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The Relationship Between Histomorphological Patterns and Clinicopathological Features In High-Grade Serous Ovarian Carcinoma

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ABSTRACT

High-grade serous ovarian carcinoma (HGSC) is heterogeneous tumors in terms of morphology, genetics, and clinical presentation. The SET pattern (solid, pseudoendometrioid, and transitional-like) is associated with BRCA mutations and reflect distinct biological behavior. The present study was conducted with the objective of evaluating the relationship between SET and non-SET patterns, and their clinicopathological and genetic characteristics.

The present study comprised 83 patients diagnosed with HGSC between the years 2010-2020. Patients with any SET pattern (SET-predominant or focal-SET) were compared with non-SET cases, and SET-predominant cases with non-SET cases after excluding focal-SET. A comprehensive comparison was conducted between the groups with respect to age, FIGO stage, regional lymph node involvement, regional and distant metastasis, ascites cytology, CA-125 level, and BRCA mutation status.

The SET-predominant pattern was detected in 41.0% of cases while focal SET cases were 15.7%. Advanced FIGO stage (III–IV) was more prevalent in the non-SET group. Regional lymph node involvement was significantly high in the non-SET group compared to the SET-predominant group (41.7%vs.14.7%; p=0.017). Regional and distant metastasis rates were higher in the non-SET group. Median CA-125 levels tended to be lower in the SET-predominant group. The prevalence of the BRCA mutation was found to be significantly higher in the SET-predominant and SET-focal/predominant groups compared to the non-SET group (61.8% and 51.1%vs.2.8%, respectively; p=0.001).

The SET pattern in HGSC is strongly associated with the presence of a BRCA mutation. The findings of this study indicate that the reporting of the SET pattern in routine pathological evaluation is clinically and biologically significant.

Keywords: ovary, serous, carcinoma, BRCA, mutation, SET, pattern

Introduction

High-grade serous carcinoma (HGSC) of the ovary is among the most prevalent malignant gynecological neoplasms in women, with a high mortality rate, and more than 70% of patients are diagnosed at an advanced stage (1, 2). The HGSC group is characterized by a considerable degree of heterogeneity, as evidenced by the presence of a wide range of neoplasms that manifest in a variety of forms, possess distinct genetic characteristics, and exhibit diverse clinical and biological features (3-6). Despite the fact that platinum-based chemotherapy is the standard first-line treatment, resistance is frequently observed, highlighting the importance of identifying tumor characteristics that may influence treatment response and clinical management.

BRCA1 and BRCA2 alterations have been shown to play a crucial role in the pathogenesis of HGSC, with inactivation reported in approximately 30–40% of cases. Such alterations may occur as germline or somatic mutations, or through BRCA1 promoter methylation (3-6). It has been hypothesized by scholars in the field that tumors exhibiting a specific mutation in the BRCA gene may manifest distinctive morphological characteristics that differ from those observed in tumors that do not carry this mutation. It is well established that HGSCs typically manifest as papillary, micropapillary, or labyrinthine (slit-like) architectural patterns. Conversely, tumors that

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exhibit a specific pattern of mutations, known as the "SET pattern", have been observed to manifest distinct morphologies, including solid, pseudoendometrioid, and transitional-like features (7). In addition to the SET morphology, there is a growing body of literature highlighting the presence of prominent tumor-infiltrating lymphocytes, high mitotic activity, and necrosis in cases of BRCA-mutated tumors (7, 8).

It has been hypothesized by several studies that tumors which exhibit SET pattern and are characterized by a mutation in the BRCA gene may demonstrate an enhanced response to platinum-based chemotherapy and potentially more favorable clinical outcomes when compared with non-mutated tumors. However, it should be noted that the current evidence for this hypothesis remains limited (5, 6, 9-11). Furthermore, the administration of polyADP-ribose polymerase (PARP) inhibitors has been demonstrated to be significantly efficacious in ovarian carcinoma patients with BRCA1 or BRCA2 mutations, thus further emphasizing the clinical importance of identifying features associated with a positive BRCA status (12-14). Despite the significance of both BRCA status and homologous recombination deficiency as predictive markers, the availability of reliable and readily applicable morphological indicators remains limited.

The present study was conducted with the objective of investigating the association between SET and non-SET morphological patterns and clinicopathological and genetic characteristics at the time of diagnosis in patients with HGSC.

Materials and Methods

The present retrospective study comprised 83 patients diagnosed with HGSC between 2010 and 2020. Due to the retrospective design of the study, no a priori sample size calculation was performed. The sample size was based on all eligible patients identified during the study period. The evaluation of all hematoxylin–eosin (H&E) stained slides was conducted independently by two pathologists who were blinded to the clinical data. Following confirmation of the diagnosis, the tumors were evaluated according to the architectural patterns defined in the 5th Edition of the WHO Classification of Female Genital Tumors Book, including papillary, micropapillary, labyrinthine (slit-like), pseudoendometrioid, solid, and transitional-like patterns (2). The following patterns are described as Micropapillary pattern: characterized by the formation of finger-like projections that do not contain fibrovascular cores (Figure 1A). Papillary: The neoplastic cells that arranged in a pattern that consists of a lining of neoplastic cells around fibrovascular cores (Figure 1B). Labyrinthine (slit-like): a pattern consisting of irregularly arranged neoplastic cells containing fine slit-like spaces (Figure 1C). Solid: patterns consisting of arrangement of tumor cells in layers that do not conform to other morphologies (Figure 2A). Cribriform-glandular (pseudoendometrioid) pattern: a pattern consisting of neoplastic cells forming islands or glandular structures and pinhole-like spaces (Figure 2B). Transitional-like: a pattern consisting of broad papillary structures containing stratified tumor cell layers (Figure 2C). SET pattern: solid, pseudoendometrioid and transitional-like pattern (Figure 2D). Non-SET pattern: papillary, micropapillary, and labyrinth (slit-like) patterns (7).

Tumors exhibiting a greater than 50% prevalence of SET patterns were designated as SET-predominant, while those with 5-50% SET pattern were categorized as focal SET (15). Cases containing less than 5% SET pattern were evaluated as non-SET, and the pattern present in the highest percentage was designated the predominant pattern. As posited by Soslow et al., the percentages of the three patterns (solid, pseudoendometrioid, transitional-like) in the SET pattern were aggregated to derive the ultimate percentage (7).

The demographic and clinicopathological data were obtained from the hospital information system. The evaluated variables included age at diagnosis, regional lymph node involvement (pelvic or paraaortic), regional metastasis (pelvic peritoneum or omentum involvement), distant metastasis, serum CA-125 level, ascites cytology status, FIGO stage, and BRCA mutation (in blood) status. The study was approved by the institutional ethics committee (approval number: 2025/02) and conducted in accordance with the Declaration of Helsinki.

Statistical Analysis: The statistical analyses were conducted using R software (version 4.5.0; R Foundation for Statistical Computing, Vienna, Austria). The normality of continuous variables was assessed using visual methods and the Shapiro–Wilk test. Continuous variables were presented as mean ± standard deviation (SD) or median (interquartile range, IQR), as appropriate. Categorical variables were expressed as number and percentage.

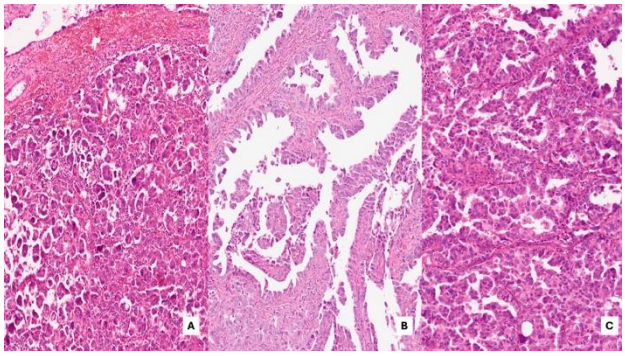

Fig. 1. A: Micropapillary pattern H&E x40 B: Papillary pattern H&E x40 C: Labyrinthine (slit-like) pattern H&E x40

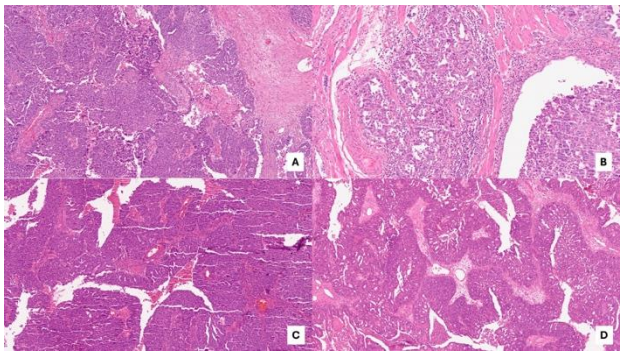

Fig. 2. A: Solid pattern with necrosis H&E x40 B: Glandular/cribriform-pseudoendometrioid pattern H&E x40 C: Transitional-like pattern H&E x40 D: SET pattern H&E x20

Comparisons were performed according to the predefined analysis plan, including comparisons between SET-pattern (SET-predominant and focal SET combined) and non-SET groups, as well as between SET-predominant and non-SET groups after exclusion of focal SET cases. Student's t-test or Mann–Whitney U test was used for continuous variables depending on data distribution, and the chi-square test or Fisher's exact test was used for categorical variables.

Inter-observer agreement between the two pathologists was assessed using Cohen's kappa coefficient (0.83). A two-sided p value <0.05 was considered statistically significant.

Results

The study comprised a total of 83 patients diagnosed with high-grade serous ovarian carcinoma. The mean age of the study population was 54.8 ± 10.1 years. The majority of patients (80.7%) were diagnosed at an advanced stage (FIGO III–IV). The presence of regional metastasis was observed in 83.1% of patients, while distant metastasis was detected in 59.0% of cases. Furthermore, ascites cytology positivity was identified in 83.1% of patients. The most prevalent site of distant metastasis was the liver (33/49, 67.3%). A total of 30.1% of cases exhibited a positive detection of a BRCA mutation. The baseline clinicopathological characteristics of the study population are summarized in Table 1. The inter-observer agreement between the two pathologists was 0.83 (Cohen's κ).

The distribution of histologic growth patterns is presented in Table 2. The prevalence of SET was observed to be 41.0% among the patient cohort, while focal SET was identified in 15.7%, papillary in 15.7%, micropapillary in 15.7%, and labyrinthine patterns in 12.0%.

The clinicopathological characteristics according to histomorphology are shown in Table 3.

An additional analysis was performed comparing patients with predominant SET morphology and those with non-SET patterns after excluding focal SET cases (Table 4).

The cases were examined in three groups: non-SET, SET patterns (focal SET + SET predominant patterns), and SET predominant. The mean age was found to be 53.9 ± 9.3 years in the SET-predominant group, 53.9 ± 9.7 years in the SET-focal/predominant group, and 56.0 ± 10.7 years in the non-SET group. There was no significant difference between SET focal/predominant and Non-SET (p=0.374), even between SET-predominant and Non-SET (p=0.379). Furthermore, the advanced FIGO stage (III–IV) was observed in 70.6% and 88.9% of patients in the SET-predominant and non-SET groups, respectively (p=0.075). The presence of regional lymph node involvement was observed in 14.7% of patients with SET-predominant disease, 23.4% of those with SET-focal/predominant disease, and 41.7% of patients with non-SET disease (p=0.017).

The presence of regional metastasis was observed in 70.6%, and 91.7% of patients with SET-predominant and non-SET patterns respectively (p=0.032). Similarly, distant metastasis was detected in 47.1% and 69.4% of patients, respectively (p=0.089).

The median (IQR) CA-125 levels were as follows: 405 (131–1201) in the SET predominant group, and 745 (336–2094) in the non-SET group. There was no significance between two groups (p=0.074). Ascites cytology positivity was observed in 73.5%, 80.9%, and 86.1% of patients (p=0.238). The prevalence of a BRCA mutation

Table 1: Baseline Clinicopathological Characteristics of The Study Population (n=83)

Variable	n (%) or value
Age, years (mean ± SD)	54.8 ± 10.1
Advanced FIGO stage (III–IV)	67 (80.7%)
Regional lymph node involvement	26 (31.3%)
Regional metastasis	69 (83.1%)
Distant metastasis	49 (59.0%)
Positive ascites cytology	69 (83.1%)
BRCA mutation	25 (30.1%)
CA-125 at diagnosis, median (IQR)	1717 (10–18653)

Data are presented as mean ± SD, median (IQR), or n (%). FIGO: International Federation of Gynecology and Obstetrics

Table 2: Histomorphological Pattern Distribution

Pattern	n (%)
Papillary	13 (15.7%)
Labyrinthine (slit-like)	10 (12%)
Micropapillary	13 (15.7%)
Focal SET	13 (15.7%)
SET	34 (41.0%)
Data are presented as n (%).	

Table 3: Clinicopathological Characteristics According to SET Morphology

Variable	SET patterns (SET focal/predominant) (n=47)	Non-SET (n=36)	p value
Age, years (mean ± SD)	53.9 ± 9.7	56.0 ± 10.7	0.374
Advanced FIGO stage (III–IV), n (%)	35 (74.5%)	32 (88.9%)	0.159
Regional lymph node involvement, n (%)	11 (23.4%)	15 (41.7%)	0.097
Regional metastasis, n (%)	36 (76.6%)	33 (91.7%)	0.083
Distant metastasis, n (%)	24 (51.1%)	25 (69.4%)	0.117
CA-125 at diagnosis, median (IQR)	517 (171–1331)	745 (336–2095)	0.272
Ascites cytology positive, n (%)	38 (80.9%)	31 (86.1%)	0.570
BRCA mutation, n (%)	24 (51.1%)	1 (2.8%)	0.001

Continuous variables are presented as mean ± SD or median (IQR), and categorical variables as n (%). Student's t-test or Mann–Whitney U test was used for continuous variables, and the chi-square or Fisher's exact test was used for categorical variables. FIGO: International Federation of Gynecology and Obstetrics; CA-125: Cancer antigen 125.

Table 4: Clinicopathological Characteristics Comparing Predominant SET Morphology With Non-SET Patterns (focal SET Cases Excluded)

Variable	SET-predominant (n=34)	Non-SET (n=36)	p value
Age, years (mean ± SD)	53.9 ± 9.3	56.0 ± 10.7	0.379
Advanced FIGO stage (III–IV), n (%)	24 (70.6%)	32 (88.9%)	0.075
Regional lymph node involvement, n (%)	5 (14.7%)	15 (41.7%)	0.017
Regional metastasis, n (%)	24 (70.6%)	33 (91.7%)	0.032
Distant metastasis, n (%)	16 (47.1%)	25 (69.4%)	0.089
CA-125 at diagnosis, median (IQR)	405 (131–1201)	745 (336–2094)	0.074
Ascites cytology positive, n (%)	25 (73.5%)	31 (86.1%)	0.238
BRCA mutation, n (%)	21 (61.8%)	1 (2.8%)	0.001

Continuous variables are presented as mean ± SD or median (IQR), and categorical variables as n (%). Student's t-test or Mann–Whitney U test was used for continuous variables, and the chi-square or Fisher's exact test was used for categorical variables. FIGO: International Federation of Gynecology and Obstetrics; CA-125: Cancer antigen 125

was detected in 61.8% of patients diagnosed with SET-predominant, 51.1% of those diagnosed with SET-focal/predominant, and 2.8% of patients diagnosed with non-SET (p=0.001).

Discussion

High-grade serous ovarian carcinomas are a heterogeneous group of diseases that can vary considerably in their morphological appearance, genotypic and biological characteristics, as well as their prognosis [3-6]. Research conducted over the last two decades has reported that HGSCs largely originate from tubal epithelium, show BRCA mutations in approximately 40% of cases, and that BRCA mutant ovarian carcinomas may be associated with specific morphological patterns (3, 4). The most frequently observed pattern associated with a BRCA mutation is the SET pattern (solid, pseudoendometrioid, transitional-like) (7,16,17). The incidence of the SET pattern in HGSCs remains unclear; however, some studies have reported that the SET-predominant pattern manifests in approximately 40% of cases (15). In the present study, cases exhibiting SET-predominance constituted 41% of the total cases, and when combined with focal SET cases, this rate increased to 56.7%. Despite the absence of a statistically significant disparity in the mean patient age between SET and non-SET cohorts within the present study, cases exhibiting the SET pattern were observed to be, on average, two years younger than those demonstrating non-SET patterns. A plethora of studies in the extant literature also report a 2-year discrepancy between SET and non-SET patterns (15, 18). HGSCs typically being diagnosed at an advanced stage, 87% of the cases in this study were found to be at an advanced stage (FIGO III-IV) at the time of diagnosis. Research has indicated that approximately 96.6% of HGSCs are diagnosed at an advanced stage, irrespective of pattern (19). In the present study, cases exhibiting a SET predominant pattern were diagnosed at an earlier stage in comparison to cases displaying SET-focal/predominant and non-SET patterns (70.6% vs. 74.5%, 88.9%); however, no significant difference was observed between these groups. A review of the literature reveals a paucity of studies reporting any difference in FIGO stage between SET and non-SET patterns (15). Research has indicated that approximately 64% of cases of HGSC present with regional lymph node metastasis at diagnosis (19). However, in the present study, this rate was found to be 31.3%, indicating a significant difference between SET and non-SET patterns (14.7% vs. 41.7%). The present study detected regional metastasis in 83.1% of cases, a figure lower than the 90% threshold documented in the extant literature (19).

Although distant metastasis and positive ascites cytology were less prevalent in cases exhibiting the SET pattern compared to non-SET cases, no statistical significance was identified. Levels of the CA-125 antigen were found to be significantly lower at the time of diagnosis in cases where the predominant manifestation was SET, as compared to cases where the predominant manifestation was non-SET (405 vs. 745). This discrepancy can be attributed to the disparate aggressive courses exhibited by the two patterns. CA-125 has been identified as a potentially effective prognostic factor in high-grade serous ovarian carcinomas. This finding was consistent with the literature (20).

The BRCA mutation is a significant genetic alteration that plays a crucial role in the development of ovarian carcinoma. It has been observed to be associated with specific morphological patterns in ovarian carcinomas. The presence of the BRCA mutation has been observed to be particularly prevalent in ovarian carcinomas exhibiting solid, pseudoendometrioid, and transitional-like patterns. The presence of necrosis, a high mitotic index, and tumor-infiltrating lymphocytes, in addition to the SET pattern, have also been associated with the presence of the BRCA mutation. It has also been reported that nuclear pleomorphism may be associated with the BRCA mutation (7). The presence of the BRCA mutation has been documented in 30-40% of HGSC cases, with a rate of 50% in the SET pattern and 5-25% in non-SET cases (18). This variability is attributable to inter-observer differences in the interpretation of the SET pattern, as well as the unclear relationship between the focal SET pattern and BRCA. In the present study, the presence of a BRCA mutation was observed in 61.8% of cases exhibiting SET-predominant characteristics, while this rate was recorded at 2.8% in cases exhibiting non-SET characteristics. The presence of BRCA mutations in 3 of the 13 cases (23%) with focal SET pattern demonstrates the necessity of indicating the presence of SET pattern in pathology reports, regardless of its prevalence (21-22). The SET pattern is also crucial in predicting prognosis. Research has indicated that the median survival duration for cases characterised by SET is 81 months, 59 months for those with focal SET, and 44 months for cases not involving SET (15). Furthermore, it has been documented that cases exhibiting the SET pattern demonstrate a heightened response to chemotherapy, consequently exhibiting a more favourable prognosis in comparison to non-SET cases (17). In contrast, the extant literature includes studies that demonstrate a correlation between the presence of breast cancer and the SET pattern. However, these studies report no statistically significant differences in survival rates or chemotherapy sensitivity between patients with these two distinct morphological classifications (18). Mean survival and chemotherapy response are outside the scope of this article and constitute a limited aspect of the study.

The present study has demonstrated that the SET histomorphological pattern in high-grade serous ovarian carcinomas is associated with distinct clinicopathological and genetic features. SET-predominant cases are distinguished by a reduced degree of regional lymph node involvement and lower CA-125 levels at the time of diagnosis in comparison with non-SET cases. These findings suggest that the SET pattern may reflect a less aggressive biological behaviour. Despite the absence of statistically significant differences between the groups with regard to FIGO stage, regional and distant metastasis rates, and positive ascites cytology, a consistent trend towards superior clinical outcomes was observed in cases exhibiting the SET pattern. The most striking finding was the high rate of BRCA mutation in SET-predominant and focal SET cases, compared to an extremely low rate in non-SET cases.

The results of this study indicate that the SET pattern may serve as a viable and cost-effective morphological marker for the identification of BRCA mutations, and its inclusion in pathology reports, even in cases where the mutation is focal, is essential. In the future, the execution of prospective studies incorporating survival and treatment response data will serve to more clearly reveal the prognostic and predictive value of the SET pattern.

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