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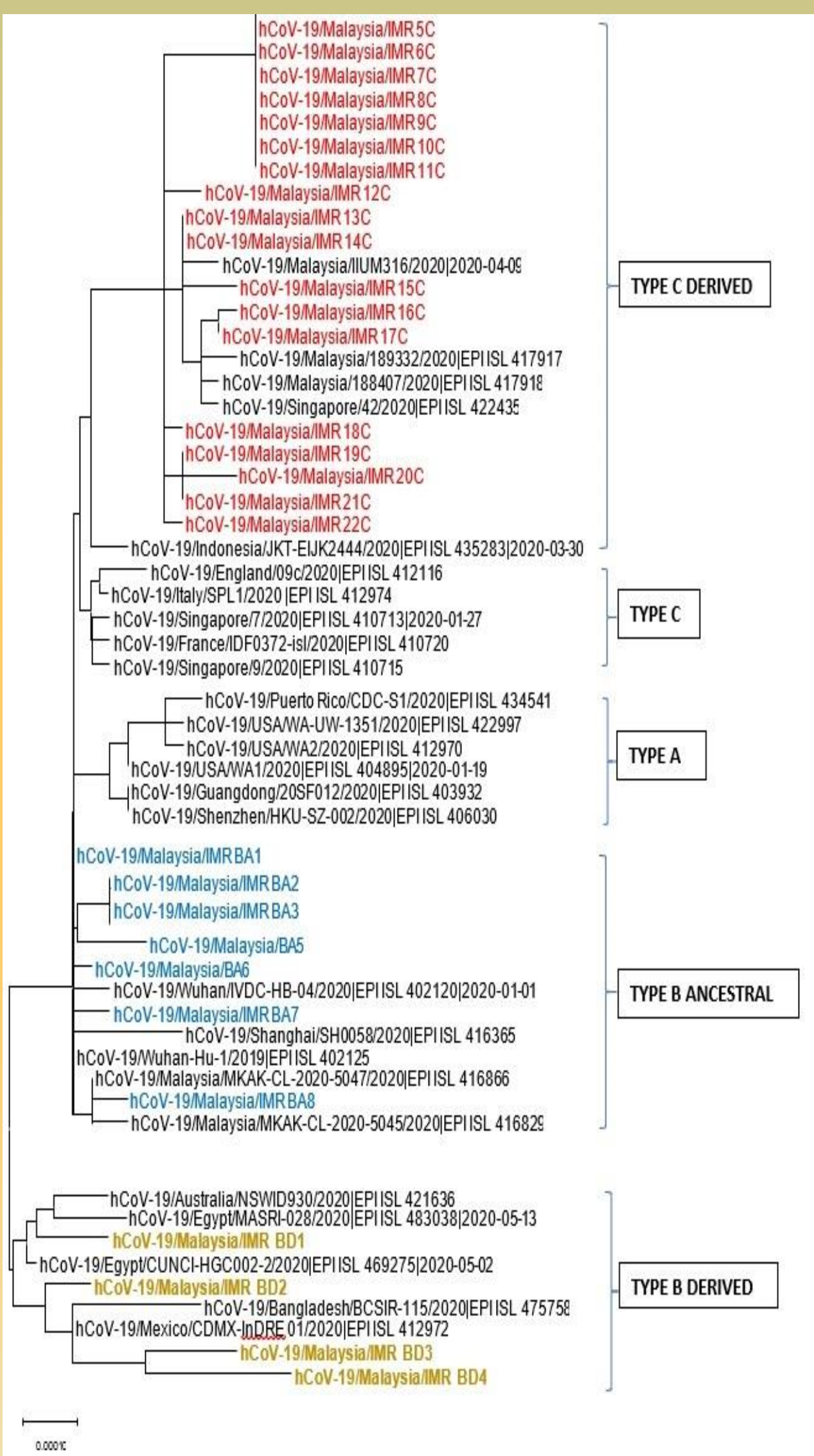
INTRODUCTION

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) was identified as an aetiology agent of clustered cases of pneumonia in Wuhan, China and the disease is called Coronavirus Disease (COVID-19). The COVID-19 outbreak in Malaysia is categorized according to clusters. However, information on the genomic nature and diversity of the circulating strains is sparsely available. Hence, the study was aimed to characterize the virus and identify mutations.

METHODOLOGY

SARS-CoV-2 viral RNA was extracted from isolates and original specimen and subjected to next generation sequencing on Illumina NextSeq 500 platform. Full genome sequences were obtained by assembling against reference genomes using BBDuk and MEGAHIT softwares. Phylogenetic tree was constructed using Neighbour-joining & Tamura-Nei model and mutations were identified via MEGA X alignment.

RESULTS & DISCUSSION



1 Variation in type

- 3 types of circulating Malaysian SARS-CoV-2: TYPE B ancestral, TYPE B derived and TYPE C derived.
- Note: 36 full genomes of SARS-CoV-2 (~29000 bp length) were sequenced and only representative sequences are included in the phylogenetic tree in colored fonts.

2 Early & current strains

- Early strains : Type B ancestral, closely related to Wuhan strains.
- Current strains: Type C derived.
- Imported strains : Type B derived.

3 Comparison by clusters

- Tabligh cluster marked the point where type C-derived emerged.
- Depot immigration cluster was closely related to local strains in the C-derived type indicating acquired infection from local transmission, seems to be rooted out from the tabligh cluster.
- Imported strains were closely related to global strains.

4 Mutations summary

- 23 active mutations in ORF1AB, 4 mutations in ORF3A, 4 mutations in Spike gene, 3 mutations in Membrane gene, 3 mutations in Nucleocapsid.
- E gene is highly conserved with no mutations found, a good target for diagnostic tool.

5 Unique mutations

- Evident in the TABLIGH and DEPOT IMMIGRATION clusters

6 Virulent mutations

- Example: D614G (spike protein), Q57H (Orf3a), G204R and R203K (N gene).
- Found among imported cases

CONCLUSION

Genomic diversity of the Malaysian SARS-CoV-2 is apparent through the circulating type and unique mutations. Comparison of early outbreak and current strains have shown a shift from type B to C. Unique mutations identified exclusively among Malaysian SARS-CoV-2 is indicative of rapidly evolving virus. This could pose a challenge in vaccine development. Characterization of the SARS-CoV-2 virus by molecular epidemiology carries significant information for preventive measures, diagnosis, and therapy of infectious diseases.

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