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A NEW POTENTIAL INDEPENDENT PROGNOSTIC MARKER FOR OVARIAN CANCER

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Objectives: Many members of the human kallikrein gene family were found to be differentially expressed in various malignancies and some are useful cancer diagnostic/prognostic markers. KLK9 is a newly discovered kallikrein gene that is expressed in several tissues. Like other kallikreins, the KLK9 gene was found to be regulated by steroid hormones in cancer cell lines. We hypothesized that KLK9, similar to other kallikreins, is differentially expressed in ovarian cancer. **Methods:** We studied the expression of KLK9 by quantitative RT-PCR in 182 ovarian tumors of different stages, grades and histological types. **Results:** KLK9 expression was significantly higher in patients with early stages (I or II) ($p=0.037$) and in patients with optimal debulking ($p=0.011$). Kaplan-Meier survival curves demonstrated that patients with KLK9-positive tumors have substantially longer progression-free and overall survival ($p < 0.001$ and $p = 0.018$, respectively). When the Cox proportional hazard regression analysis was applied to subgroups of patients, KLK9 expression was found to be a significant predictor of the progression-free survival in the subgroup of patients with low grade tumors (Hazard Ratio "HR" = 0.12, $p < 0.001$), early stage (HR = 0.10, $p = 0.028$) and those with optimal debulking (HR = 0.31, $p = 0.018$). After adjusting for other known prognostic variables, KLK9 retained its independent prognostic value. A negative correlation was found between the expression levels of CA 125 and KLK9 ($r_s = 0.351$, $p = 0.002$). **Conclusion:** KLK9 is a potential new favorable prognostic marker for ovarian cancer.