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

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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.

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).

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 (68.1 and 68.2).

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

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).

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 supernatant).

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

<table>
<thead>
<tr>
<th>Genetic characterization</th>
<th>Mean age (years)</th>
<th>p</th>
</tr>
</thead>
<tbody>
<tr>
<td>(-)</td>
<td>49.2</td>
<td>0.382</td>
</tr>
<tr>
<td>(+)</td>
<td>46.0</td>
<td></td>
</tr>
</tbody>
</table>

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

<table>
<thead>
<tr>
<th>Ct value</th>
<th>n (%)</th>
<th>&quot;A(H1)pdm09&quot; characterized/Total selected viruses</th>
</tr>
</thead>
<tbody>
<tr>
<td>&lt;20</td>
<td>(93/116) (6/6)</td>
<td>(23/31) (4/6)</td>
</tr>
<tr>
<td>20-29</td>
<td>100.0%</td>
<td>80.2%</td>
</tr>
<tr>
<td>30-35</td>
<td>82.2%</td>
<td>74.2%</td>
</tr>
<tr>
<td>&gt;35</td>
<td>66.7%</td>
<td>74.2%</td>
</tr>
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Notes: Ct value - threshold cycle of Protein Chain Reaction (PCR)

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.

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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