ERRATUM

Erratum to: A confirmation of sapovirus re-infection gastroenteritis cases with different genogroups and genetic shifts in the evolving sapovirus genotypes, 2002-2011

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In the original publication, the text on page 2002 in print and online version should be replaced with the following text:
The 139 SaV strains detected from 2002 to 2011 were classified into four genogroups and 11 genotypes: GI.1 ($n = 29$), GI.2 ($n = 3$), GI.3 ($n = 2$), GI.5 ($n = 4$), GII.1 ($n = 9$), GII.2 ($n = 4$), GII.3 ($n = 29$), GII.4 ($n = 1$), GII.7 ($n = 1$), GIV ($n = 51$) and GV ($n = 6$) (Table 2).

Furthermore, Table 2 was incorrectly published and the correct version is given below:

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Table 2 Sapovirus genotypes in gastroenteritis outpatients at three pediatric clinics in the same area between June 2002 and March 2011

	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec	Total number of SaV cases in each year
2002	NA	NA	NA	NA	NA							GI.1 (2)	2
2003		GI.1 (1) GII.1 (1) GII.2 (1)	GII.4 (1)	GII.2 (1)								GII.3 (2)	7
2004						GV (1)						GV (1)	2
2005	GI.1 (1)										GI.1 (1) GI.5 (1)	GI.1 (1) GI.5 (3)	7
2006									GI.1 (1)		GI.1 (1) GV (1)	GI.1 (3) GII.1 (3) GII.2 (1)	10
2007	GI.1 (2)								GIV(1)	GIV(11)	GIV (29)	GIV (10)	53
2008		**GII.7 (1)**		**GII.3 (1)** **GV (1)**	**GII.3 (2)**	**GII.3 (1)**				**GII.3 (1)**	**GII.3 (3)**	**GII.3 (1)**	**11**
2009	**GI.1 (1)** **GII.1 (1)** **GII.3 (1)**	**GI.1 (3)** **GI.3 (2)**	**GII.3 (6)**	**GI.1 (1)** **GII.3 (2)**	**GII.3 (1)**					**GII.3 (3)**	**GII.3 (1)**		**22**
2010		**GI.1 (1)**	**GI.1 (4)**	**GI.1 (4)** **GII.3 (1)**	**GI.2 (3)**	**GI.1 (1)** **GII.1 (1)**	**GII.2 (1)**				**GII.3 (2)**	**GI.1 (1)** **GII.1 (1)** **GII.3 (1)** **GV (1)**	**22**
2011			**GII.1 (2)** **GV (1)**	NA	NA	NA	NA	NA	NA	NA	NA	NA	**3**
Total numbers of SaV in each month	6	10	14	11	6	4	1	0	2	15	39	31	139

The 58 strains detected from 2008 to 2011 are indicated in bold

Nucleotide sequences for the 81 SaV strains detected from 2002 to 2007 were deposited in GenBank/EMBL/DDBJ under accession numbers AB429079-AB429159 [ref 8]

Nucleotide sequences for the 58 SaV strains detected from 2008 to 2011 were deposited in GenBank/EMBL/DDBJ under accession numbers AB689798-AB689855

Genotype numbers are according to the classification scheme by Oka et al. [ref 18]

The numbers detected are indicated in parentheses

NA: no samples were available