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Ye-Hui Lv, Jian-Long Ma, Hui Pan, Heng Zhang, Wen-Can Li, Ai-Min Xue, Hui-Jun Wang, Kai-Jun Ma, Long Chen

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RNA degradation as described by a mathematical model for postmortem interval determination

Lv Ye-Hui[a,b,c], Ma Jian-Long[a], Pan Hui[a], Zhang Heng[a,b], Li Wen-Can[d], Xue Ai-Min[a], Wang Hui-Jun[e], Ma Kai-Jun[f],Chen Long[a*]

[a]Department of Forensic Medicine, School of Basic Medical Sciences, Fudan University, 131 Dongan Road, Shanghai, 200032, People's Republic of China

[b]Department of Physiology & Pathophysiology, School of Basic Medical Sciences, Fudan University, 131 Dongan Road, Shanghai, 200032, People's Republic of China

[c]Shanghai University of Medicine & Health Sciences, 21 Meilong Road, Shanghai, 200030, People's Republic of China

[d]Shanghai Public Security Bureau, Pudong Branch ,655 Dingxiang Road, Shanghai, 200032, People's Republic of China

[e]Children's Hospital of Fudan University, 399 Wanyuan Road, Shanghai, 201102, People's Republic of China

[f]Forensic lab, Criminal Science and Technology Institute, Shanghai Public Security Bureau, 803 North Zhongshan Road, Shanghai, 200082, People's Republic of China

[*]**Corresponding authors: Long Chen, Email: chenlong@shmu.edu.cn.**

Abstract

Precisely determining the postmortem interval (PMI) is crucial to civil, criminal and forensic cases. A technique to exploit the postmortem RNA transcript level was developed to increase the accuracy and practicality of PMI estimation. For this purpose, lung tissues and muscle tissues were removed at twelve time points (0-144 h) from rat corpses that had been stored at three different temperatures (10, 20 and 30°C). Human tissues were collected at autopsy from twelve real cases with known PMI values and other parameters. After the RNA was extracted from all these samples, the transcript levels of nine biomarkers were analyzed by real-time quantitative PCR (RT-qPCR). With the assistance of geNorm, *miR-195*, *miR-200c*, *5S*, *U6* and *RPS29* were selected as reference biomarkers for lung specimens; *miR-1*, *miR-206*, *5S* and *RPS29* were chosen as control markers for muscle tissues. On the contrary, *ACTB* and *GAPDH* were significantly correlated with the PMI. The mathematical models using these target biomarkers were constructed to describe the characteristic relationship between ΔCt values (normalized to reference biomarkers) and the observed PMI for each temperature group. Following validation, the relatively low error rates (7.4% and 12.5% for rat and human samples, respectively) demonstrated the accuracy and reliability of the mathematical model. We believe these results indicate that the multi-parametric mathematical model can become a practical tool for PMI estimation.