Molecular landscape in high-grade serous ovarian cancer: The correlation between BRCA mutational status and stromal p16 expression

The effect of BRCA mutational status on biological feature and survival outcome in advanced-stage (IIb-IV stage) high-grade serous ovarian cancer (HGSOC) seems to confer a better prognosis. The aim of our preliminary work is to investigate the stromal p16 expression for HGSOC in advanced-stage (IIb-IV stage), using immunohistochemistry, and differences in the expression status depending on the mutational status of BRCA. Alterations in p16 protein expression have been reported to be associated with tumor development and progression. p16 expression status in the peritumoral stroma has been rarely investigated.

Methodology This is a retrospective study included 33 patients diagnosed with FIGO stage IIb-IV HGSOC who underwent primary debulking surgery (PDS) at the Departments of Gynecology and Obstetrics of the University of Pisa between January 2019 and April 2020. The stromal p16 expression in HGSOC was investigated by using immunohistochemistry, and the differences in p16 immunoreactivity linked with the BRCA mutational status were analyzed.

Result(s) BRCA1/2 mutations were observed in 15 women (45%). Wild-type -BRCA advanced HGSOCs exhibited diffuse, moderate-to-strong p16 immunoreactivity in 46.66% of cases, instead mutated-BRCA advanced HGSOCs showed elevated stromal p16 expression in 33.33% of cases.

Conclusion This study introduces a new and interesting result: the correlation between stromal expression of p16 and BRCA mutational status. The majority of malignant lesions exhibited diffuse and moderate-to-strong p16 immunoreactivity, suggesting that stromal p16 expression can be used as an adjunctive predictive and prognostic biomarker for HGSOC. Further studies are necessary to confirm our preliminary results and to explain the different outcome of wt- and m-BRCA HGSOC.

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