PLOS PATHOGENS

CORRECTION

Correction: Site-specific analysis of N-glycans from different sheep prion strains

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There are glycopeptide structures missing in both Fig 2 and Fig 6. Please see the correct Fig 2 and Fig 6 here.

Also, in Fig 7 the m/z value 1255.8162 is associated with the wrong glycan composition and should be assigned to H5N6S1F2. Please see the correct Fig 7 here.

OPEN ACCESS

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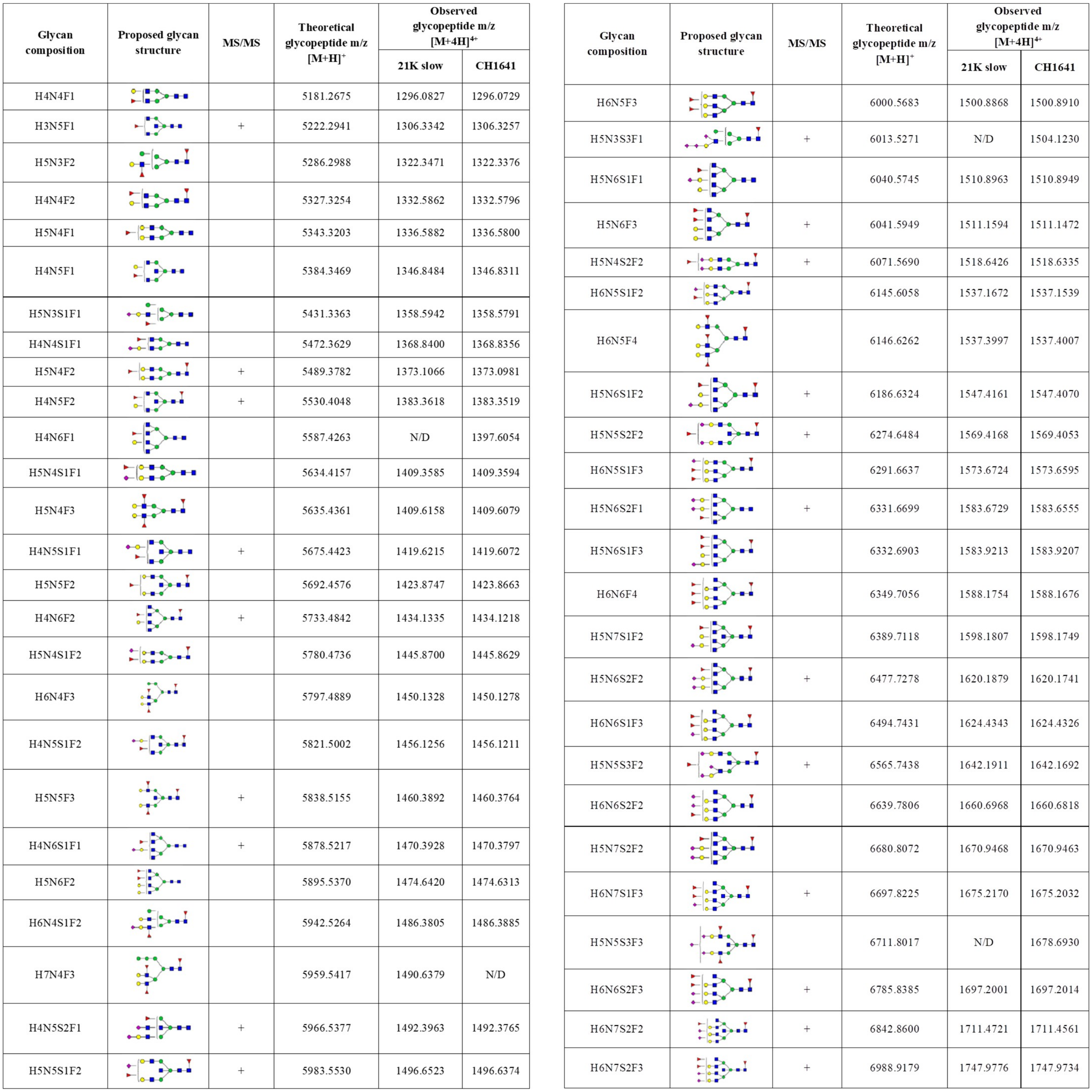

Glycan composition	Proposed glycan structure	MS/MS	Theoretical glycopeptide m/z $[M+H]^+$	Observed glycopeptide m/z $[M+4H]^{4+}$	
				21K slow	CH1641
H4N4F1			5181.2675	1296.0827	1296.0729
H3N5F1		+	5222.2941	1306.3342	1306.3257
H5N3F2			5286.2988	1322.3471	1322.3376
H4N4F2			5327.3254	1332.5862	1332.5796
H5N4F1			5343.3203	1336.5882	1336.5800
H4N5F1			5384.3469	1346.8484	1346.8311
H5N3S1F1			5431.3363	1358.5942	1358.5791
H4N4S1F1			5472.3629	1368.8400	1368.8356
H5N4F2		+	5489.3782	1373.1066	1373.0981
H4N5F2		+	5530.4048	1383.3618	1383.3519
H4N6F1			5587.4263	N/D	1397.6054
H5N4S1F1			5634.4157	1409.3585	1409.3594
H5N4F3			5635.4361	1409.6158	1409.6079
H4N5S1F1		+	5675.4423	1419.6215	1419.6072
H5N5F2			5692.4576	1423.8747	1423.8663
H4N6F2		+	5733.4842	1434.1335	1434.1218
H5N4S1F2			5780.4736	1445.8700	1445.8629
H6N4F3			5797.4889	1450.1328	1450.1278
H4N5S1F2			5821.5002	1456.1256	1456.1211
H5N5F3		+	5838.5155	1460.3892	1460.3764
H4N6S1F1		+	5878.5217	1470.3928	1470.3797
H5N6F2			5895.5370	1474.6420	1474.6313
H6N4S1F2			5942.5264	1486.3805	1486.3885
H7N4F3			5959.5417	1490.6379	N/D
H4N5S2F1		+	5966.5377	1492.3963	1492.3765
H5N5S1F2		+	5983.5530	1496.6523	1496.6374

Glycan composition	Proposed glycan structure	MS/MS	Theoretical glycopeptide m/z $[M+H]^+$	Observed glycopeptide m/z $[M+4H]^{4+}$	
				21K slow	CH1641
H6N5F3			6000.5683	1500.8868	1500.8910
H5N3S3F1		+	6013.5271	N/D	1504.1230
H5N6S1F1			6040.5745	1510.8963	1510.8949
H5N6F3		+	6041.5949	1511.1594	1511.1472
H5N4S2F2		+	6071.5690	1518.6426	1518.6335
H6N5S1F2			6145.6058	1537.1672	1537.1539
H6N5F4			6146.6262	1537.3997	1537.4007
H5N6S1F2		+	6186.6324	1547.4161	1547.4070
H5N5S2F2		+	6274.6484	1569.4168	1569.4053
H6N5S1F3			6291.6637	1573.6724	1573.6595
H5N6S2F1		+	6331.6699	1583.6729	1583.6555
H5N6S1F3			6332.6903	1583.9213	1583.9207
H6N6F4			6349.7056	1588.1754	1588.1676
H5N7S1F2			6389.7118	1598.1807	1598.1749
H5N6S2F2		+	6477.7278	1620.1879	1620.1741
H6N6S1F3			6494.7431	1624.4343	1624.4326
H5N5S3F2		+	6565.7438	1642.1911	1642.1692
H6N6S2F2			6639.7806	1660.6968	1660.6818
H5N7S2F2			6680.8072	1670.9468	1670.9463
H6N7S1F3		+	6697.8225	1675.2170	1675.2032
H5N5S3F3			6711.8017	N/D	1678.6930
H6N6S2F3		+	6785.8385	1697.2001	1697.2014
H6N7S2F2		+	6842.8600	1711.4721	1711.4561
H6N7S2F3		+	6988.9179	1747.9776	1747.9734

Fig 2. Detected N-184 glycopeptides on both prion strains. Proposed glycan structures found on N-184 glycosylation site with the theoretical and observed m/z values of the detected glycopeptides. H–hexose, N–*N*-acetylhexosamine, F–fucose and S–*N*-acetylneuraminic acid (sialic acid). Blue square–N-acetylglucosamine (GlcNAc), green circle–mannose (Man), red triangle–fucose (Fuc), yellow circle–galactose (Gal), purple diamond–N-acetylneuraminic acid (Neu5Ac). The presence of MS/MS spectrum is indicated with +. N/D–not determined.

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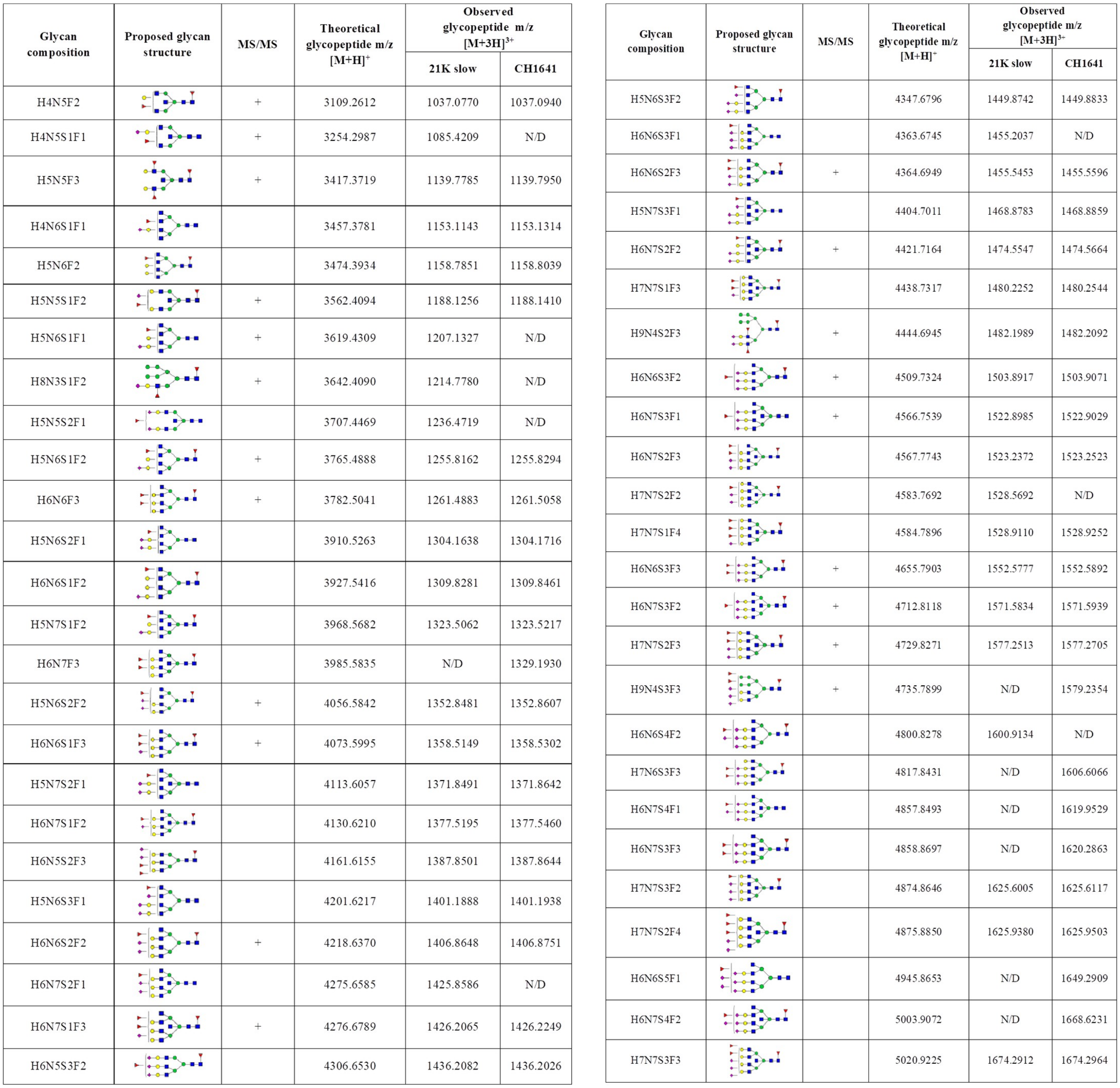

Glycan composition	Proposed glycan structure	MS/MS	Theoretical glycopeptide m/z $[M+H]^+$	Observed glycopeptide m/z $[M+3H]^{3+}$	
				21K slow	CH1641
H4N5F2		+	3109.2612	1037.0770	1037.0940
H4N5S1F1		+	3254.2987	1085.4209	N/D
H5N5F3		+	3417.3719	1139.7785	1139.7950
H4N6S1F1			3457.3781	1153.1143	1153.1314
H5N6F2			3474.3934	1158.7851	1158.8039
H5N5S1F2		+	3562.4094	1188.1256	1188.1410
H5N6S1F1		+	3619.4309	1207.1327	N/D
H8N3S1F2		+	3642.4090	1214.7780	N/D
H5N5S2F1			3707.4469	1236.4719	N/D
H5N6S1F2		+	3765.4888	1255.8162	1255.8294
H6N6F3		+	3782.5041	1261.4883	1261.5058
H5N6S2F1			3910.5263	1304.1638	1304.1716
H6N6S1F2			3927.5416	1309.8281	1309.8461
H5N7S1F2			3968.5682	1323.5062	1323.5217
H6N7F3			3985.5835	N/D	1329.1930
H5N6S2F2		+	4056.5842	1352.8481	1352.8607
H6N6S1F3		+	4073.5995	1358.5149	1358.5302
H5N7S2F1			4113.6057	1371.8491	1371.8642
H6N7S1F2			4130.6210	1377.5195	1377.5460
H6N5S2F3			4161.6155	1387.8501	1387.8644
H5N6S3F1			4201.6217	1401.1888	1401.1938
H6N6S2F2		+	4218.6370	1406.8648	1406.8751
H6N7S2F1			4275.6585	1425.8586	N/D
H6N7S1F3		+	4276.6789	1426.2065	1426.2249
H6N5S3F2			4306.6530	1436.2082	1436.2026
H5N6S3F2			4347.6796	1449.8742	1449.8833
H6N6S3F1			4363.6745	1455.2037	N/D
H6N6S2F3		+	4364.6949	1455.5453	1455.5596
H5N7S3F1			4404.7011	1468.8783	1468.8859
H6N7S2F2		+	4421.7164	1474.5547	1474.5664
H7N7S1F3			4438.7317	1480.2252	1480.2544
H9N4S2F3		+	4444.6945	1482.1989	1482.2092
H6N6S3F2		+	4509.7324	1503.8917	1503.9071
H6N7S3F1		+	4566.7539	1522.8985	1522.9029
H6N7S2F3			4567.7743	1523.2372	1523.2523
H7N7S2F2			4583.7692	1528.5692	N/D
H7N7S1F4			4584.7896	1528.9110	1528.9252
H6N6S3F3		+	4655.7903	1552.5777	1552.5892
H6N7S3F2		+	4712.8118	1571.5834	1571.5939
H7N7S2F3		+	4729.8271	1577.2513	1577.2705
H9N4S3F3		+	4735.7899	N/D	1579.2354
H6N6S4F2			4800.8278	1600.9134	N/D
H7N6S3F3			4817.8431	N/D	1606.6066
H6N7S4F1			4857.8493	N/D	1619.9529
H6N7S3F3			4858.8697	N/D	1620.2863
H7N7S3F2			4874.8646	1625.6005	1625.6117
H7N7S2F4			4875.8850	1625.9380	1625.9503
H6N6S5F1			4945.8653	N/D	1649.2909
H6N7S4F2			5003.9072	N/D	1668.6231
H7N7S3F3			5020.9225	1674.2912	1674.2964

Fig 6. Identified N-200 glycopeptides on both prion strains. Proposed glycan structures found on N-200 glycosylation site with the theoretical and observed m/z values of the detected glycopeptides. H–hexose, N–*N*-acetylhexosamine, F–fucose and S–*N*-acetylneuraminic acid (sialic acid). Blue square–N-acetylglucosamine (GlcNAc), green circle–mannose (Man), red triangle–fucose (Fuc), yellow circle–galactose (Gal), purple diamond–N-acetylneuraminic acid (Neu5Ac). The presence of MS/MS spectrum is indicated with +. N/D–not determined.

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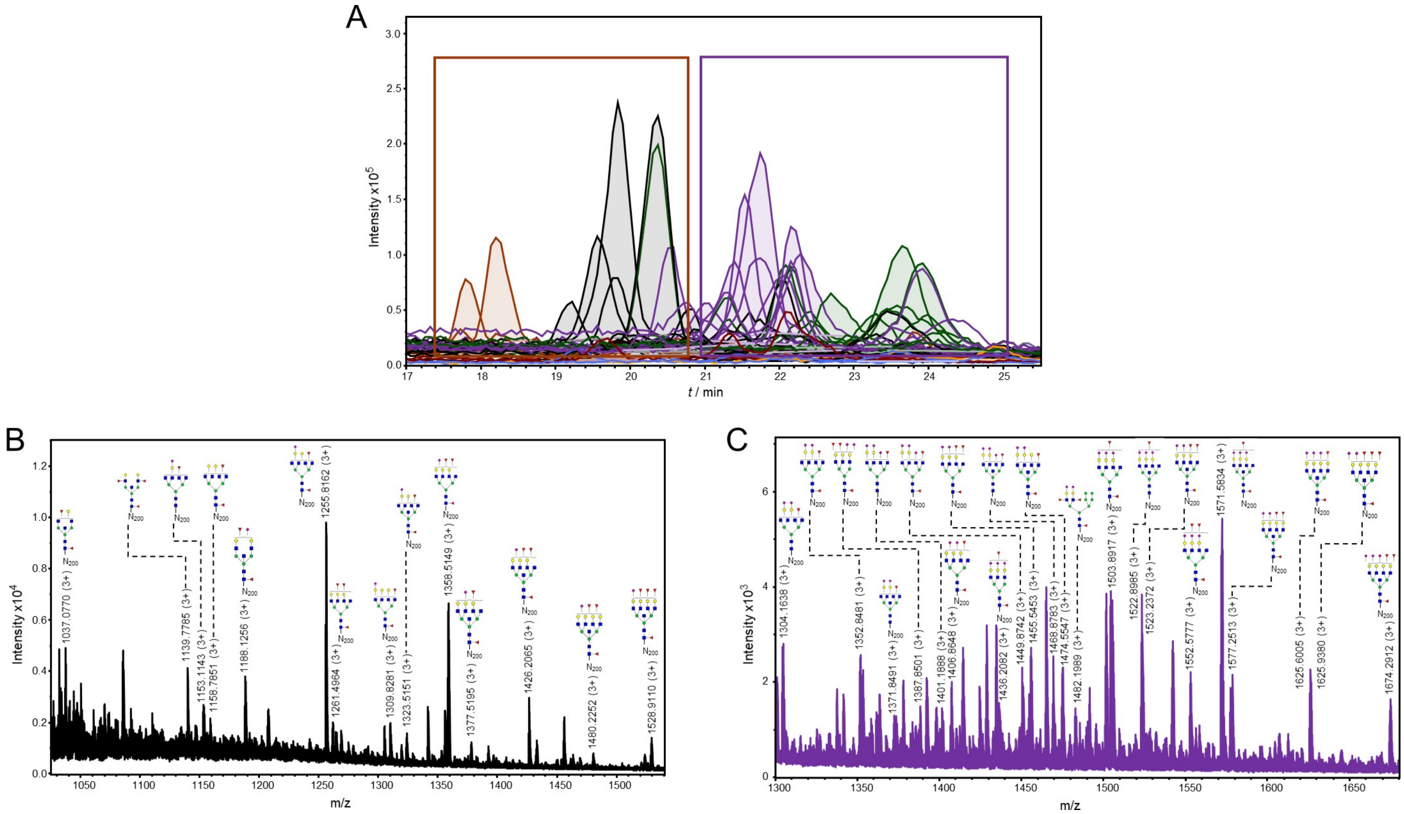

Fig 7. Representation of detected glycoforms on the N-200 glycosylation site of 21K slow prion strain. A) Extracted ion chromatograms with mutual 35 glycoforms detected. **B)** Assigned glycoforms in MS spectrum with N-200 peptide backbone: neutral and monosialylated, **C)** disialylated and trisialylated glycoforms. Blue square–*N*-acetylglucosamine (GlcNAc), green circle–mannose (Man), red triangle–fucose (Fuc), yellow circle–galactose (Gal), purple diamond–*N*-acetylneuraminic acid (Neu5Ac).

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Reference

1. Nakić N, Tran TH, Novokmet M, Andreoletti O, Lauc G, Legname G (2021) Site-specific analysis of N-glycans from different sheep prion strains. PLoS Pathog 17(2): e1009232. https://doi.org/10.1371/journal.ppat.1009232 PMID: 33600485