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Respiratory virus genomic quantification usefulness in surveillance influenza (flu) season

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Background: Surveillance Influenza season is the highest period of both child and adult respiratory circulation virus detection. Thus genomic quantification allows diagnose the respiratory disease causal virus.

Material/methods: From September-2015 to March-2016, 5369 respiratory samples were recluted: 2969 from children(3.3±3.2 years), and 2370 from adults(58.3±24.5 years)(age of 30 patients was unknown) showing respiratory signs. Samples were processed according to the laboratory protocols: immunofluorescence, cell-cultures, and genomic detection. Genomic extraction was performed by Magnapure/Ampliprep systems(Roche). From the genomic quantification, multiple Real-Time PCR were performed for virus: Influenza A(IA), Influenza B(IB), Respiratory syncytial virus(RSV)/Enterovirus(ETV), Human parainfluenza viruses(HPIVs), Metapneumovirus(MPVh)/Rhinovirus, Adenovirus(ADV) and Coronavirus(CoV). After standarized Betaglobin Ct and Respiratory Virus Ct with both known human cells and betaglobin copies numbers, and known copies respiratory virus and cycles of viruses, we compared them with the corresponding virus to genomic quantification. Thus genomic quantification was measured in copies/10^3cells.

Results: 3478(64.7%)samples were positive: 2320(78.1%)from childrens and 1137(48%)from adults(age of 22 patients was unknown). The distribution of the virus detected in children was: 584(19.7%)ADV, 524(17.6%)RSV, 367(12.3%)IA, 286(9.6%)ETV, 242(8.1%)IB, 157(5.3%)Rhinovirus, 119(4%)CoV, 41(1.4%)MPVh, 32(1.1%)HPIVs and in adults was: 489(20.6%)IA, 204(8.6%)VRS, 131(5.5%)ADV, 97(4.1%)IB, 94(3.4%)CoV, 54(2.3%)Rhinovirus, 50(2.1%)ETV, 189(0.8%)MPVh and 15(0.6%)HPIVs.

Double-virus infections were detected in 450 cases, and 17 triple-virus. Most frequent co-infections were: ADV(238), RSV(216), ETV(128), IA(89), CoV(83), IB(53), Rhinovirus(56), MPVh(21) and

HPIVs(19)(Table1). Implicated virus quantifications are showed in Table I. Among the 450 double virus infections, 396(88%) of them were due to only one of the detected virus, according to the viral load. The genomic quantification of the virus responsible for the infection was on average 3.1log/10^3cells greater than the other/s virus/es detected. All triple virus detection was attributed to only one virus by genomic quantification overload. A quantification of <500 copies/10^3cells for the two virus was obtained in 52 samples, and in 6 samples the same quantification was detected.

Table1. Co-infections and quantification overload from implicated virus.

	IA	IB	CoV	ETV	MPVh	HPIVs	Rhino	RSV	ADV
IA	**52/89**	4/14	1/3	3/7	0/1	0/1	0/3	33/40	11/20
IB	4/14	**18/52**	2/3	0/6				4/10	8/21
CoV	1/3	0/3	**24/83**	1/9	3/10	1/2	0/3	7/14	11/39
ETV	3/7	6/6	7/9	**84/128**		2/2	9/12	28/47	29/45
MPVh	1/1		5/10		**14/21**	1/1		1/2	6/7
HPIVs	1/1		0/2	0/2	0/1	**8/19**	1/2	3/4	3/7
Rhino	3/3		2/3	2/12		1/2	**32/56**	11/18	13/18
RSV	5/40	5/10	4/14	19/47	0/2	1/4	6/18	**66/216**	26/81
ADV	6/20	9/21	22/39	15/45	1/7	4/7	3/18	38/81	**98/238**

*etiological virus due to greater viral load/number of cases in which virus was detected.

Conclusions: -Quantification of betaglobin has an essential role in the virus quantification of heterogeneous respiratory samples, which allows the etiologic diagnostic of respiratory infections.

-ADV and VRS were more frecuent in children and IA was more frecuent in adults.