Global and Regional Laboratory Network for Rotavirus Surveillance

Regional Meeting on Sentinel Surveillance of Rotavirus, Bacterial Meningitis and Pneumonia

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Cancun – Mexico, 09 December 2013.
Outline

• Global Rotavirus Laboratory network
• Global Rotavirus Genotypes Identification
• Regional Rotavirus Laboratory Network
• Regional Rotavirus Genotypes identification
• Summary
• Challenges
Global Rotavirus Laboratory network
Component of
WHO Sentinel Hospital VPD Surveillance Networks

Dr. Fatima Serhan
Laboratory Coordinator, New Vaccines Surveillance
IVB department, EPI Unit, WHO HQ
GLOBAL ROTAVIRUS SURVEILLANCE
- COUNTRIES THAT HAVE INTRODUCTED OR PLANNED TO INTRODUCE ROTAVIRUS VACCINE

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153 participating labs: 1 GRL, 9 RRL, 36 NL and 107 SHL
Strategic Review process: Laboratory component

• Laboratory network supporting system in the most effective/efficient manner?
  – Meeting 2008 objectives
  – Technical support provided (Training, lab assessments, lab procedures, SOPs)
  – Genotyping data-global, regional and over time (2009-2012)
  – Quality control and quality assurance
Accomplishments: Laboratory component

- Met the 2008 objectives for
  - presence of disease
  - monitoring disease trends over time
  - genotype distribution
- Excellent technical support and optimization of laboratory procedures
- Technical working group: designation of "common" and "uncommon" strains
- Adequate EQA programme and development of QC programmes
Overarching Issues

- Some Regional variation requires further network cohesion, as feasible
- Limited ability to use data for real time monitoring of site or lab performance
  - lack of case level data in standard format
  - difficulty linking laboratory results with the clinical and epidemiologic data
- Resources needed for network of this size are insufficient and need more strategic allocation
  - Resources for network data management and analysis
  - Reference Lab capacity (tests, site visits) need to match number of sentinel sites supported
Global Rotavirus Genotypes Identification
Global Rotavirus Genotype Distribution by Year, 2009-2012

Note: EMR data excluded for 2009, 2011 and 2012.
Countries included in 2009 – Indonesia, Myanmar, Nepal, Sri Lanka

Countries included in 2010 – Myanmar, Nepal

Countries included in 2011 - Indonesia

Countries included in 2012 - Myanmar, Nepal, Sri Lanka

Updated on 30 Aug 2013
Rotavirus surveillance and vaccine introduction in countries of the Americas

2004 start rotavirus (RV) surveillance in three countries: El Salvador, Paraguay and Venezuela.

2006 seven countries introduce the RV vaccine: BRA, SLV, MEX, NIC, PAN, VEN & USA.

15 countries and 1 territory have implemented the surveillance until 2013.
Regional Rotavirus Laboratory Network
Regional Laboratory Network for Rotavirus Sentinel Surveillance

Technical capacity Implemented
1 GRL with ELISA, RT-PCR, SEQUENCING, other assays & reagents production
1 RRL with ELISA, RT-PCR, SEQUENCING
8 NLs with ELISA & RT-PCR
6 NLs with ELISA

Regional Rotavirus Lab Network
- 14 National Laboratories
- 1 Regional Reference Labs
- 1 Global Reference Lab

Source: FGL/IM
## Sentinel Rotavirus Surveillance
### The Americas Region, 2010 – 2012

<table>
<thead>
<tr>
<th>REGIONAL SENTINEL ROTAVIRUS SURVEILLANCE</th>
<th>2010</th>
<th>2011</th>
<th>2012</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>n</td>
<td>%</td>
<td>n</td>
</tr>
<tr>
<td># hospitalizations in children &lt;5 years</td>
<td>286,557</td>
<td>100.0</td>
<td>333,979</td>
</tr>
<tr>
<td># hospitalizations with diarrhea in children &lt;5 years</td>
<td>35,530</td>
<td>12.4</td>
<td>43,303</td>
</tr>
<tr>
<td># children &lt;5 years who meet criteria for suspected case</td>
<td>20,636</td>
<td>58.1</td>
<td>16,611</td>
</tr>
<tr>
<td># children &lt;5 years with format and specimens collected</td>
<td>15,566</td>
<td>75.4</td>
<td>11,961</td>
</tr>
<tr>
<td># positives specimens for rotavirus in children &lt;5 years</td>
<td>4,575</td>
<td>29.4</td>
<td>3,297</td>
</tr>
<tr>
<td># countries reporting to Vinuva</td>
<td>16</td>
<td>15</td>
<td>15</td>
</tr>
</tbody>
</table>

Source: Country report to PAHO (Vinuva).
Data until 06 December 2013.
Sentinel Rotavirus Surveillance, positivity and % genotyping in one selected LA country, 2007 – 2012

<table>
<thead>
<tr>
<th>REGIONAL SENTINEL ROTAVIRUS SURVEILLANCE</th>
<th>2007</th>
<th>2008</th>
<th>2009</th>
<th>2010</th>
<th>2011</th>
<th>2012</th>
</tr>
</thead>
<tbody>
<tr>
<td># children &lt;5 years who meet criteria for suspected case</td>
<td>3188</td>
<td>1935</td>
<td>1499</td>
<td>2396</td>
<td>2396</td>
<td>5244</td>
</tr>
<tr>
<td># children &lt;5 years with format and specimens collected</td>
<td>2950</td>
<td>1853</td>
<td>1328</td>
<td>2191</td>
<td>2132</td>
<td>2255</td>
</tr>
<tr>
<td># specimens positives for rotavirus in &lt;5 años</td>
<td>1,142</td>
<td>201</td>
<td>344</td>
<td>524</td>
<td>653</td>
<td>543</td>
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<tr>
<td>% specimens RV positives</td>
<td>39</td>
<td>11</td>
<td>26</td>
<td>24</td>
<td>31</td>
<td>24</td>
</tr>
<tr>
<td># specimens genotyped</td>
<td>97</td>
<td>147</td>
<td>125</td>
<td>67</td>
<td>131</td>
<td>117</td>
</tr>
<tr>
<td>% specimens genotyped</td>
<td><strong>8.5</strong></td>
<td><strong>73.1</strong></td>
<td><strong>36.3</strong></td>
<td><strong>12.8</strong></td>
<td><strong>20.1</strong></td>
<td><strong>21.5</strong></td>
</tr>
</tbody>
</table>

Source: Country report to PAHO (Vinuva). Data until 06 December 2013.
Rotavirus genotypes
In one selected LA country, 2007 – 2012

Source: Country report to PAHO (Vinuva).
Data until July 2013.
Workshop on Rotavirus Detection and Genotyping, 2013

Hands on workshop
Recommendations focus on how to improve genotype identification (sample preservation, use of kits for RNA extraction and RT-PCR, use of standardize primers) and QA/QC in the Regional Lab Net
### Regional Rotavirus LabNet, EQAP Pilot 2012

<table>
<thead>
<tr>
<th>LAB</th>
<th>ELISA</th>
<th>GENOTYP</th>
</tr>
</thead>
<tbody>
<tr>
<td>LAB1</td>
<td>87.5%</td>
<td>87.5%</td>
</tr>
<tr>
<td>LAB2</td>
<td>100%</td>
<td>81.2%</td>
</tr>
<tr>
<td>LAB3</td>
<td>100%</td>
<td>87.5%</td>
</tr>
<tr>
<td>LAB4</td>
<td>100%</td>
<td>100%</td>
</tr>
<tr>
<td>Mean</td>
<td>96.7%</td>
<td>89.1%</td>
</tr>
</tbody>
</table>

St Vincent
Regional Rotavirus LabNet, EQAP 2013

Summary PT Panel 2013

<table>
<thead>
<tr>
<th>LABs</th>
<th>ELISA</th>
<th>GENOTYP</th>
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</thead>
<tbody>
<tr>
<td># received</td>
<td>16</td>
<td>8</td>
</tr>
<tr>
<td># answered</td>
<td>14</td>
<td>8</td>
</tr>
<tr>
<td>Score &gt; 80%</td>
<td>14</td>
<td>4</td>
</tr>
<tr>
<td>Mean</td>
<td>97.3%</td>
<td>80.2%</td>
</tr>
</tbody>
</table>

*Note: 5 labs penalized with minus 5 points, for late response.

<table>
<thead>
<tr>
<th>LAB CODE</th>
<th>ELISA</th>
<th>GENOTYP</th>
</tr>
</thead>
<tbody>
<tr>
<td>AMR01*</td>
<td>95</td>
<td>88.8</td>
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<tr>
<td>AMR02*</td>
<td>95</td>
<td>NA</td>
</tr>
<tr>
<td>AMR03</td>
<td>100</td>
<td>87.5</td>
</tr>
<tr>
<td>AMR05*</td>
<td>95</td>
<td>79.4</td>
</tr>
<tr>
<td>AMR06</td>
<td>100</td>
<td>75</td>
</tr>
<tr>
<td>AMR07*</td>
<td>95</td>
<td>NA</td>
</tr>
<tr>
<td>AMR08</td>
<td>100</td>
<td>NA</td>
</tr>
<tr>
<td>AMR09</td>
<td>100</td>
<td>90.6</td>
</tr>
<tr>
<td>AMR10</td>
<td>100</td>
<td>68.8</td>
</tr>
<tr>
<td>AMR11*</td>
<td>95</td>
<td>70</td>
</tr>
<tr>
<td>AMR12</td>
<td>100</td>
<td>81.3</td>
</tr>
<tr>
<td>AMR13</td>
<td>87.5</td>
<td>NA</td>
</tr>
<tr>
<td>AMR14</td>
<td>100</td>
<td>NA</td>
</tr>
<tr>
<td>AMR15</td>
<td>100</td>
<td>NA</td>
</tr>
</tbody>
</table>

Mix! New strains!!
Regional Rotavirus Genotypes Identification
Regional Rotavirus Genotypes in selected LAC countries, pre and post vaccine introduction.

**Castello et al, 2004**

1995-2003

- **G1** P[8] 27%
- **G2** P[4] 20%
- **G3** P[8] 4%
- **G4** [P8] 5%
- **G9** [P8] 7%
- Mix 12%
- **G12** P[8] 2%
- Others 4%
- **NT** 20%

Source: Country report to PAHO

n=1989

2007-2009

- **G1** P[8] 37%
- **G2** P[4] 24%
- **G3** P[8] 7%
- **G4** [P8] 1%
- **G9** [P8] 7%
- Mix 4%
- Others 4%
- **NT** 8%

Source: Country report to PAHO

n=1915

2010-2012

- **G1** P[8] 5%
- **G2** P[4] 31%
- **G3** P[6] 16%
- **G9** P[4] 16%
- **G12** P[8] 11%
- **G12** P[6] 1%
- Others 3%
- **NT** 6%

Source: Country report to PAHO

n=4437

Countries without vaccine

- G1 P[8] 55%
- G9 P[4] 14%
- G4 [P8] 4%
- G3 P[8] 0%
- G2 P[4] 2%
- G12 P[6] 3%
- G9 P[8] 0%
- Mix 4%
- Others 6%
- NT 6%

n=1419

Countries with vaccine

- G1 P[8] 37%
- G2 P[4] 24%
- G9 [P8] 7%
- G1 P[4] 1%
- G12 P[8] 2%
- Mix 4%
- Others 4%
- NT 8%

n=1915

Regional 2007-2009
Regional Rotavirus Genotypes in selected LA countries, Sub-Regional variability, 2010-2012.

2010-2012 Mexico

- **G1 P8**: 41%
- **G2 P4**: 31%
- **G3 P8**: 5%
- **G9 P4**: 4%
- **G12 P8**: 11%
- **Others**: 3%
- **Mix**: 6%
- **NT**: 1%

Central-America

- **G1 P8**: 27%
- **G2 P4**: 21%
- **G3 P8**: 15%
- **G9 P4**: 15%
- **G3 P6**: 6%
- **Others**: 4%
- **Mix**: 3%
- **NT**: 1%

“Regional 2010-2012”

- **G1 P8**: 31%
- **G2 P4**: 16%
- **G3 P8**: 17%
- **G9 P4**: 11%
- **G12 P8**: 9%
- **Others**: 3%
- **Mix**: 3%
- **NT**: 6%

Countries with vaccine introduction
Regional Rotavirus Genotypes in selected LA countries, Sub-Regional variability, 2010-2012.

**Andean**
- G2 P[4] 37%
- G3 P[8] 36%
- G9 P[8] 5%
- Others 6%
- Mix 2%
- NT 1%
- G1 P[8] 8%
- G1 P[6] 1%

**2010-2012 Brasil**
- G2 P[4] 49%
- G3 P[8] 11%
- G9 P[8] 12%
- G3 P[6] 11%
- G12 P[8] 1%
- Mix 1%
- Others 6%
- NT 8%
- G1 P[8] 7%

**“Regional 2010-2012”**
- G3 P[8] 17%
- G2 P[4] 31%
- G9 P[4] 16%
- G12 P[8] 11%
- G4 [P8] 0%
- G9 [P8] 4%
- G1 [P6] 0%
- Mix 3%
- NT 6%
- Others 3%

**Countries with vaccine introduction**

Pan American Health Organization

World Health Organization

Regional office for the Americas
Regional Rotavirus Genotypes in selected LA countries, Regional annual variability, 2010-2012.

Source: Countries with vaccine introduction that report to PAHO

2010
- G9 P[4] 38%
- G2 P[4] 36%
- G1 P[8] 6%
- Others 2%
- Mix 4%
- G12 P[8] 0%
- G3 P[6] 1%
- G9 P[8] 0%
- G4 P[8] 0%
- NT 5%

2011
- G2 P[4] 34%
- G9 P[4] 31%
- G4 [P8] 31%
- Mix 1%
- NT 7%
- Others 3%
- G3 P[6] 8%
- G1 P[6] 5%
- G9 [P8] 6%
- G1 P[6] 6%
- G3 P[6] 5%
- G9 P[4] 8%
- G12 P[8] 31%
- Others 3%
- Mix 1%
- NT 3%

2012
- G3 P[8] 31%
- G1 P[8] 24%
- G2 P[4] 16%
- Mix 3%
- NT 6%
- Others 4%
- G1 P[6] 6%
- G4 [P8] 6%
- G9 [P8] 4%
- G9 P[4] 3%
- G3 P[6] 6%
- G12 P[8] 31%

n=1470
n=1367
n=1600
Regional Rotavirus Genotypes in selected Caribbean countries, 2004-2012.

<table>
<thead>
<tr>
<th>Year</th>
<th>Genotype</th>
<th>G1</th>
<th>G2</th>
<th>G3</th>
<th>G4</th>
<th>G8</th>
<th>G9</th>
<th>G12</th>
<th>Mix</th>
<th>NT</th>
</tr>
</thead>
<tbody>
<tr>
<td>2004-2006</td>
<td></td>
<td>18%</td>
<td>1%</td>
<td>1%</td>
<td>3%</td>
<td>18%</td>
<td>15%</td>
<td>15%</td>
<td>1%</td>
<td>2%</td>
</tr>
<tr>
<td>2007-2009</td>
<td></td>
<td>69%</td>
<td>2%</td>
<td>41%</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
</tr>
<tr>
<td>2010-2012</td>
<td></td>
<td>8%</td>
<td>1%</td>
<td>17%</td>
<td>8%</td>
<td>41%</td>
<td>19%</td>
<td>8%</td>
<td>1%</td>
<td>3%</td>
</tr>
</tbody>
</table>

Source: CARPHA report to PAHO
Summary

• The Regional Laboratory Network is being strengthened, building capacity and improving the QA/QC
• Rotavirus genotypes data have been improve in some LAC countries
• Different genotypes distribution and annual variability have been identified at Regional, SubRegional and country level
• The genotypes distribution is changing in most of the countries (with or without vaccine introduction)
• Data limitations: genotypes not linked to age, sex, origin and onset
Challenges

• Integrate laboratory data with clinical and epi data
• Follow up the implementation of recommendations of the workshop held in RJ 2013
• Improve the report of genotype data systematically (twice a year) to MoH and PAHO
• Incorporate the SAGE and TWG recommendations in the Regional Rotavirus Lab Network
• Resources available to support the Regional LabNet that permit continue building capacity
Strategic Review recommendations:
SAGE endorsed

• **Network technically strong** (TWG, RLs, etc.); need to consider how to bring further 'cohesion' to the network, while maintaining needed Regional individuality

• **Use data for real time monitoring**
  – Monitoring of reagents, site or lab performance
  – Requires link laboratory results with clinical - epi data on the same patient
  – Consider linking case-based data to genotype data

• **Genotyping:**
  – Report genotype data 2x per year
  – Standardize sample selection for genotyping
  – Examine country-level genotype distribution
Acknowledgements

• WHO-HQ, Fatima Serhan & Mary Agocs
• CDC, Jon Gentsch & Mike Bowen
• FIOCRUZ, Jose P. Leite et al.
• National Rotavirus Laboratories
• Hospital Sentinel Laboratories
• PAHO FGL/IM, Lúcia de Oliveira
# Rotavirus genotyping report

## Did the country use rotavirus vaccine in its national immunization programme during this reporting period?

<table>
<thead>
<tr>
<th>Name of RRL</th>
<th>No. of rotavirus positive specimens sent to RRL for typing this reporting period</th>
<th>No. (%) of rotavirus positive (ELISA confirmed) specimens sent to RRL that are confirmed to be positive by the RRL</th>
<th>Strain characterization technique used in RRL</th>
<th>No. (%) of genotype results reported back to the country/site within 6 months</th>
<th>Genotyping Additional Results:</th>
<th>Sequencing Results:</th>
</tr>
</thead>
<tbody>
<tr>
<td>Yes / No</td>
<td>No.</td>
<td>%</td>
<td>No.</td>
<td>%</td>
<td>mixed</td>
<td>untypeable</td>
</tr>
</tbody>
</table>

* Please specify mixed infection by entering data such as G1G2 or P[4]P[8]

## Genotype Results

Please enter the total number of genotype found in the table below. Feel free to add as many columns and rows as necessary.

<table>
<thead>
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<tbody>
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<td>G1</td>
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