Feasibility Study of Molecular Profiling of Gastric Cancer Specimens From Rwanda

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Background: Gastric cancer is associated with high mortality in Rwanda. Geographic or genetic differences may lead to variations in somatic mutations and novel therapies. Overseas collaboration to determine gastric cancer molecular profiles is paramount. We undertook this work to determine the feasibility of collaboration between researchers in Rwanda and the United States by creating a research platform for gastric and other cancers in Rwanda.

Methods: Patients consented for biopsy. Cases that were confirmed as gastric adenocarcinoma were included. Formalin-fixed paraffin-embedded tissue blocks or eight unstained sections (4 μm) were transported to the United States. DNA extraction and library preparation was performed by using 50 ng gDNA. Samples were normalized, pooled, and sequenced by using the Pillar NGS SLIMamp Lung Hot Spot Panel (Pillar Biosciences, Natick, MA). FASTq files were uploaded to Pillar Biosciences to perform sequence alignment, annotation, and variant classification.

Results: Fifty-seven samples were received and 35 were excluded because of low DNA yield or quality (18 and 17, respectively). Mutations were detected in nine (41%) of 22 samples. One sample contained three mutations, other cases had one to two mutations identified. In total, 12 mutations were identified: TP53 (four), SMAD4 (two), ERBB4 (two; S341L and D228N), PTEN (two; K267RfsTer9 and C136Y), FBXW7 (one), and KRAS (one).

Conclusion: Overseas collaboration for the molecular profiling of gastric cancer samples is feasible. Quality improved with larger biopsies or tissue blocks. Frequency of mutations is lower than expected. ERBB4 mutations identified are not known to be pathogenic. PTEN mutations are considered pathogenic—a potential target for therapy in larger trials. A larger fusion panel may be more effective in identifying potential targets.

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