Gait Variability correlates with p-SP1<sup>453</sup> Expression in the Motor Cortex in Experimental Subarachnoid Hemorrhage

Zhi Yuan ZHENG, PhD<sup>1*</sup>, Gang LU, MD<sup>2*</sup>, Zhi Qiang XIONG<sup>1</sup>, Chi Kwan LEUNG, PhD<sup>2</sup>, Xian Wei SU, PhD<sup>2</sup>, Tu LI<sup>2</sup>, Wai Sang POON, MD<sup>1</sup>, Wai Yee CHAN, PhD<sup>2</sup>, and George Kwok Chu WONG, MD<sup>1#</sup>

1. Division of Neurosurgery, Department of Surgery, Prince of Wales Hospital, The Chinese University of Hong Kong, Hong Kong, China
2. CUHK-SDU Joint Laboratory on Reproductive Genetics, School of Biomedical Sciences, the Chinese University of Hong Kong, Hong Kong, China
3. Bioinformatics Unit, SDIVF R&D Centre, Hong Kong Science and Technology Parks, Hong Kong, China

Object: Gait variability analysis has been adopted in clinical settings to characterize the presentation of various neurological diseases. However, literature and practice lack a comprehensive murine model assessment of the gait deficits that result from subarachnoid hemorrhage (SAH). Further, correlations between gait parameters and the gene expression profiles associated with SAH have yet to be identified. The present study quantitatively assesses gait deficits through a clinically relevant murine model of SAH to determine associations between gait deficits and SAH-related gene expressions.

Methods: A total of 159 dynamic and static gait parameters from the endovascular perforation murine model for simulating clinical human SAH were measured using the CatWalk system. Pearson’s correlation analysis was applied, and 88 genes associated with SAH were identified from the Ingenuity Pathway Analysis database to aid the investigation of the relationship between gait variability and gene expression profiles.

Results: Eighty gait parameters and the mRNA expression levels of 35 of the 88 SAH-associated genes exhibited significant change in the SAH models (p < 0.05). Totals of 42 and 38 gait parameters correlated with the 35 SAH-associated genes positively and negatively with Pearson’s correlation coefficients of > 0.7 and < -0.7, respectively. p-SP1<sup>453</sup> expression in the motor cortex in SAH animal models displays a significant correlation with a subset of gait parameters associated with muscular strength and coordination of limb movements.

Conclusion: This examination of gait variability and its strong correlation to gene expression profiles provides a quantitative and reliable assessment of the SAH model’s motor performance. This research provides valuable insights into the study of disease progression and offers novel therapeutic interventions in the murine modeling of SAH. p-SP1<sup>453</sup> expression could act as a biomarker to monitor SAH pathological development and a therapeutic target for SAH.

Keyword: Gait variability, subarachnoid hemorrhage, stroke, CatWalk, SP1