfactin analogues (Srf1-4) (Fig. 4a; Table S4).”
- Page 9: “In the ESI-MS spectrum of the 70% fraction, a cluster of m/z peaks with a difference of approximately 14 or 22 or 28 atomic mass units (amu) in their molecular ion species were detected, revealing five groups of analogue molecules (Fig. 4b). The spectra in

Fig. 4 Electrospray ionisation mass spectrometry (ESI-MS) of the cell-free supernatant of *Bacillus amyloliquefaciens* DPN123 obtained after reverse phase chromatography. **a** 50% isopropanol fraction and **b** 70% isopropanol fraction. High resolution molecular ion mass spectra of the two lipopeptide complexes are shown and annotated with their putative identities (*Srf* surfactin, *BmD* bacillomycin D). The multi-protonated positive ion spectrum was deconvoluted with MaxEnt 3 from MassLynx 4.01. Refer to Table S4 and S5 for more information on the identities and expected m/z and Mr values

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positive mode showed the main groups of molecular ions at m/z 1017.5, 1031.6 and 1045.6 which corresponded to the deaminated charged species $[M + 3H_2O - 3NH_3]^+$ (Fig. 4b; Table S5). Corresponding potassium adducts $[M + K]^+$ at m/z 1053.5 and 1067.5 and

Table S5 Isoforms of bacillomycin D lipopeptide extracted from isolate DPN123 and detected using high resolution mass spectrometry. The top value is the experimentally detected monoisotopic M_r of themolecular ion and bottom value the theoretical M_r of the peptide species. The mass error in ppm is given in brackets

Primary Structure	Monoisotopic M_r	$[M+H]^+$	$[M+Na]^+$	$[M+K]^+$
cyclo[(Beta-N-C12)-L-Asn-D-Tyr-D-Asn-L-Pro-L-Glu-D-Ser-L-Thr]	1016.5212	1017.5450 (16) 1017.5290	1039.5110	1055.4849
cyclo[(Beta-N-C13)-L-Asn-D-Tyr-D-Asn-L-Pro-L-Glu-D-Ser-L-Thr]	1030.5368	1031.5415 (-3) 1031.5447	1053.5227 (4) 1053.5266	1069.4890 (-11) 1069.5005
cyclo[(Beta-N-C14)-L-Asn-D-Tyr-D-Asn-L-Pro-L-Glu-D-Ser-L-Thr]	1044.5525	1045.5656 (5) 1045.5603	1067.5483 (6) 1067.5423	1083.5333 (16) 1083.5162

hydrogenated adducts $[M+OH]$ at m/z 1083.5 were also detected (Fig. 4b; Table S5). The singly charged protonated molecular species and their corresponding singly charged potassium molecules all differed by 14 or 28 amu (Table S5). High-resolution M_r values (< 10 ppm) of the possible iturin A1 analogues in the 50% fraction corresponded to that of the C12, C14, C15 and C16 iturin A1 analogues (Fig. 4b; Table S5). The same results were reported by Ndlovu et al. [44]. Production of lipopeptides surfactin and iturin A1 by *B. amyloliquefaciens* strains have been well documented [70–72].” should read “In the ESI-MS spectrum of the 70% fraction, a cluster of m/z peaks with a difference of approximately 14 or 22 or 28 atomic mass units (amu) in their molecular ion species were detected, revealing three analogue molecules (Fig. 4b). The spectra in positive mode showed the main groups of molecular ions at m/z 1017.5, 1031.5 and 1045.6 which corresponded to singly protonated species $[M+H]^+$ (Fig. 4b; Table S5). Corresponding sodium adducts $[M+Na]^+$ at m/z 1053.5 and 1067.5, as well as potassium adducts $[M+K]^+$ at m/z 1069.5 and 1083.5 were also detected (Fig. 4b; Table S5). The singly charged protonated molecular species and their corresponding

singly charged potassium molecules all differed by 14 or 28 amu (Table S5). High-resolution M_r values (ppm < 15) of the possible iturin analogues in the 50% fraction corresponded to that of the C12, C13 and C14 of bacillomycin D, which are lipopeptides in the iturin group (Fig. 4b; Table S5). Production of lipopeptides surfactin and iturins by *B. amyloliquefaciens* strains have been well documented [70–72].”

- (d) “Antimicrobial lipopeptides surfactin and iturin A1 were produced by *B. amyloliquefaciens* DPN123...” should read “Antimicrobial lipopeptides surfactin and bacillomycin D from the iturin group were produced by *B. amyloliquefaciens* DPN123...”
- (e) Corrected Figure:
- (f) The revised Fig. 4 and Table S5 of the supplementary document is shown.

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