ABSTRACT

Background/Aim: In endometrial cancer (EC), lymph node (LN) metastasis significantly impacts prognosis. Thus far, no studies have reported the molecular genetics of each metastatic lesion. This study aimed to investigate the molecular characteristics of primary and metastatic LNs and their association with clinical outcomes. Patients and Methods: The clinicopathological and molecular characteristics of 33 patients with EC with regional LN metastasis (FIGO stage IIIC) were investigated; we evaluated the mutational status of p53 and DNA mismatch repair (MMR) proteins in the primary lesion, all the positive LNs (102 lesions), mutational variation between primary and paired metastatic lesions, inter-lesion heterogeneity, and their association with clinical outcomes. Results: Immunohistochemically, 12 patients (36.4%) displayed aberrant p53 expression in metastatic lesions, and a concordant rate of 93.4% was observed between primary and metastatic lesions. Inter-lesion heterogeneity was observed in 20 cases (60.6%). In Kaplan–Meier analysis, patients with aberrant p53 expression in metastatic LNs exhibited worse progression-free survival (PFS) than those with wild-type p53 expression (p=0.008). Wild-type p53 expression in primary lesion with inter-lesion heterogeneity had a significantly worse PFS (p=0.049) than those without heterogeneity. In the Cox univariate analysis, p53 expression in metastatic LNs was significantly associated with recurrence (p=0.013). Genetic diversity between primary and metastatic lesions and among metastases was validated by evaluating p53 and MMR proteins by using immunohistochemistry (IHC) analysis. Conclusion: The molecular characteristics of metastatic lesions in addition to those of primary lesions could provide beneficial prognostic information in patients with EC with regional LN metastasis.