Conclusion

This study is the first to describe characteristics of real-world patients who initiated 1LM niraparib monotherapy based on niraparib’s approval status. Study findings suggest that BRCA/HRD testing has increased over time. Moreover, understanding dosing patterns and associated treatment duration can help optimise disease management. These outcomes will be explored in the next study phase.

Abstract 2022-RA-618-ESGO Table 1

| Demographic and clinical characteristic of the primary and stratified cohorts |
|---------------------------------|-----------------|-----------------|
| Primary study cohort (n=234) | Niraparib pre-1LM approval cohort (index dates before 23April2020) (n=96) | Niraparib post-1LM approval cohort (index dates on or after 23April2020) (n=138) |

Demographic characteristics
- Median age at index (Q1, Q3), years: 68.0 (62.9, 75.0), 67.5 (62.9, 75.0), 68.0 (61.0, 75.0)
- Predictive type, n (%)
  - Academic: 60 (16.0%), 17 (18.9%), 43 (18.1%)
  - Community: 332 (88.8%), 81 (90.0%), 251 (88.4%)

Clinical characteristics
- Stage at initial EOC diagnosis, n (%)
  - I: 20 (5.3%), 5 (5.6%), 15 (5.9%)
  - II: 188 (50.3%), 33 (36.5%), 155 (54.6%)
  - III: 130 (24.6%), 44 (48.9%), 86 (30.3%)
  - Unknown/Not documented: 36 (9.6%), 8 (8.9%), 28 (9.9%)
- BRCA mutation status, n (%)
  - Mutated: 30 (10.2%), 19 (21.1%), 19 (6.7%)
  - Wild-type: 313 (83.3%), 57 (63.3%), 256 (89.1%)
  - Unknown: 23 (6.1%), 14 (15.5%), 9 (3.2%)
- HRD status, n (%)
  - Positive: 59 (16.8%), 9 (9.8%), 51 (18.0%)
  - Negative: 592 (16.8%), 6 (6.7%), 53 (18.7%)
  - Unknown: 256 (60.4%), 76 (84.4%), 180 (63.4%)

Residual disease status following initial surgery for EOC, n (%)
- No residual disease: 62 (26.5%), 24 (26.7%), 38 (13.4%)
- No visible residual disease: 148 (39.9%), 33 (36.1%), 115 (40.5%)
- Visible residual disease: 82 (21.9%), 22 (24.4%), 60 (21.1%)
- Unknown: 82 (21.9%), 11 (12.2%), 71 (25.0%)

Notes:
1. Patients with records in academic and community practices are counted in both categories; therefore, percentages may sum to more than 100%.
2. Results with counts less than 5 are masked by combining categories.
3. Data do not differentiate between somatic and germline mutations.
4. Adverse events: 1LM, first-line maintenance; HRD, homologous recombination deficiency; HRD, homologous recombination deficient; HRD, homologous recombination proficient; HRD, not otherwise specified; GC, ovarian cancer; Q, quartile.

Methodology

This is a retrospective, multicentre cohort study that included patients who underwent cytoreductive surgery for primary advanced or relapsed ovarian cancer with colorectal resection and anastomosis between January 2011 and June 2021. From patients already included in the previous predictive model were not considered in the present analysis.

Results

848 out of 1159 recruited patients were finally included in the multivariable logistic regression model validation. The AUC of the new cohort was 0.63. Considering a cut-off point of 22.1% to be ‘positive’ (to get a leak) this would provide a sensitivity of 0.45, specificity of 0.80, predictive positive value of 0.09 and predictive negative value of 0.97 for anastomotic leak. If we consider this cut-off point to select patients for bowel diversion, up to 22.5% of the sampled patients would undergo a diverting ileostomy and 47% (18/40) of the anastomotic leaks would be ‘protected’ with the stoma. Nevertheless, if we consider only the ‘clinical criteria’ for performing or not a diverting ileostomy, only 12.5% (5/40) of the leaks would be ‘protected’ with a stoma, with a rate of diverting ileostomy of up to 24.3%.

Conclusion

Compared with subjective clinical criteria, the use of a predictive model for anastomotic leak improves the selection of patients who would benefit from a diverting ileostomy without increasing the rate of stoma use.

Abstract 2022-RA-630-ESGO

OVEREXPRESSION OF PDEA1 IS A PREDICTIVE BIOMARKER FOR PLATINUM RESISTANCE AND POOR PROGnosis IN EPITHELIAL OVARIAN CANCER BY REGULATING CELL CYCLE


Introduction/Background

Phosphodiesterase 1A (PDE1A) belongs to a class of phosphohydrolytic enzymes that modulate the intensity of intracellular second messenger signaling and resulting in the integration of Ca2+ and cyclic nucleotide mediated in various disease such as cancers in expression and clinicopathological features, while its role also role in epithelial ovarian cancer (EOC) has not been clarified yet. Therefore, in this study we aim to evaluate the function, molecular mechanism and clinicopathological significance of PDE1A in EOC.

Methodology

The qPCR, western blotting and public data sets were used to evaluate the expression level of PDE1A. Also, expression levels of PDE1A and clinicopathological characteristics were evaluated by immunohistochemistry staining of EOC, borderline, benign and normal epithelial tissues. Its functional role and association with cell cycle were evaluated in EOC cell lines.