Methods One hundred and thirty-six bladder cancer patients with occupational history were included in the study. Serum DNA-methylation levels of DNA methyltransferase 1 (DNMT1) were analyzed using methylation-specific PCR (MS-PCR) and methylation-sensitive high-resolution melting (MS-HRM) analysis. DNA-methylation levels were quantified using the TMS reagent kit and MS-PCR. The melting temperature of the methylated DNA was used to determine the degree of methylation.

Results The DNA-methylation levels of DNMT1 were significantly lower in the bladder cancer patients compared to the control group. The methylation patterns were significantly different between the two groups, with a higher percentage of unmethylated DNA in the bladder cancer patients. These findings suggest that DNMT1 may play a role in the development of bladder cancer through its DNA-methylation status.

Conclusions Our study highlights the potential role of DNMT1 in the pathogenesis of bladder cancer and suggests that DNA-methylation analysis could be a useful tool for the detection and risk assessment of this disease.