**Phenotypic and Genotypic Features of von Willebrand Disease in Hong Kong**

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# Abstract

**Background**: While the molecular pathogenesis of von Willebrand disease (VWD) is well-studied, the genetic landscape of VWD in the Hong Kong population is less clear.

**Methods**: 71 patients from 64 families were enrolled. A multitude of VWF assays were performed. While whole exome sequencing was performed for the newly recruited patients, previous genetic data generated by targeted NGS gene panels or Sanger sequencing were also included for analysis.

**Results**: Majority of the patients had either type 1 VWD / low VWF (41%), or type 2 VWD (52%). 45 *VWF* variants, including seven novel variants, were detected in 41 patients. Three novel variants, namely *VWF* p.C1165Y, p.L1384P and p.A1461T, were classified as likely pathogenic for type 2 VWD. Type 2 VWD showed good genotype-phenotype correlation, but the correlation in type 1 VWD was less clear. Negative *VWF* genotyping results provided diagnostic clues to alternative diagnoses including haemophilia A and acquired von Willebrand syndrome. Some issues regarding the phenotypic and genotypic diagnosis of VWD were observed.

**Conclusion**: The phenotypes of the Hong Kong patients with novel variants may provide insights into the complex pathogenesis of VWD. Moreover, the role of genetic tests in enabling correct diagnosis in a simplified manner is highlighted.