



# Low 5-methylcytosine expression as an aggressive biomarker for the urothelial carcinoma: an immunohistochemical study

Chi-Jung Chung<sup>1,2</sup>, Chao-Hsiang Chang<sup>3,4</sup>, Yi-Huei Chang<sup>3</sup>, Mu-Chi Chung<sup>5</sup>, Han Chang<sup>6,7</sup>

<sup>1</sup>Department of Health Risk Management, College of Public Health, China Medical University, Taichung, Taiwan;

<sup>2</sup>Department of Medical Research, China Medical University Hospital, Taichung, Taiwan;

<sup>3</sup>Department of Urology, China Medical University and Hospital, Taichung, Taiwan;

<sup>4</sup>Department of Medicine, College of Medicine, China Medical University and Hospital, Taichung, Taiwan;

<sup>5</sup>Division of Nephrology, Department of Internal Medicine, Taichung Veterans General Hospital, Taichung, Taiwan;

<sup>6</sup>Department of Pathology, School of medicine, China Medical University, Taichung, Taiwan;

<sup>7</sup>Department of Pathology, China Medical University Hospital, Taichung, Taiwan.

## Introduction

❖ Previous studies suggested that global DNA methylation is involved in breast, lung, and colon carcinogenesis. However, only a few studies showed the association between global DNA methylation and urothelial carcinoma (UC).

## Aims

❖ We constructed a tissue array to elucidate the role of global DNA methylation in UC carcinogenesis.

## Material and Methods

❖ Two tissue microarrays were purchased from US Biomax, Inc. (MD, USA), including 155 tissue cores with 22 normal urothelium samples and 133 urothelium samples with UC. Global DNA methylation (5-methylcytosine; 5-MeC) was measured using the immunohistochemistry (IHC) method (H score) and image analysis (total intensity). Nonparametric analysis with Wilcoxon rank-sum test or the Kruskal–Wallis test was applied to compare the differences in 5-MeC levels and the clinical variables between the two groups.

**Table I. Clinical information of urothelial carcinoma patients and normal subjects**

Variables	Normal (n = 22)	Urothelial Carcinoma (n = 133)
Age	31.64 ± 12.37	61.67 ± 12.11
Sex		
Male	11 (50.00%)	106 (79.70%)
Female	11 (50.00%)	27 (20.30%)
Tumor grade		
Low	-	76 (57.14%)
High	-	57 (42.86%)
Cancer stage		
Early*	-	101 (75.94%)
Advanced**	-	32 (24.06%)
TNM stage		
T1N0M0	-	38 (28.57%)
T2a/bN0M0	-	62 (46.62%)
T3a/bN0M0	-	33 (24.81%)

\*Early stage indicates cases with cancer stages I and II.

\*\*Advanced stage indicates cases with cancer stage III.

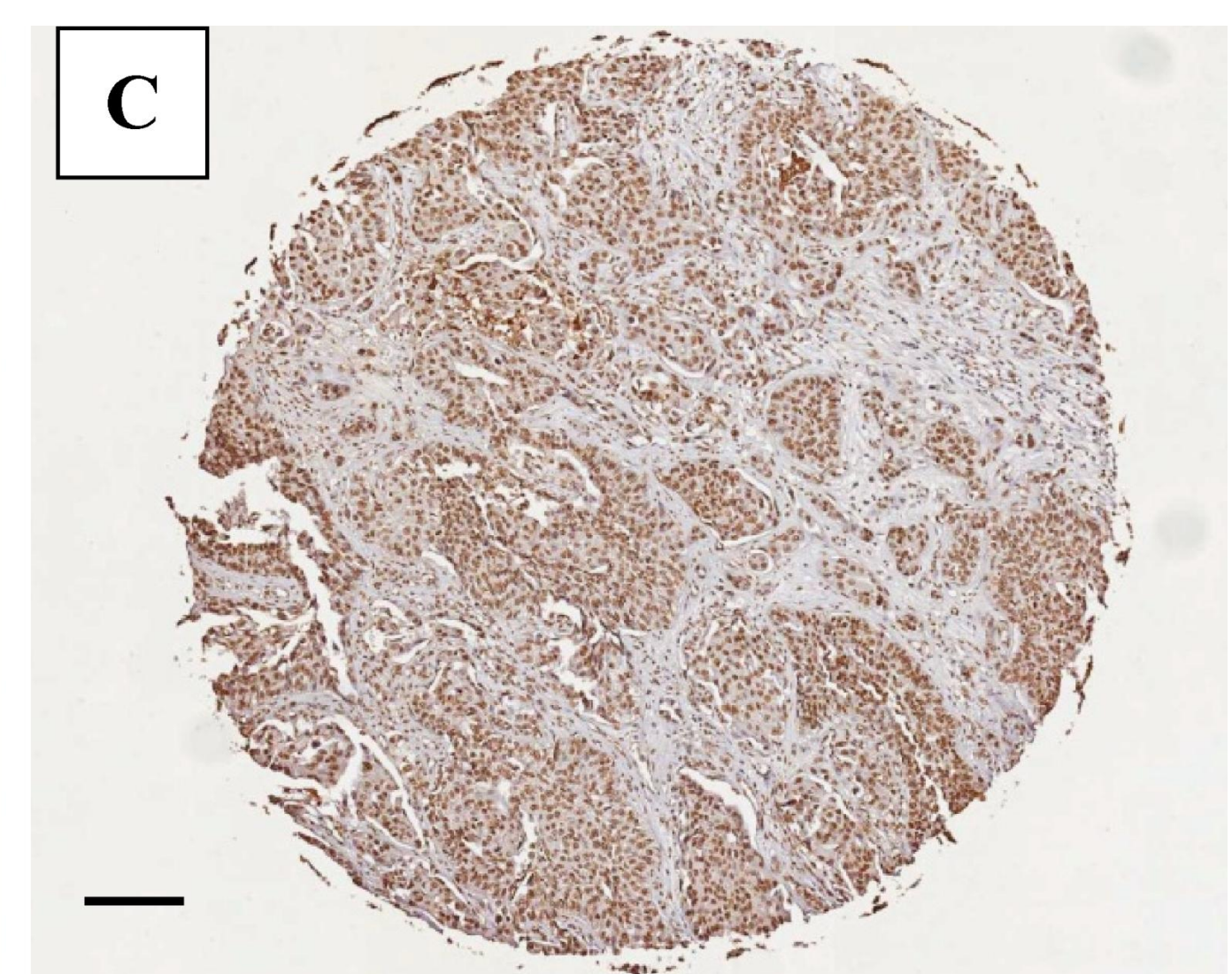
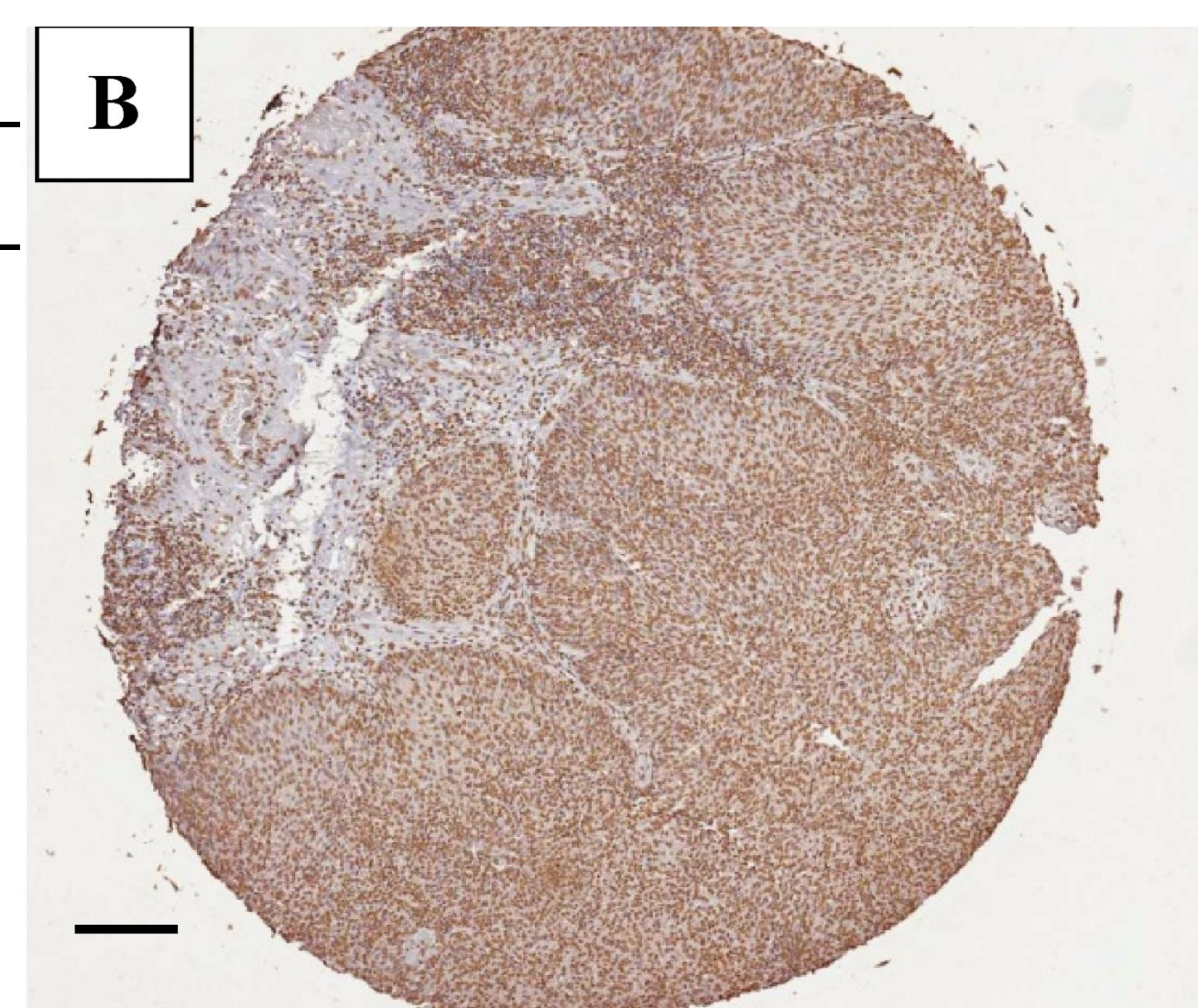
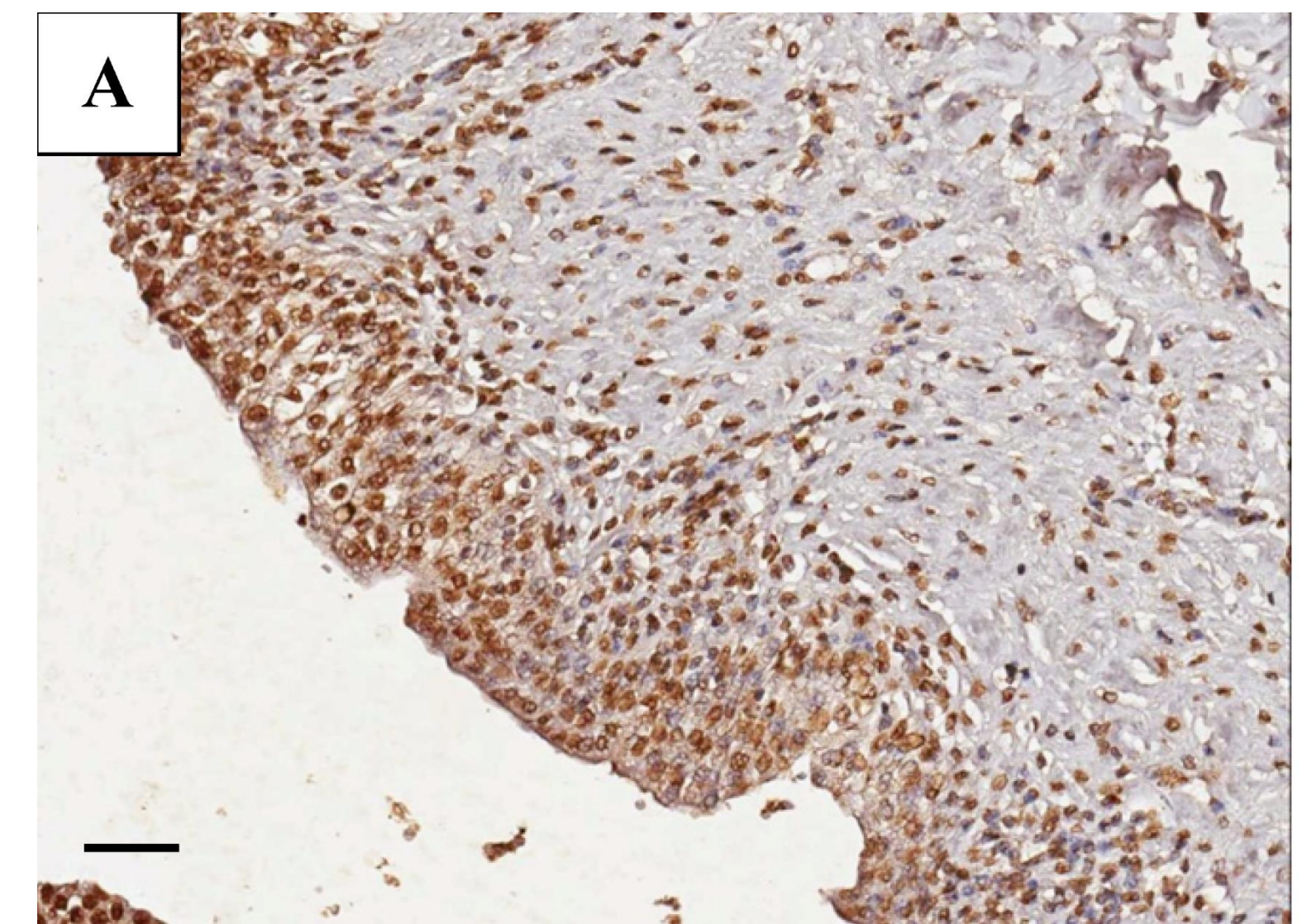
**Table III. DNA methylation levels stratified by clinical variables in urothelial carcinoma cases (n=133)**

Variables	H score	p Value	Total Intensity	p Value
Sex		0.99		0.90
Male	76.32 ± 61.02		106.70 ± 86.84	
Female	68.33 ± 45.09		96.67 ± 68.95	
Tumor grade		0.55		0.41
Low	75.33 ± 52.16		106.05 ± 73.41	
High	73.86 ± 65.62		102.81 ± 95.71	
Cancer stage		0.01		0.04
Early	81.14 ± 57.11		112.38 ± 82.29	
Advanced	54.38 ± 57.25		80.31 ± 83.34	
TNM stage		0.04		0.09
T1N0M0	72.11 ± 46.96		99.74 ± 66.68	
T2a/bN0M0	86.77 ± 62.67		120.32 ± 90.77	
T3a/bN0M0	55.00 ± 56.46		80.91 ± 82.10	

**Table II. DNA methylation levels\* for urothelial carcinoma and normal urothelium**

Methods	Normal (n = 22)	Urothelial Carcinoma (n = 133)	p Value
H score	107.73 ± 64.80	74.70 ± 58.08	0.026
Total intensity	154.55 ± 92.31	104.66 ± 83.37	0.013

\* DNA methylation levels were detected using two methods. H score was examined by a pathologist under a light microscope and total intensity was calculated by imaging software.



**Figure 1. Anti-MC immunohistochemistry in normal urothelium and UC.**

A. Normal urothelium with high expression. Bar, 100 µm.

B. Invasive UC with high expression. Bar, 400 µm.

C. Invasive UC with low expression. Bar, 400 µm.

## Conclusions

❖ The 5-MeC levels measured by IHC might be a good method for clinicians to evaluate global DNA methylation in UC progression.