

human conflicts. We must empower the responsible authorities in such regions to establish proper locust monitoring and to implement environmentally friendly locust control in core areas of new locust outbreaks. Success will require ensuring that equipment remains functional and finding a way to access unsafe areas.

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## Appropriate names for COVID-19 variants

Multiple severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) variants are now circulating globally. Those with mutations in functional domains such as the receptor binding domain of the spike protein are of particular concern (1). In December 2020, three new variants of concern (VOC) with a common mutation at position 501 in the spike protein were reported: VOC-202012/01 (B.1.1.7, 501Y.V1, 20I) (2) was first identified in the United Kingdom, 501Y.V2 (B.1.351, 20H) (1) was first described by South African researchers, and P.1 (501Y.V3, 20J) was first identified in Japan and described by Brazilian researchers (3). Unfortunately, variants are widely being referred to by their country of first description. This naming convention should be avoided.

Using geographical regions to distinguish variants is harmful, as demonstrated by the term "China" virus, which has been used to blame and stigmatize China. The connotation that the variants were created and spread by their

respective first locations has already generated political backlash through travel bans [e.g., (4)] and negative perceptions of these countries and their people. The risk of being associated with a new variant also disincentivizes country-level genomic surveillance and transparent reporting of their results.

The descriptions are also inaccurate. It is not known whether patient zero of each variant was a resident of or visitor to that country, and all variants have been identified well beyond the first countries in which they were identified (5). Variants that are more transmissible quickly become the dominant circulating variant in many countries, just like the D614G variant that rapidly became the dominant global variant early in the COVID-19 pandemic (6).

Admittedly, mutation-based or lineage names are difficult to say and write. The World Health Organization is expected to announce a standard nomenclature soon (7). Until then, scientific and media reports should not refer to variants by country names.

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