

Supplemental table ST2.

Number of influenza virus haemagglutinin (HA) gene full length sequences retrieved with GISAID EpiFlu database accession number and analysed in this report, by subtype/lineage and country, EU/EEA, weeks 40/2022 to 39/2023.

Country/HA sequences	A(H1N1)pdm09	A(H3N2)	B/Victoria
Austria	13	5	
Denmark	341	187	369
Finland	32	60	7
France	47	231	15
Germany	79	575	220
Greece		15	
Ireland	69	86	
Italy	14	23	7
Luxembourg	21	190	161
Netherlands	581	322	439
Norway	494	292	346
Portugal	49	197	34
Romania	146	91	17
Slovenia	47	51	2
Spain	431	826	405
Sweden	101	88	94
Total number of HA sequences	2466	3240	2116

Supplemental table ST3. Influenza subtypes and lineages with and without reduced inhibition/susceptibility following antiviral susceptibility testing reported to TESSy by drug tested, EU/EEA, weeks 40/2022 to 39/2023. HRI: Highly reduced inhibition; RI: Reduced inhibition; NI: Normal inhibition; RS: Reduced susceptibility; NS: Normal susceptibility; INP: Interpretation not possible because full NA or PA segment was not sequenced; prefix 'AA': Amino acid, refers to genotypic testing result. For isolates which were tested both phenotypically and genotypically, only the phenotypical result is reported in this table.

Osetamivir	HRI n (%)	NI n (%)	AAHRI n (%)	AARI n (%)	AANI n (%)	AAINP n(%)	Total
A(H1)pdm09	2 (0.1%)	249 (10.7%)	5 (0.2%)	1 (0%)	2080 (89%)	0 (0%)	2337
A(H3)	1 (0%)	399 (19%)	0 (0%)	0 (0%)	1695 (80.9%)	0 (0%)	2095
B/Vic	0 (0%)	370 (19.4%)	0 (0%)	0 (0%)	1540 (80.6%)	0 (0%)	1910
Total	3 (0%)	1018 (16.1%)	5 (0.1%)	1 (0%)	5315 (83.8%)	0 (0%)	6342
Zanamivir	HRI n (%)	NI n (%)	AAHRI n (%)	AARI n (%)	AANI n (%)	AAINP n(%)	Total
A(H1)pdm09	0 (0%)	229 (9.8%)	0 (0%)	1 (0%)	2105 (90.1%)	0 (0%)	2335
A(H3)	0 (0%)	387 (18.6%)	0 (0%)	0 (0%)	1696 (81.4%)	0 (0%)	2083
B/Vic	0 (0%)	359 (18.9%)	0 (0%)	1 (0.1%)	1544 (81.1%)	0 (0%)	1904
Total	0 (0%)	975 (15.4%)	0 (0%)	2 (0%)	5345 (84.5%)	0 (0%)	6322
M2-Blocker	HRI n (%)	NI n (%)	AAHRI n (%)	AARI n (%)	AANI n (%)	AAINP n(%)	Total
A(H1)pdm09	0 (0%)	0 (0%)	865 (100%)	0.00	0 (0%)	0 (0%)	865
A(H3)	0 (0%)	0 (0%)	1154 (100%)	0.00	0 (0%)	0 (0%)	1154
B/Vic*	-	-	-	-	-	-	-
Total	0 (0%)	0 (0%)	(100%)	0.00	0 (0%)	0 (0%)	2019
Baloxavir marboxil	-	-	-	AARS n (%)	AANS n (%)	AAINP n (%)	Total
A(H1)pdm09	-	-	-	0 (0%)	1231 (96.5%)	44 (3.5%)	1275
A(H3)	-	-	-	0 (0%)	1982 (99%)	21 (1%)	2003
B/Vic	-	-	-	0 (0%)	1242 (93%)	94 (7%)	1336
Total	-	-	-	0 (0%)	4455 (96.6%)	159 (3.4%)	4614

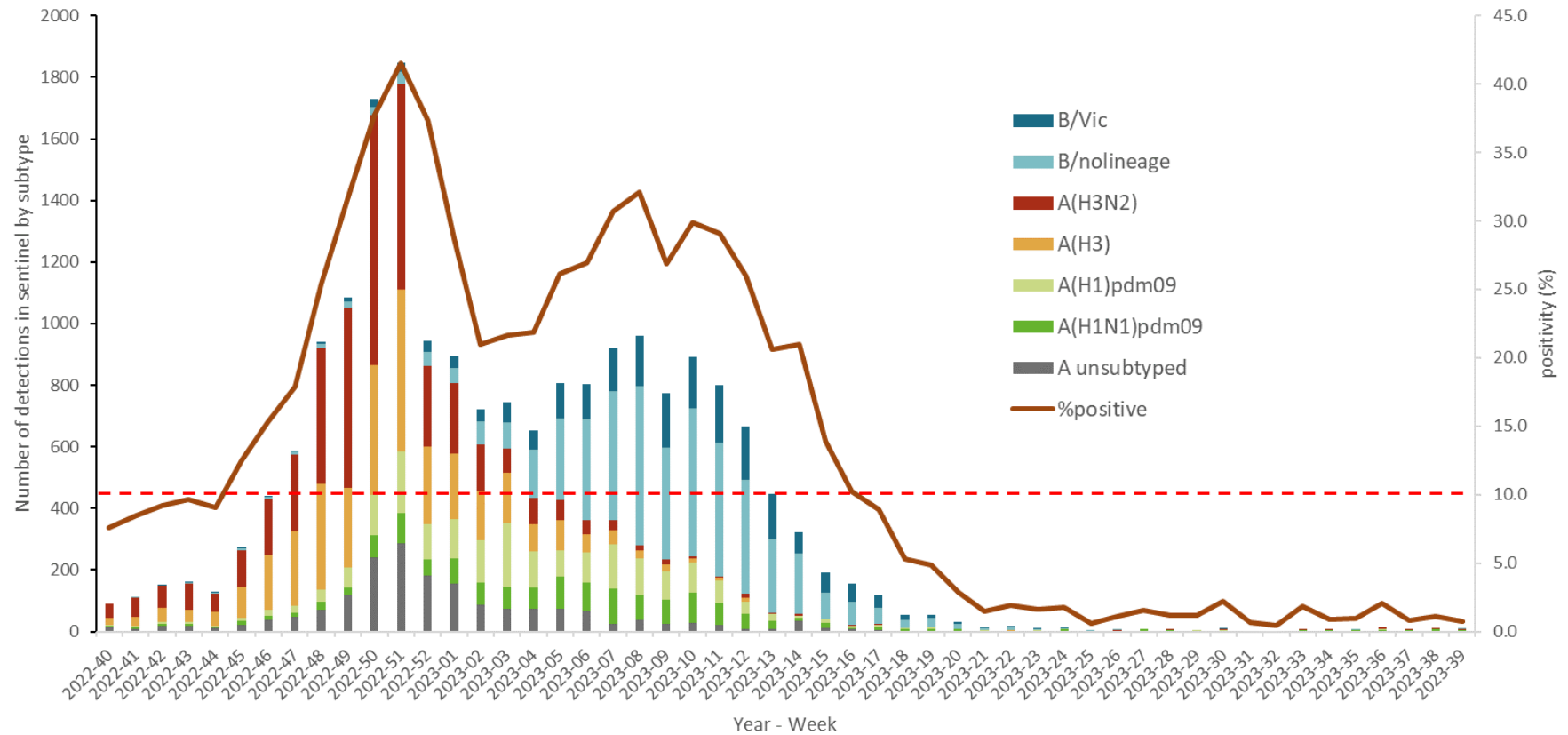
*: M2 blockers are not relevant for influenza B viruses. Detected HRI for M2 blockers were genotypic predictions based on presence of mutations M2:L26F, M2:V27I, M2:V27A and/or M2:S31N.

Supplemental table ST4. List of viruses reported with reduced inhibition or susceptibility by antiviral, subtypes and lineages, phenotypic or genotypic testing as well as corresponding GISAID id and interpretation defining mutation. TESSy, weeks 40/2022 to 39/2023, EU/EEA. AST: Antiviral susceptibility testing; HRI: Highly reduced inhibition; RI: Reduced inhibition; prefix 'AA': Amino acid, refers to genotypic testing result. N/A: Not available.

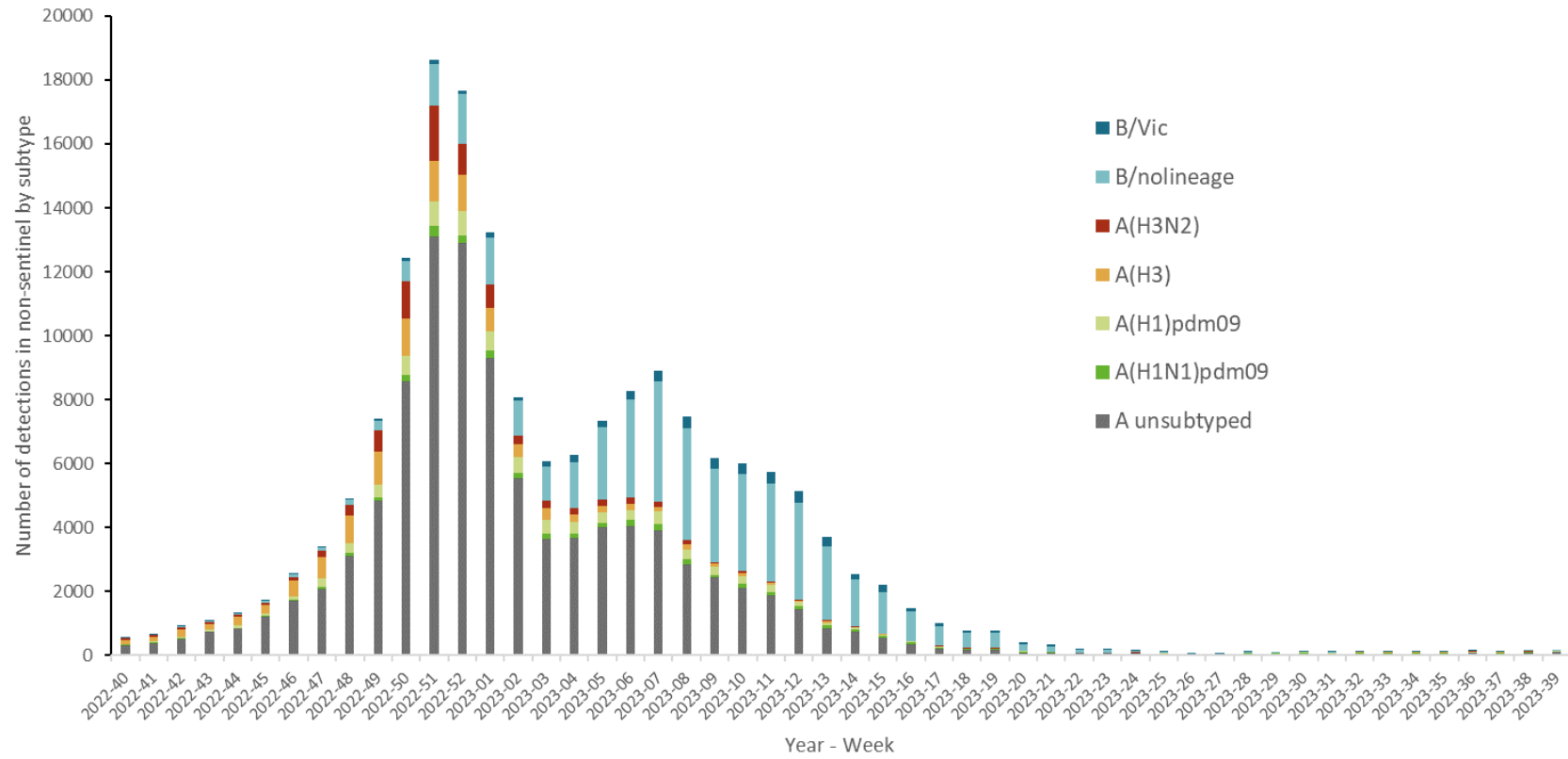
Oseltamivir					
GISAID ID	Virus	AST	Interpretation	NAISD	NAAAMutations
A/Netherlands/10294/2023	A(H1)pdm09	Phenotypic	HRI	EPI2660412	D199G (24%), H275Y (75%)
A/Schweiz/1/2023	A(H1)pdm09	Phenotypic	HRI	EPI2459759	H275Y
A/Arad/547046/2023	A(H3)	Phenotypic	HRI	N/A	N/A
A/Athens.GR/72/2023	A(H1)pdm09	Genotypic	AAHRI	EPI2689324	H275Y
A/Athens.GR/73/2023	A(H1)pdm09	Genotypic	AAHRI	EPI2689325	H275Y
A/Norway/05139/2023	A(H1)pdm09	Genotypic	AAHRI	EPI2529589	H275Y
A/PaisVasco/4350/2022	A(H1)pdm09	Genotypic	AAHRI	EPI2273970	H275Y
A/Arges/545719/2023	A(H1)pdm09	Genotypic	AAHRI	EPI2547045	H275Y
A/CastillaLaMancha/934/2023	A(H1)pdm09	Genotypic	AARI	EPI2520166	I223R
Zanamivir					
GISAID ID	Virus	AST	Interpretation	NAISD	NAAAMutations
A/CastillaLaMancha/934/2023	A(H1)pdm09	Genotypic	AARI	EPI2520166	I223R
B/Luxembourg/LNS8679822/2023	B/Vic	Genotypic	AARI	EPI2683836	G407S

Supplemental figure SF1. Number of specimens positive for influenza in primary care (A) sentinel and (B) non-sentinel surveillance and proportions of positive specimens among those tested, EU/EEA, week 40/2022 – week 39/2023. Viruses reported as A(H1)pdm09 or A(H3) have not been subtyped for neuraminidase (NA) gene, while those reported as A(H1N1)pdm09 or A(H3N2) have been subtyped also for NA gene.

A.

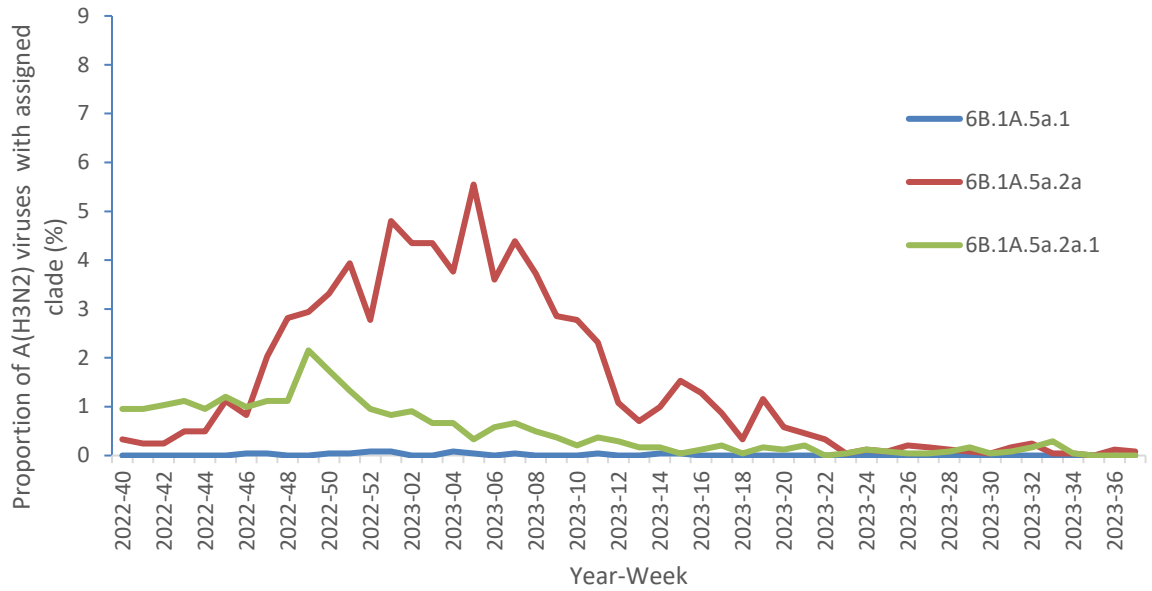


B.

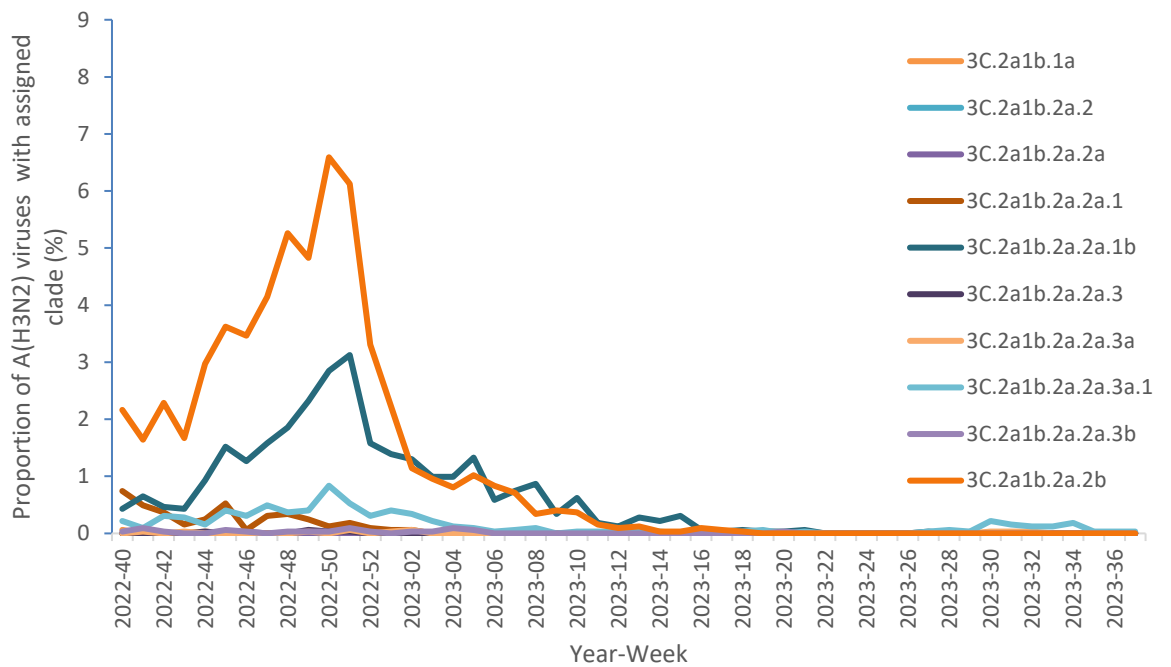


Supplemental figure SF2. Proportion (number of viruses per week by total number of viruses in that subtype/lineage) of viruses by assigned clade by subtype (A, A(H1N1)pdm09; B, A(H3N2); C, B/Victoria) and week, EU/EEA, weeks 40/2022- 39/2023.

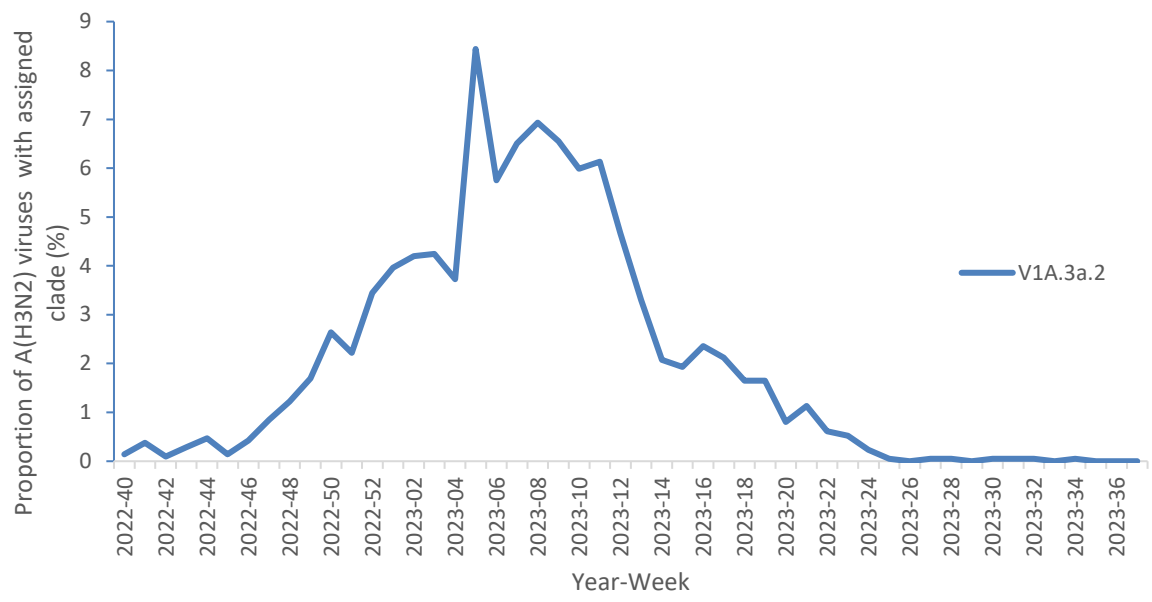
A. A(H1N1)pdm09



B. A(H3N2)



C. B/Victoria



Supplemental figure SF3: Number of antigenic and genetic clade categoric reports and number of countries reporting each type of data to TESSy, by influenza season, EU/EEA countries, 2016-2023.



