

**Correspondence**

To the Editors

**Molecular genetic surveillance of important infectious disease and calculation for mutation rate: a simple but not-to-be-forgotten error regarding accumulation effect**

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Dear Editors,

There are several important infectious diseases at present. In clinical paediatrics, mutation of the pathogens is reported worldwide and might be associated with change of the natural history of disease. The molecular genetic surveillance of important infectious diseases is a contemporary practice for monitoring of pathogen resistance and evolution such as surveillance of vaccine escape mutant<sup>1</sup> or new mutated viral pathogenic strain<sup>2</sup>. Additionally, the same concept can be applied for monitoring of genetic disorder such inborn error of metabolism<sup>3</sup>. For surveillance during a certain period, the derived data will include overall number of mutants during that period. A common value that is a determinant for magnitude of mutation is mutation rate. Briefly, it is generally calculated by “overall all number of mutants during observation period/period of time”. However, this calculation can give an estimate but not an accurate rate. A common forgotten error by non-epidemiologist expert is the accumulation effect. This is the same case as a summation of deposited money in a bank. There is a fixed interest rate and if the period is more than 1 year, there will be compound interest. This concept is the same for calculation of the mutation rate. Effect of accumulation or compound interest should not be overlooked.

For example, in a setting, monitoring of mutant of pathogen for hand food and mouth syndrome is done. Based on 10-year period data, there are overall 100 detected mutants giving a crude number of mutation equalling 10/year. If we use a rough estimation, the % mutation rate will be 10% (which is from 10/100). However, if accumulation effect is considered, there will be a big error, up to 47.1% (Table 1). (If we use a programme for calculation correct % mutation rate will be

7.4918%). Hence, the estimated rate in % will give a big error. This is a basic easily forgotten concept in epidemiological interpretation of mutation surveillance, which is a common activity during pandemic crises.

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**Table 1: Estimated number of mutants at each year with and without accumulation effect, giving fax rate increasing 10%**

Year	Without accumulation effect		With accumulation effect	
	Background sum	New mutants	Background sum	New mutants
0	0	0	0	0
1	10	10	10	10
2	20	10	20.1	10.1
3	30	10	31.21	11.11
4	40	10	43.43	12.22
5	50	10	56.87	13.44
6	60	10	71.66	14.79
7	70	10	87.93	16.27
8	80	10	105.82	17.89
9	90	10	125.50	19.68
10	100	10	147.15	21.65
Total	100	100	147	147