Virological data integration on influenza vaccine effectiveness, Portugal 2015/16

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1 Background

Regarding the wide genetic and antigenic variability of *Influenza* viruses, overall or subtype *Influenza* vaccine effectiveness (IVE) estimates may not be sufficient to assess vaccine protection against circulating strains. This is particularly important when low IVE against a specific clade is suspicious or a new drifted virus is emerging.

Viral genetic characterization is routinely performed in *Influenza* surveillance but viruses are selected according patient age, severity and vaccine status. For instance, last season genetic characterized cases were more vaccinated than those not selected.

DESCRIPTION OF THE PROBLEM

A protocol for virological data integration on IVE studies within I-MOVE network was performed. It intended to solve the following:

- Selection of the clade of interest to provide IVE;
- Determination of the number of cases needed for genetic characterization;
- Selection of cases for genetic characterization independently of patient features.

2 Materials and methods

SELECTION OF TARGET *INFLUENZA* VIRUS

Dominant *Influenza* virus in circulation was identified and the subtype of interest for virus characterization was targeted using surveillance data (National and European level).

RANDOM CASE SELECTION BY *INFLUENZA* PHASE

Case selection for genetic characterization was performed in three phases established according to influenza activity (Figure 1).

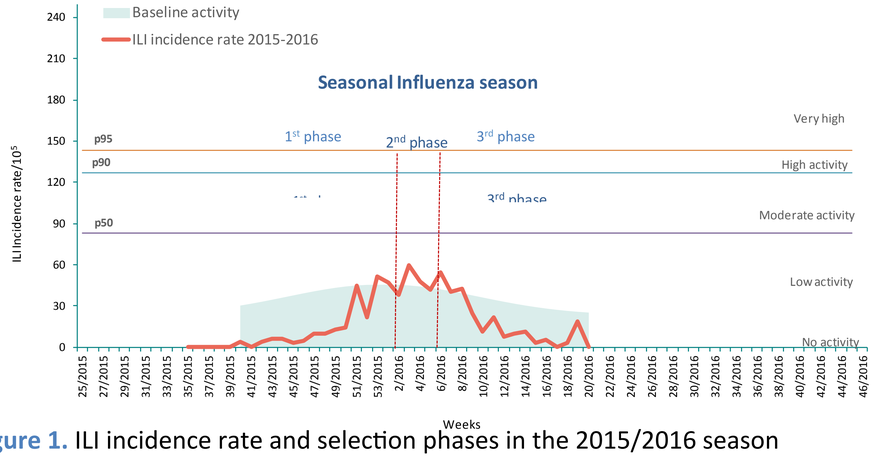

Figure 1. ILI incidence rate and selection phases in the 2015/2016 season

PERFORMANCE OF GENETIC CHARACTERIZATION

Sequencing was performed directly from the clinical specimen. Only when amplification cannot be obtained in the primary sample, sequence was performed in isolated virus (cell culture supernantant).

3 Results

During the 2015/2016 season, a closely contact between epidemiological and laboratorial teams allows to perform a random selection of influenza cases for genetic characterization independently of cases features.

Influenza A(H1N1)pdm09 was the selected subtype given its predominance and the emergence of new subclades (6B.1 and 6B. 2).

A total of 133 samples were genetic characterized distributed in the 3 phases. (Figure 2).

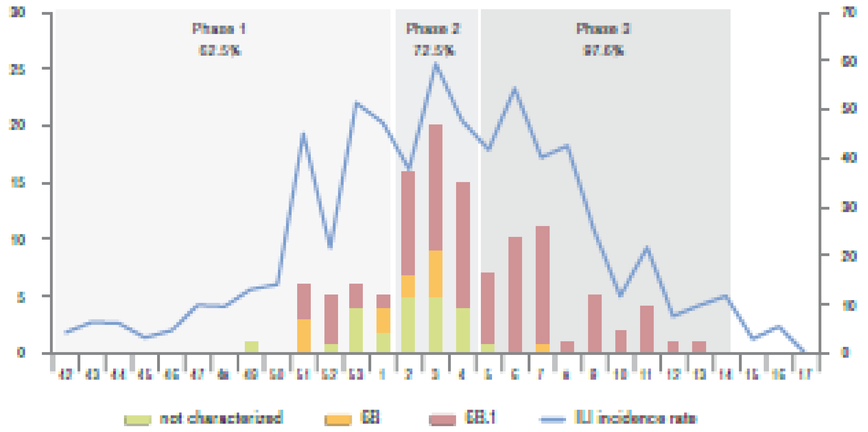

Figure 2. Distribution of genetic clades and ILI incidence rate per week of symptoms onset; identification of selection phases and respective characterization rates (%).

No differences regarding age, sex and influenza seasonal vaccination status were found between selected and unselected cases for genetic characterization (Table 1).

The success of the genetic characterization decreases with increasing Ct value, ranging from 100% of success in samples with Ct < 20 to 66.7% in samples with Ct >35 (Table 2).

Table 1. Characteristics of 2015/2016 EuroEVA cases by genetic characterization

	Genetic characterization (-)	Genetic characterization (+)	p
Mean age (years)	49.2	46.0	0.382
Female (%)	35.0	56.5	0.062
Influenza seasonal vaccine (%)	18.2	10.1	0.468

***Notes*:** p - p value

Table 2. *Influenza* A(H1)pdm09 viruses selected for genetic characterization during 2015/2016 season

	n (%)	Ct value <20	Ct value 20-29	Ct value 30-35	Ct value >35
A(H1)pdm09 characterized / Total selected viruses	(93/116)	(6/6)	(60/73)	(23/31)	(4/6)
	80.2%	100.0 %	82.2%	74.2%	66.7%

***Notes*:** Ct value - threshold cycle of Protein Chain Reaction (PCR)

4 Discussion and conclusions

The large sample size needed to estimate IVE against a specific clade requires an important effort on genetic characterization behind virological surveillance.

However, random selection of cases for genetic characterization along season seems to be feasible without interfering with virological surveillance and allows to obtain a representative sample of cases of the clade of interest.

5 Key messages

- Virological data from randomly selected cases will permit to estimate IVE against a specific clade during *Influenza* season.
- An extra effort on influenza genetic characterization is necessary to achieve the needed sample size.

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