

Systematically mapping clinical features of infections with classical endemic human coronaviruses

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Dear editor,

The classical endemic human coronaviruses including HKU1, OC43, NL63 and 229E are widely circulating among the global population. However, research on these coronaviruses has been largely neglected, until the recent outbreak of SARS-CoV-2 that caused COVID-19 pandemic. Emerging evidence indicates cross-reactive immunity towards SARS-CoV-2 by pre-exposure of endemic coronaviruses, which may induce possible protective effects but could also interfere with serological diagnosis of COVID-19 [1]. Therefore, several recent studies have investigated the prevalence of these endemic coronaviruses [2-4]. In line with these studies, Cummings et al [5] found that 8% of healthcare personnel were infected with endemic coronavirus, and they further investigated risk factors of the infection. However, little efforts have been dedicated to understand their clinical features. Such knowledge is essentially required for assessing the burden of endemic coronavirus infection *per se*, but also for better understanding the implications in COVID-19 pandemic.

In this study, we performed a systematic review and meta-analysis to comprehensively characterize the epidemiology and clinical features of endemic coronavirus infection (supplementary data). From 3225 searched records, we identified 157 eligible studies originated from 44 countries/territories across six continents. Among the reported 282162 outpatient clinic or hospitalized patients with respiratory symptoms, OC43 was estimated as the most prevalent genotype (2.40%, 95% CI 2.15-2.66%, $I^2=95\%$), followed by NL63 (1.60%, 95% CI 1.39-1.82%, $I^2= 95\%$), HKU1 (1.04%, 95% CI 0.85-1.25%, $I^2= 94\%$) and 229E (0.97%, 95% CI 0.82-1.15%, $I^2= 95\%$) (Figure 1A, supplementary data). Interestingly, the young children group with 0-9 years

old has the highest infection rate of 4.71% (95% CI 3.89-5.60%; $I^2=94%$), as compared to 0.94% and 2.35% in two older age groups (Figure 1B, supplementary data). This appears in line with the findings of Cummings et al [5] that younger healthcare personnel, those who saw pediatric patients and those with household members under the age of five are at increased risk of infection.

In total, 18 types of clinical symptoms and features have been identified among endemic coronavirus confirmed patients by pooling all the studies irrespective of the genotypes or possible co-infection with multiple genotypes. Fever, cough, rhinorrhea, sore throat and headache commonly occurred in over half of the confirmed patients. Diarrhea was reported in about 5% of patients. Unexpectedly, over 25% patients developed pneumonia potentially resulting in serious complications, although the severity of pneumonia was not specified in these studies (Figure 1C). We further stratified patients with mono-infection of 229E, HKU1, NL63 or OC43, and characterized their clinical symptoms and features respectively (Figure 1D). Strikingly, pneumonia was reported in over 40% patients with NL63 or OC43 infection, although the included patient number is small (supplementary data).

In summary, this study comprehensively characterized the clinical features of endemic coronavirus infection. Despite the intrinsic limitations of retrospective meta-analysis with potential selection and publication bias, our findings suggest that endemic coronavirus can impose substantial clinical burden in a subset of patients, which deserves more attention.

NOTES

Authors contributions

P.L., M.P.P., Z.M. and Q.P. conceived the idea and interpreted data. P.L., A.I. and Q.P. conducted data analysis. P.L. wrote the manuscript. Q.P. critically revised the manuscript.

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Conflict of interest

All the authors declare that they have no conflict of interest.

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Figure legend

Figure 1. (A) The estimated global prevalence of four endemic coronaviruses including OC43, NL63, HKU1 and 229E. (B) Forest plot of subgroups. (Note: country classification is based on development levels). (C) Forest plot of overall clinical characteristics in endemic coronavirus confirmed patients. (D) Forest plot of clinical characteristics in patients with mono-infection of an individual genotype of endemic coronavirus.

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Figure 1

