

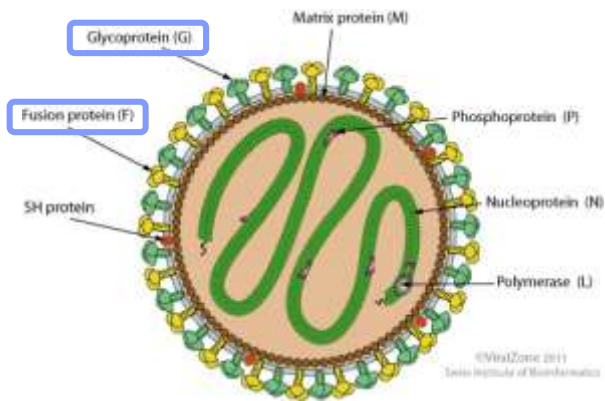
# A novel HMPV carrying 180- and 111-nucleotide duplications within the G gene detected at a tertiary university hospital in Catalonia since the 2014-2015 season

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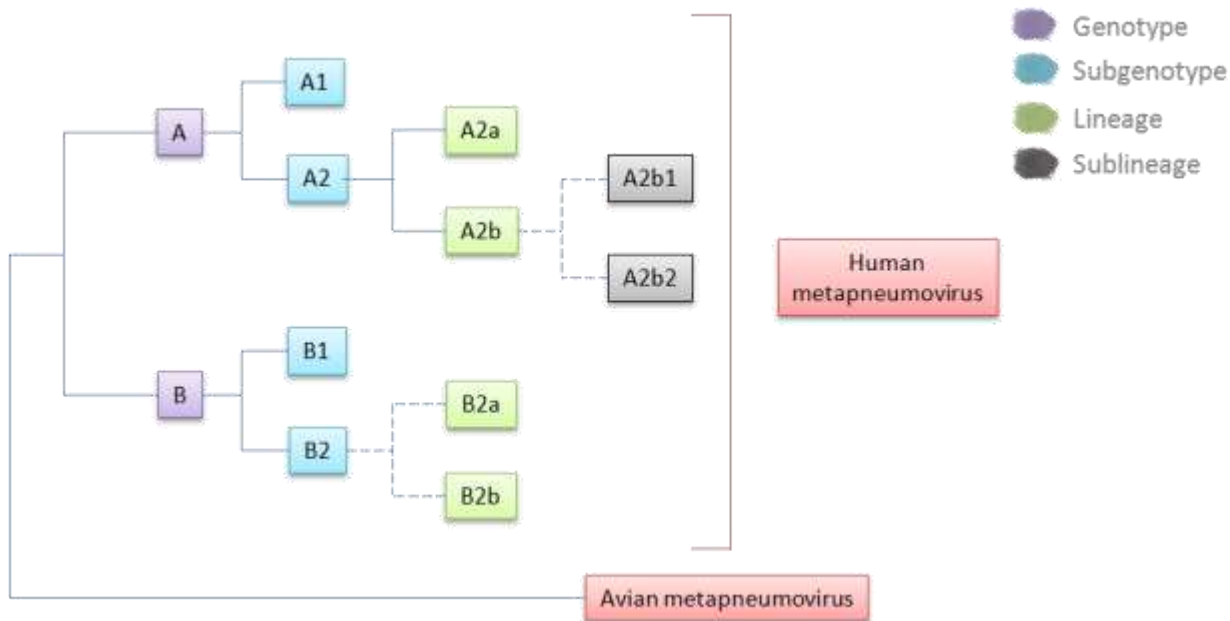
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# Human metapneumovirus

Order	Family	Genus
Mononegvirales	Pneumoviridae	Metapneumovirus



<http://viralzone.expasy.org/>



# Objectives



To describe the prevalence and epidemiology of HMPV



To describe the genetic diversity of HMPV strains in respiratory samples from patients attended in the Hospital Universitari Vall d'Hebron (HUVH) in Barcelona, Spain

# Methodology

Sample collection

## Respiratory specimens

2014-2015 season (weeks 40/2014 – 20/2015)  
2015 inter-season (weeks 21/2015 – 39/2015)  
2015-2016 season (weeks 40/2015 – 20/2016)  
2016 inter-season (weeks 21/2016 – 39/2016)  
2016-2017 season (weeks 40/2016 – 13/2017)

Respiratory viruses'  
detection

## Samples

Upper respiratory tract → nasopharyngeal aspirates or swabs  
Lower respiratory tract → bronchoalveolar lavages, bronchoaspirates  
and tracheal aspirates

## Procedure

1. Respiratory viruses' detection
2. Partial Sanger sequencing of F and G coding protein regions
3. Maximum likelihood phylogenetic analysis with MEGA v5.2
4. Collapse of haplotypes with ALTER server
5. Prediction of potential N- and O-glycosylations with the NetNGlyc and NetOGlyc servers

Genotyping and  
molecular  
characterisation

# Results and Discussion

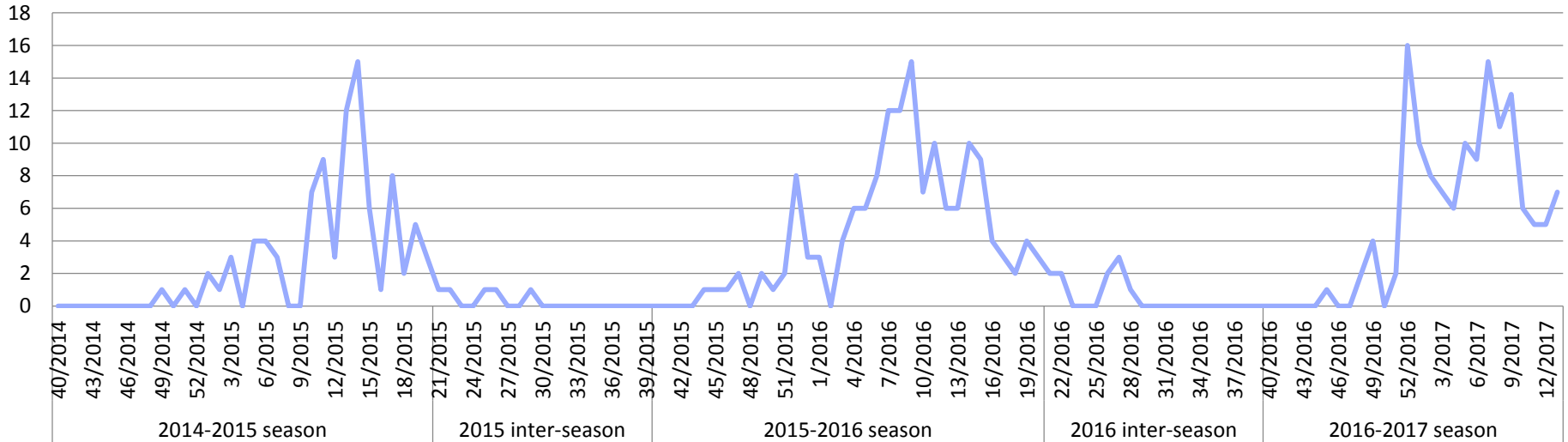
## Prevalence

Season	Samples	Patients	Laboratory-confirmed HMPV	
			Samples	Patients
2014-2015	5,190	3,683	98 (1.89%)	90 (2.44%)
2015 inter-season	1,017	741	5 (0.49%)	5 (0.67%)
2015-2016	6,498	4,800	157 (2.42%)	151 (3.15%)
2016 inter-season	1,046	786	10 (0.96%)	10 (1.27%)
2016-2017	5,786	4,423	137 (2.37%)	137 (3.09%)
<b>Total</b>	<b>19,537</b>	<b>14,433</b>	<b>407 (2.08%)</b>	<b>393 (2.72%)</b>

- HMPV's prevalence was similar to reported data worldwide (1.9-25%)
- There has been an increment in the prevalence over the different seasons, though it might be due to the increase of virological surveillance of respiratory viruses in HUVH

# Results and Discussion

## Seasonality



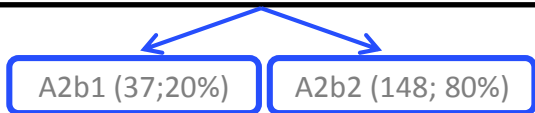
# Results and Discussion

## Genotyping

Both genotypes co-circulated

HMPV-A (196; 50%)  
HMPV-B (176; 45%)  
Not typed (20; <5%)  
A/B co-infection (1; <1%)

Season	A1	A2a	A2b	B1	B2
2014-2015	0 (0%)	9 (10%)	25 (29%)	<b>37 (42%)</b>	17 (19%)
2015 inter-season	0 (0%)	1 (20%)	0 (0%)	<b>4 (80%)</b>	0 (0%)
2015-2016	0 (0%)	0 (0%)	<b>87 (62%)</b>	22 (16%)	31 (22%)
2016 inter-season	0 (0%)	0 (0%)	<b>9 (90%)</b>	1 (10%)	0 (0%)
2016-2017	0 (0%)	1 (<1%)	<b>64 (50%)</b>	36 (28%)	28 (22%)
<b>Total</b>	<b>0 (0%)</b>	<b>11 (3%)</b>	<b>185 (50%)</b>	<b>100 (27%)</b>	<b>76 (20%)</b>



# This study is the first description of duplication events in HMPV



## 180-Nucleotide Duplication in the G Gene of Human metapneumovirus A2b Subgroup Strains Circulating in Yokohama City, Japan, since 2014

Miwako Saikusa<sup>1\*</sup>, Chiharu Kawakami<sup>1</sup>, Naganori Nao<sup>2</sup>, Makoto Takeda<sup>2</sup>, Shuzo Usuku<sup>1</sup>, Tadayoshi Sasao<sup>1</sup>, Kimiko Nishimoto<sup>1</sup> and Takahiro Toyozawa<sup>3</sup>

<sup>1</sup>Yokohama City Institute of Public Health, Yokohama, Japan, <sup>2</sup>Department of Virology III, National Institute of Infectious Diseases, Musashimurayama, Japan, <sup>3</sup>Yokohama City Public Health Center, Yokohama, Japan

Saikusa M, Kawakami C, Nao N, Takeda M, Usuku S, Sasao T, et al. 180-nucleotide duplication in the G gene of human metapneumovirus A2b subgroup strains circulating in Yokohama City, Japan, since 2014. *Frontiers in Microbiology* 8:1–11. doi: 10.3389/fmicb.2017.00402

However, during the preparation of this manuscript, a similar report of 180nt-dup was presented at the 19th Annual Meeting of the European Society for Clinical Virology held in September 2016 (Pinana et al., 2016).

**GENETIC VARIABILITY OF HUMAN METAPNEUMOVIRUS A GENOTYPE CIRCULATING IN CATALONIA DURING THE 2014-2015 AND 2015-2016 SEASONS: A 180-NUCLEOTIDE G GENE DUPLICATION REPORTED**

María Piñana, Jorgina Vila, Laura Gimferrer, María Valls, Cristina Andrés, Javier Ramón, María Gema Codina, María del Carmen Martín, Francisco Fuentes, Rosario Saz, Pilar Alcubilla, Carlos Rodrigo, Tomás Pumarola, Andrés Arán

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R T A T S S I G N H T G S M A M O K



# Results and Discussion

## 180- and 111-nucleotide duplications in the G gene

- These variants have increased in number since their emergence

Duplication	Seasons			
	2014-15	2015-16	2016 inter-season	2016-17
180 nt	2/13 (15%)	15/65 (23%)	1/8 (13%)	23/62 (37%)
111 nt	0/13 (0%)	1/65 (2%)	1/8 (13%)	10/62 (16%)

- Current human respiratory syncytial virus has a similar duplication in the glycoprotein
  - ON1 → 72-nucleotide duplication (24 amino acids)
  - BA → 60-nucleotide duplication (20 amino acids)

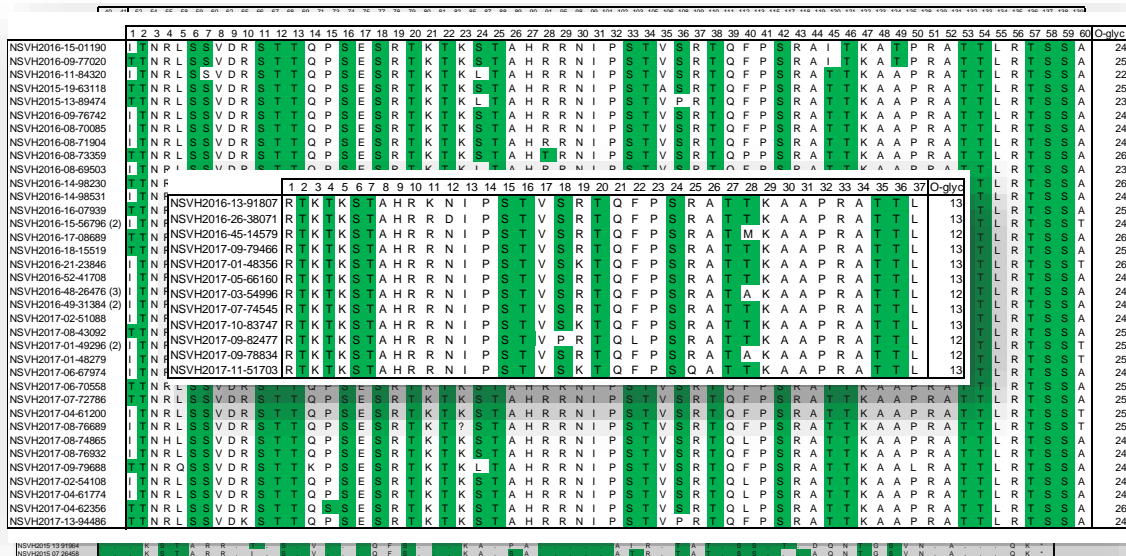
# Results and Discussion

## 180- and 111-nucleotide duplications in the G gene

- The G protein could have a shielding function due to its heavy glycosylation pattern

(Leyrat *et al*, 2014)

- 180-nt dup → 23-26 additional potential O-glycosylation sites
- 111-nt dup → 12-13 additional potential O-glycosylation sites



G protein's evolution might be affecting its own immune evasion mechanism



# Conclusions

- Recent and valuable data of prevalence, seasonality and genetic diversity of circulating HMPV in Catalonia is reported.
- Both 180- and 111-nucleotide duplications within HMPV G gene are first described here.
- The fact that both duplications have been detected in increasing numbers suggests that they might become predominant in the future, as has happened with HRSV.
- Further studies are needed to know whether these novel variants have an effect on immune evasion



The present study highlights the importance of continuous surveillance of circulating respiratory viruses. Changes in viral genetic features might affect antigenic properties, their tropism and virulence.



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