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Recommendations for genetic variation data capture in developing countries to ensure a comprehensive worldwide data collection.

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Source

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Abstract

Developing countries have significantly contributed to the elucidation of the **genetic** basis of both common and rare disorders, providing an invaluable resource of cases due to large family sizes, consanguinity, and potential founder effects. Moreover, the recognized depth of genomic **variation** in indigenous African populations, reflecting the ancient origins of humanity on the African continent, and the effect of selection pressures on the genome, will be valuable in understanding the range of both pathological and nonpathological variations. The involvement of these populations in accurately documenting the extant **genetic** heterogeneity is more than essential. Developing nations are regarded as key contributors to the Human Variome Project (HVP; http://www.humanvariomeproject.org), a major effort to systematically collect mutations that contribute to or cause human disease and create a cyber infrastructure to tie databases together. However, biomedical research has not been the primary focus in these countries even though such activities are likely to produce economic and health benefits for all. Here, we propose several **recommendations** and guidelines to facilitate participation of developing countries in **genetic variation data** documentation, ensuring an accurate and comprehensive worldwide **data** collection. We also summarize a few well-coordinated **genetic data** collection initiatives that would serve as paradigms for similar projects