

Molecular evolutionary dynamics of respiratory syncytial virus group A in recurrent epidemics in coastal Kenya

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Table S1: Frequency of IFAT and PCR diagnosed RSV cases and number sequenced over 13 successive epidemics at Kilifi, Kenya.

Epidemic Season	Number of RSV Positive samples	Number (%) of RSV A samples	Number (%) of RSV-A samples Sequenced*	Number (%) of RSV-B samples	Number (%) of RSV A+B samples	Number (%) of unique Sequences*
2012 - 2013	152	110 (72.4)	53 (48.1)	27 (17.8)	3 (2)	22 (41.5)
2011 - 2012	161	55 (34.2)	52 (94.5)	102 (63.4)	2 (1.2)	26 (50.0)
2010 - 2011	279	241 (86.4)	158 (65.6)	21 (7.5)	7 (2.5)	72 (45.6)
2009 - 2010	259	120 (46.3)	88 (73.3)	95 (36.7)	9 (3.5)	33 (37.5)
2008 - 2009	208	154 (74)	47 (30.5)	41 (19.7)	0 (0)	29 (61.7)
2007 - 2008	256	33 (12.9)	20 (60.6)	197 (77)	3 (1.2)	14 (70.0)
2006 - 2007	195	153 (78.5)	81 (52.9)	22 (11.3)	1 (.5)	32 (39.5)
2005 - 2006	239	224 (93.7)	56 (25.0)	9 (3.8)	0 (0)	21 (37.5)
2004 - 2005	183	46 (25.1)	11 (23.9)	119 (65)	3 (1.6)	5 (45.5)
2003 - 2004	114	68 (59.6)	7 (10.3)	16 (14)	0 (0)	6 (85.7)
2002 - 2003	89	42 (47.2)	25 [#]	35 (39.3)	0 (0)	8 (32.0)

2000 - 2001	N/A	N/A	19 ^o	N/A	N/A	10 (52.6)
Total	2135	1246 (58.4)	658 (46)^r	684 (32.0)	28 (1.3)	293 (44.5)

• An epidemic season defined by the time period between September of one year to August of the following year.

Highlighted in grey are the RSV-A dominated epidemics. However, we do not know for 2000-2001 and 2001-2002 which group was dominant as full surveillance was not established.

* Number sequenced as a percentage of those typed to be RSV-A.

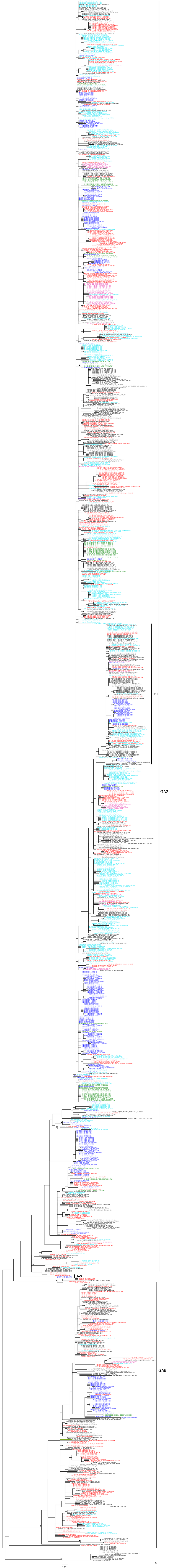
^o Unique sequences defined as sequences that differ by at least one nucleotide.

^o Percentage indeterminable as we don't have data on number of diagnosed RSV cases at the hospital during this time.

Percentage indeterminable as we only have sequences from a birth cohort in this epidemic and not the inpatient surveillance sequences.

^r The total number of RSV-A sequenced includes 633 sequences from inpatient and outpatient RSV surveillance period (2000-2012), and 25 Kilifi Birth Cohort sequences for the 2002/2003 epidemic, i.e. $633 + 25 = 658$, while the percentage is based only on the inpatient surveillance $573/1246$.

Fig. S1: Phylogenetic placement of RSV-A viruses from Kilifi, Kenya, in the global context. This is a global Maximum Likelihood phylogenetic tree of 1,415 unique RSV-A sequences from 29 countries collected between 2000 and 2012. The taxon names for Kilifi sequences ($n=284$) are in blue while the rest of Kenya ($n=56$) in green. Sequences from other countries are colour-coded as follows: Red (Europe), Cyan (Asia and Australia), Black (Americas) and Pink (Africa excluding Kenya). Branches with bootstrap values $>60\%$ are shown with a star (★).



ON1

GA2

GA5

0.005

12