

Using Influenza Vaccine Efficacy Studies for Surveillance of (Re)Emerging Respiratory viruses

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Sanofi-Pasteur:

- related to the content of the presentation

Gilead:

- not related to the content of the presentation



**ESCV WORKSHOP
ON EMERGING
VIRUS INFECTIONS**

23rd - 24th January 2020
University Clinic of Dentistry
Vienna, Austria



In cooperation with



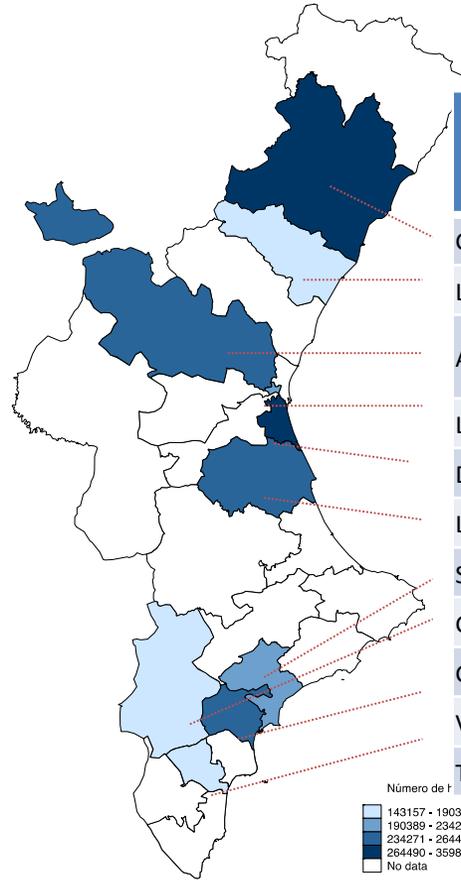
Valencia Hospital Network for the Study of Influenza and Other Respiratory viruses (VAHNSI)

Objectives

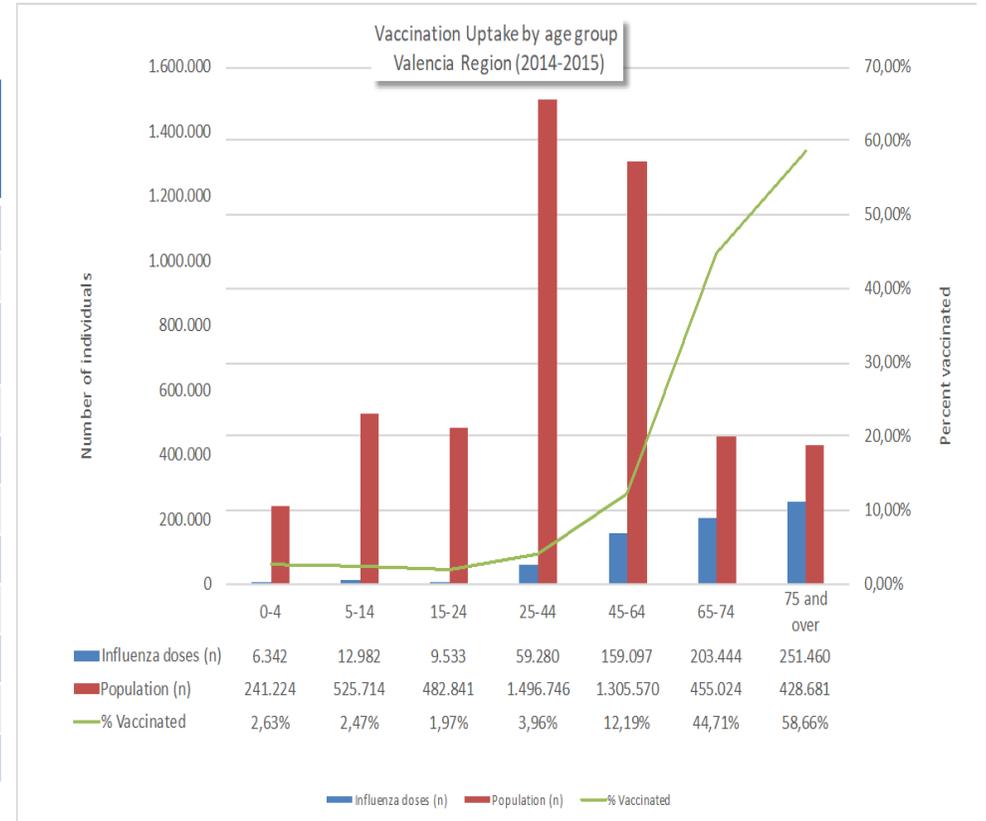
1. Estimate influenza disease burden in all age groups.
2. Estimate burden for other respiratory viruses.
3. Estimate influenza vaccine effectiveness in preventing admissions with influenza in the population targeted to vaccination in the annual influenza program (test negative approach):
 - By vaccine,
 - By age group
 - By virus type
4. Describe the epidemiology of severe influenza.
 1. Virus types involved, incidence (age-specific).
 2. Patient characteristics.
 3. Virus genetic characteristics.



Population and influenza vaccine uptake. VAHNSI and Valencia Region



Hospital	Population (n)
General de CS	277,672
La Plana	185,686
Arnau de Vilanova	255,648
La Fe	192,572
Dr Peset	359,893
La Ribera	259,125
San Juan	212,894
General Elda	190,389
General Alicante	264,490
Vinalopo	153,157
Total	2,351,526



WGS allows detecting new intra-subtype reassortants

MICROBIAL GENOMICS

RESEARCH ARTICLE

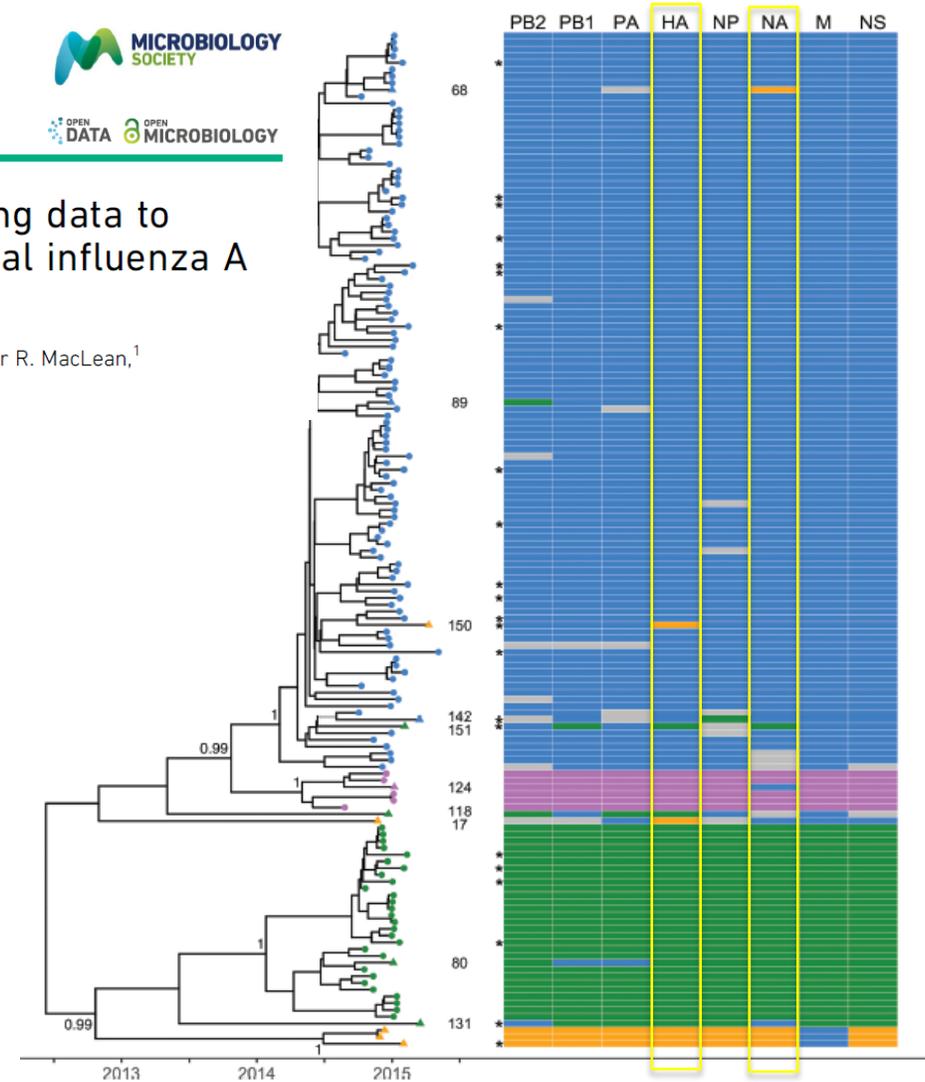
Goldstein et al., *Microbial Genomics* 2017;4
DOI 10.1099/mgen.0.000137



Integrating patient and whole-genome sequencing data to provide insights into the epidemiology of seasonal influenza A (H3N2) viruses

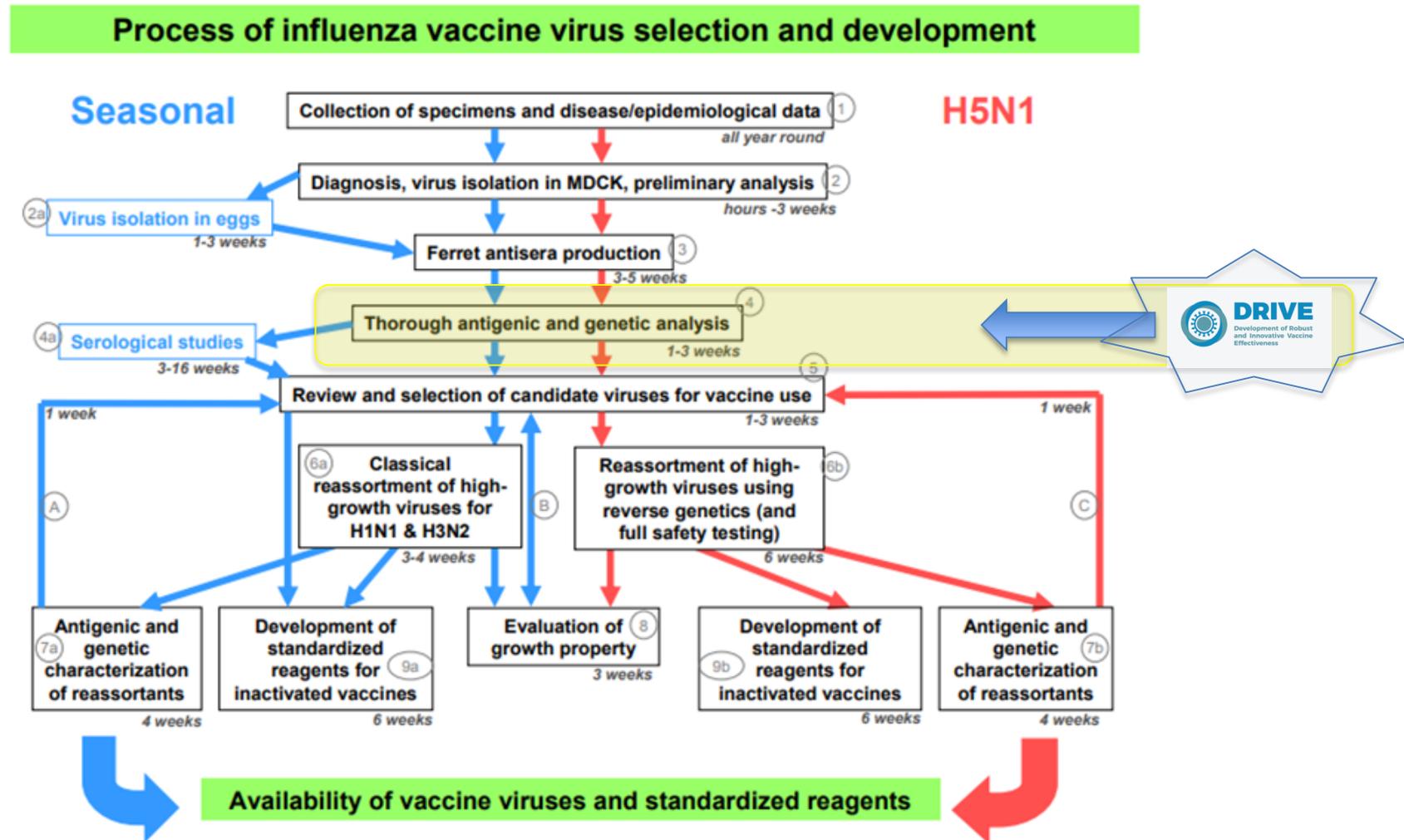
Emily J. Goldstein,^{1,*} William T. Harvey,² Gavin S. Wilkie,³ Samantha J. Shepherd,¹ Alasdair R. MacLean,¹ Pablo R. Murcia³ and Rory N. Gunson¹

- Detecting mutations in internal genes
- Resistance to new Pol complex inhibitors
- Identifies intra-subtype reassortants now unadverted by Sanger HA-NA sequencing
- Reassortant genomes may be associated with severe outcomes, antigenic drift
- Set-up 2018-19 pilot within DRIVE (Valencia and Lyon)



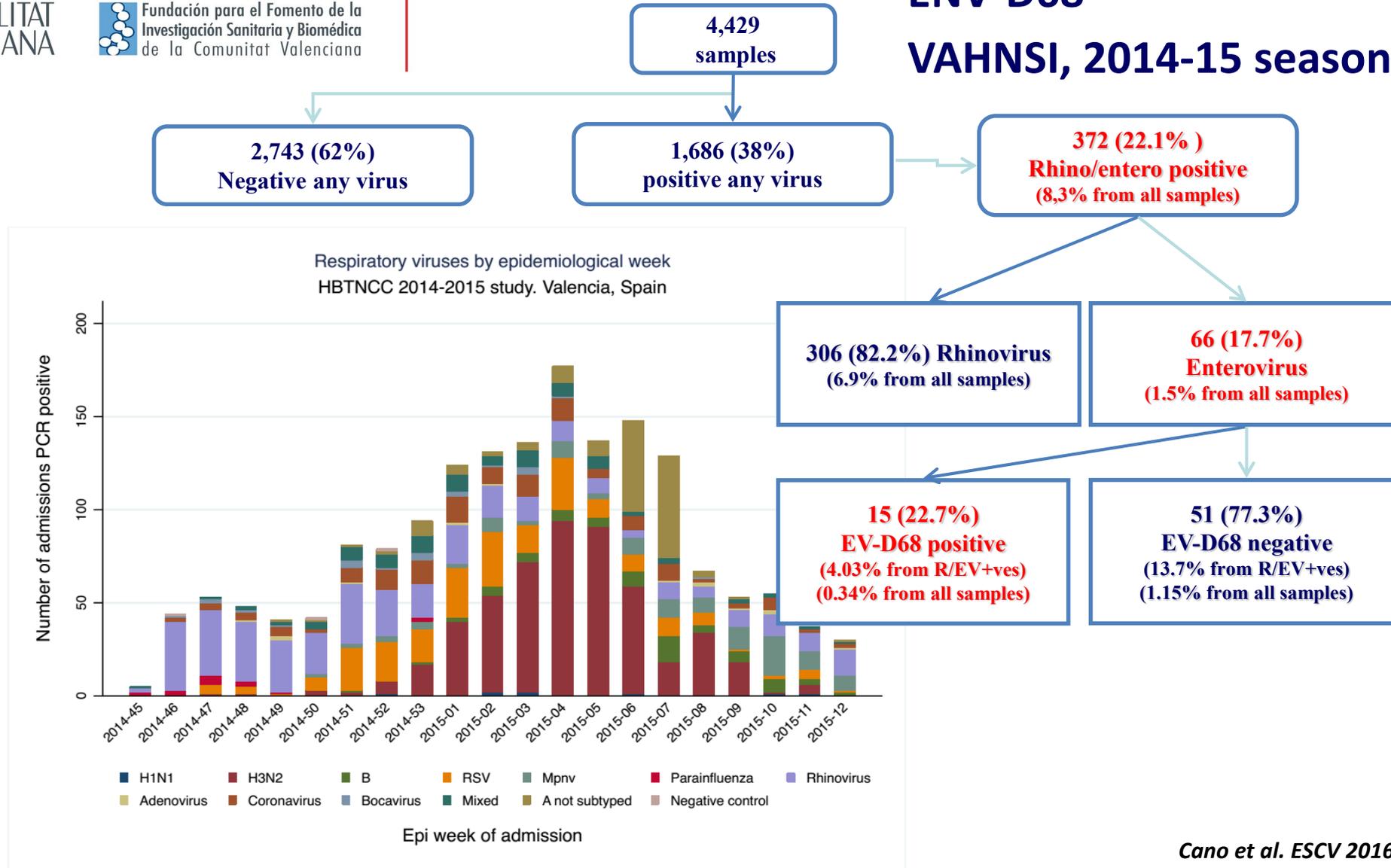
DRIVE Influenza WGS pilot

Timelines for interim and final reports



ENV-D68

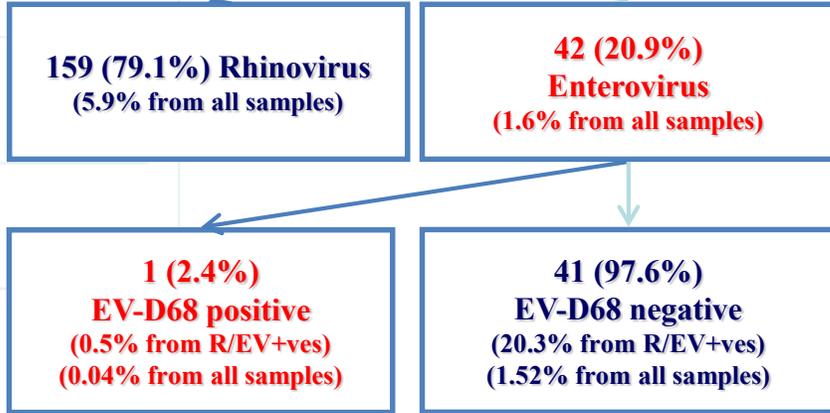
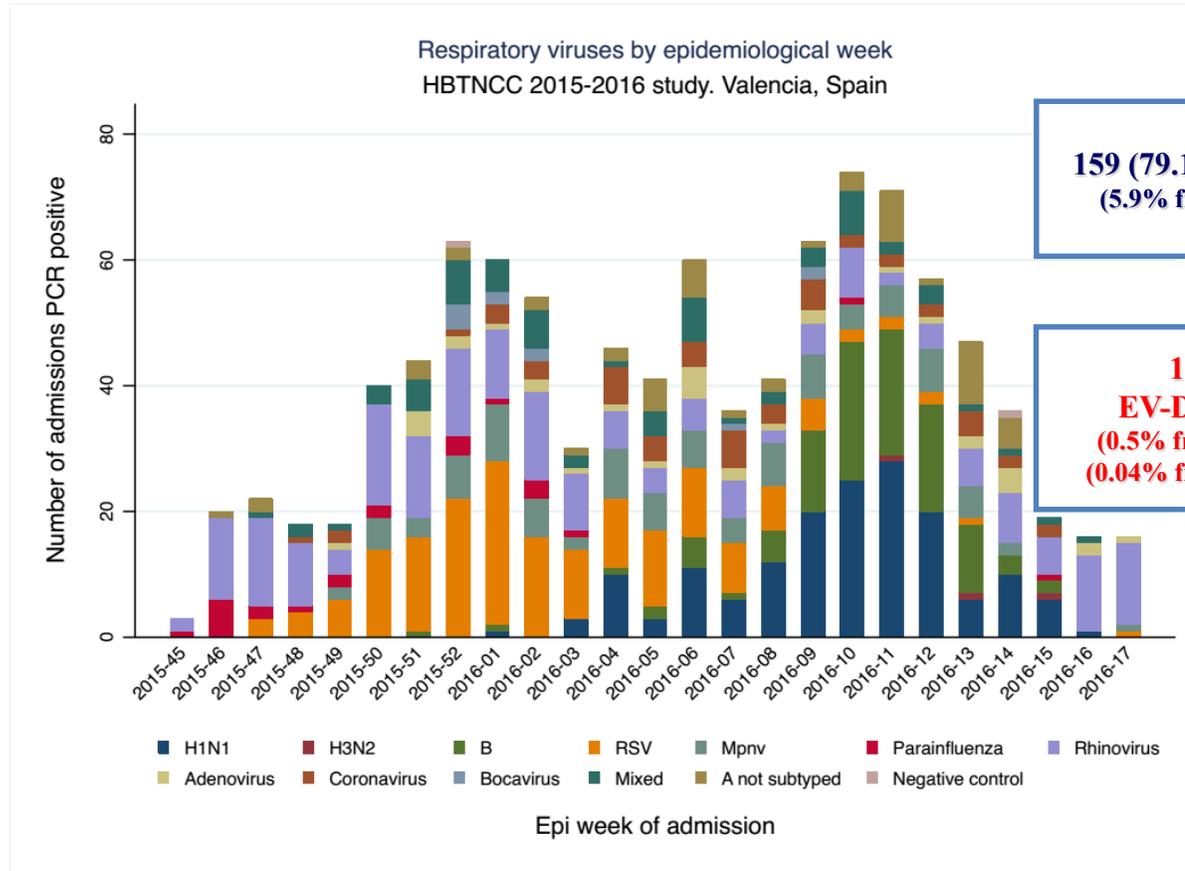
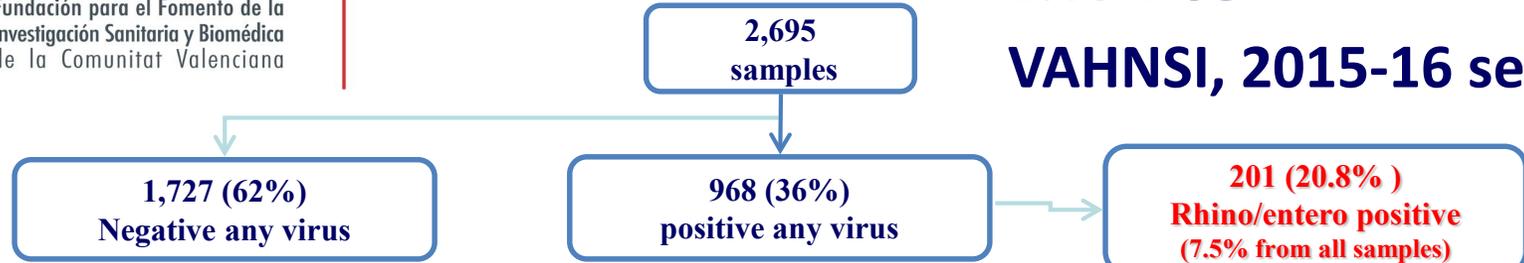
VAHNSI, 2014-15 season



Cano et al. ESCV 2016



ENV-D68 VAHNSI, 2015-16 season



Cano et al. ESCV 2016



ENV-D68

VAHNSI, Summary 2014-15 to 2018-19 seasons

	2014-15		2015-16		2016-17		2017-18		2018-19	
	N	(%)	N	(%)	N	(%)	N	(%)	N	(%)
Subjects Screened	4.429	100,0	2.695	100,0	2.263	100,0	3.046	100,0	4.707	100,0
Virus (any) positive	1.686	38,1	968	35,9	895	39,5	1.644	54,0	1.711	36,4
HRV/EV +ve	372	22,1	201	20,8	239	26,7	488	29,7	674	39,4
EV +ve	66	17,7	42	20,9	7	2,9	11	2,3	113	16,8
EV-D68 +ve	15	22,7	1	2,4	1	14,3	0	0,0	55	48,7

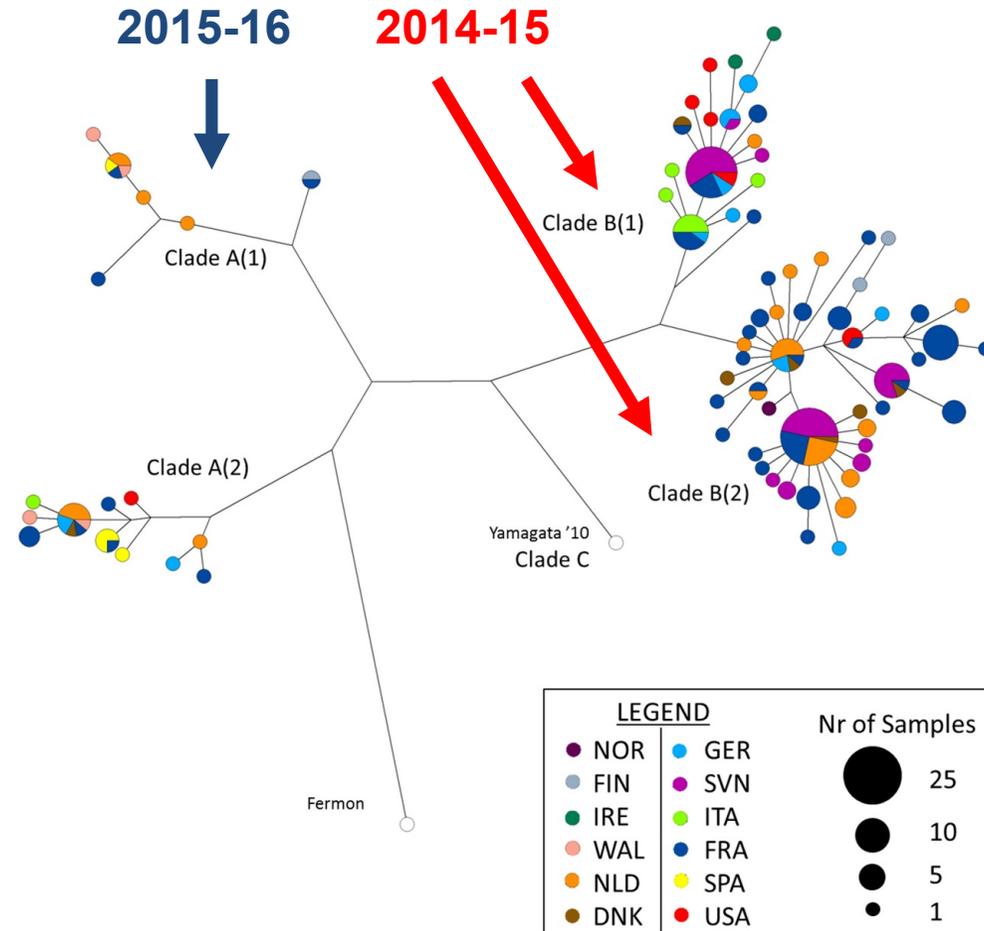
Cano et al. In preparation



ENV-D68 ESCV study: phylogenetic grouping

VAHNSI

- **2014-15 isolates (15):**
 - Clades B1 and B2
- **2015-16 isolates (1):**
 - Clade A1
- **2016-2019 isolates:**
 - Sequencing ongoing



Poelman et al. J Clin Virol 2015; 71: 1-10



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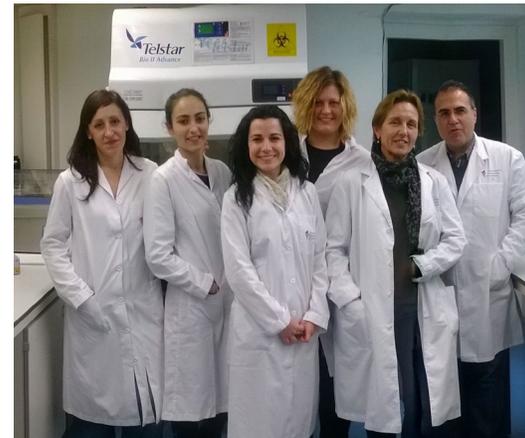
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