Weissbrich and colleagues present the first molecular epidemiology study of the newly identified human bocavirus (HBoV), from Germany. This is an important and well-written study demonstrating the worldwide distribution of HBoV, and highlighting the high degree of co-detections made in subjects infected with HBoV. The study wisely chooses a paediatric population, the most common group to be infected by respiratory viruses, and examines them with a sensitive PCR method, over several seasons.

Major Compulsory Revisions (that the author must respond to before a decision on publication can be reached)

_% in Abstract does not match value in Table 1.
_Could the authors comment in the literature on the impact of an absence of human rhinovirus and coronavirus testing data on the number of co-detections?
_Pg8,Para3. Seasonal differences of sample acquisition may account for higher prevalence values, but the authors should provide a detailed breakdown of their own seasonal data to confirm this. Do published, seasonal studies produce similar prevalence values? It seems as though this study has higher values in every sampling presented in Table 2.
_Pg7,Para1. Does the sequencing of the highly conserved NP-1 region, which yielded only 1 difference per 100nt, actually confirm that the amplicon does not result from false-positive amplification? A comment to this end should be added in the text as well as statement of how much of the amplicon was actually sequenced. Alternatively the authors could remove the suggestion that sequencing this amplicon was a diagnostic method to confirm all positives were due to true amplification from the clinical specimen rather than amplification of contaminating DNA (Pg4, Para4).

Minor Essential Revisions (such as missing labels on figures, or the wrong use of a term, which the author can be trusted to correct)

Pg3,Para1, "HKU" = HKU1.
_Pg6,Para2. % for 357 NPA samples differs from value in Table 1
_Inconsistent use of numbers, percentages and numbers followed by percentages in brackets
_Pg8,Para1. Could the authors comment on the possibility that antigen-based diagnostic methods used for the other respiratory viruses may have falsely lowered their prevalence values compared to the sensitive PCR method used for HBoV?
_Because this is a newly identified virus, it is important to ensure that all the HBoV reference are present in the reference section. Please update.
_Table 1. Spell out "Adeno". Comma in "Males" column, 59.8%.
_Pg8,Para1. "parainfluenzae".
_Table 4. How many of the clinical diagnoses can be associated with sole infection by HBoV? This may help determine its clinical impact.
_Table 2. It would be helpful for international readers if a "season" column was added.

Figure 1. It may be helpful to express the number of detections as a percentage (rather than/as well as, an absolute number) of specimens tested each month.

What next?: Accept without revision

Level of interest: An article of importance in its field

Quality of written English: Acceptable

Statistical review: No

Declaration of competing interests:

I declare that I have no competing interest