

**Global Influenza Hospital Surveillance** Network







# **RESULTS FROM THE 2018/2019 INFLUENZA SEASON IN THE VALENCIA REGION OF SPAIN**

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Hospital La Fe Population: 285,066

**Hospital Doctor Peset** Population: 278,344

**Hospital General Alicante** Population: 274,122

#### **Genetic characterization of viruses**

All the A(H1N1)pdm09 isolated viruses corresponded to the clade 6B.1 as the recommended A/Michigan/45/2015 vaccine virus, but encoding several amino acid substitutions characteristic for diversification in several distinct subclades.

Vaccine viruses Reference viruses Collection date Jan 2019 Feb 2019



# Site presentation

### **Methods**

The Valencia Hospital Network for the Study of Influenza (VAHNSI) conducts annually a prospective, active-surveillance, hospital-based study on admissions with diagnoses possibly related to influenza.

From **September to August**, all hospitalized patients were included in the study in case they:

- Gave written informed **consent**
- Were resident in one of the hospitals' catchment area
- Were not institutionalized
- Were **not** discharged from a **previous hospitalization** in the last 30 days
- Satisfied the ECDC ILI-case definition (required only for patients ≥5 years old)
- Were hospitalized within 7 days of the onset of symptoms

Clinical **information** was collected through **interview** and by **medical records** review. Information related to vaccination was obtained from the Valencia Region Vaccine **Information System.** Swabs were tested by real-time reverse transcription polymerase chain reaction (**RT-PCR**) in a centralized laboratory in FISABIO. Influenza Vaccine Effectiveness (IVE) was estimated by a **Bayesian logistic regression** following the **test-negative design**.

# Results

### **Respiratory viral infections**

2000

1500

1000

rate x100,000/se (Sept - Aug)

There were similar proportions of A(H3N2) viruses from subclades 3C.2a1b and 3C.3a, which were both predominant. None of the sequenced isolates corresponded to the 2018/19 NH clade 3C.2a1 recommended vaccine virus A/Singapore/INFIMH-16-0019/2016.

3C.2a1





Phylogenetic analysis and mutational profiles for the A(H3N2) clades and sequenced isolates.

A(H3N2) structure showing the location and frequency of amino acid substitutions found within antigenic sites as compared with the vaccine virus.

Influenza: 322; RSV: 394; HMPV: 109; PIV: 27; HRV: 609; AdV: 30; BoV: 17; CoV: 109







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	<1	1 to 4	5 to 17	18 to 49	50 to 64	65 to 74	75 to 84	≥85
→Influenza	115.57	47.49	4.67	3.96	21.44	57.98	120.63	221.04
-RSV	2080.20	142.46	0.67	1.25	8.75	20.84	80.42	161.05
HMPV	231.13	27.49	0.00	0.63	4.81	14.50	38.77	66.31
→Parainfluenza	23.11	12.50	0.67	0.21	0.87	4.53	5.74	22.10
	878.31	177.45	13.34	8.54	32.37	73.38	195.31	344.20
Adenovirus	34.67	52.49	0.67	0.21	0.87	0.00	1.44	3.16
Coronavirus	300.47	27.49	0.67	0.42	7.00	11.78	27.29	66.31
—Bocavirus	92.45	17.50	0.67	0.00	0.00	0.00	0.00	3.16

#### Influenza vaccine effectiveness (in ≥65 years old)



# **Key aspects & challenges**

Circulation of influenza A(H1N1)pdm09 and A(H3N2) with no B cases.

The influenza peak was reached at week 2019-08.

Highest influenza incidence rate was detected in 85+.

Highest RSV and RhV incidence rates were detected in <1.

IVE was moderate against overall influenza and A(H1N1)pdm09 with no significant protection against A(H3N2).

All the A(H1N1)pdm09 isolated viruses belonged to the vaccine virus clade. None of the A(H3N2) isolated viruses corresponded to the vaccine virus recommendation.

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