

Current Issues in Pharmacy and Medical Sciences

Formerly ANNALES UNIVERSITATIS MARIAE CURIE-SKŁODOWSKA, SECTIO DDD, PHARMACIA

journal homepage: <http://www.curipms.umlub.pl/>



Molecular alterations in mucinous ovarian tumors – a review

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ARTICLE INFO

Received 18 January 2024

Accepted 08 June 2024

Keywords:

mucinous ovarian tumors,
molecular alterations,
targeted therapy,
ovarian metastasis.

ABSTRACT

Mucinous ovarian tumors (MOTs) include primary and secondary neoplasms, the latter of which contribute for 80% of all cases. The most common site of origin for secondary MOTs is the gastrointestinal tract. Proper differentiation between primary and metastatic lesions is essential for effective treatment. Currently, definitive diagnosis is made based on post-operative histopathological examination with the use of immunohistochemical markers. However, the final diagnosis presents a challenge because of the histopathological similarity between mucinous metastases and primary ovarian lesions. Generally, treatment consists of cytoreductive surgery and adjuvant chemotherapy, even though malignant tumors are found to be chemo-resistant. Prognosis depends on the type of the tumor, presence of metastases and patient's general condition. Further research on the genetic background of MOTs is necessary for the better understanding of their origin and more effective treatment. This review aims to summarize recent advances in the field of the molecular features of MOTs and their implications for the diagnostic pathways and potential adjuvant therapy options. The analysis of molecular alterations might not only be an important prognostic factor, but also a useful diagnostic tool in distinguishing between primary mucinous tumors and extra-ovarian metastases or other subtypes of epithelial ovarian neoplasms. Moreover, the examination of genetic mutations seems to increase the efficiency of targeted therapy. However, more research evaluating such therapies in pre-clinical models is needed to improve the results of the diagnostics and treatment of MOTs.

INTRODUCTION

Mucinous ovarian tumors (MOTs) are a heterogeneous group of diseases that include primary tumors (PMOTs) and metastases from extra-ovarian sites, the latter of which are much more common [1]. Accurate diagnosis and treatment are challenging because of the histopathological similarity between PMOTs and mucinous metastases, especially those of gastrointestinal origin [2-4]. Deepened research on the genetics of MOTs is crucial to improve the management of the disease. Molecular alterations were once believed to be mainly prognostic factors, but current studies highlight their implications for differential diagnosis and targeted therapy [1,2,5-8]. The aim of this study is to summarize the current state of knowledge about the most common mutations in MOTs, the differences between primary and metastatic tumors, and possible therapeutic pathways in adjuvant treatment.

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Histological classification and epidemiology

Primary mucinous ovarian tumors (PMOTs) are one of the histological subtypes of epithelial ovarian neoplasms (EONs) and account for 3-15% of all primary malignancies of the ovary [1,2,9-11]. They are divided into benign (mucinous cystadenoma and mucinous adenofibroma), borderline (mucinous borderline tumor), and malignant (mucinous carcinoma) type [2,12]. PMOTs may also exhibit intestinal-type morphology or, rarely, endocervical-type morphology, and therefore be mistaken for metastases from diverse extra-ovarian sites, such as the colon, stomach, pancreas and uterus [1,2,13]. 80% of all PMOTs are benign lesions, while the incidence of mucinous carcinoma (MOC) is estimated at 3% [12,14-16]. Borderline ovarian tumors account for 10-15% of all epithelial ovarian tumors; approximately 80% being of mucinous origin [12,17,18]. MOCs, on the other hand, are divided into expansile and infiltrative subtype, both of which may co-occur. However, the expansile MOC is more common [12,19-21].

According to research, 80% of all MOC are metastases: 45% from the gastrointestinal tract, 2-20% from the pancreas, 18% from cervix and endometrium, and 8-15% from the breast [3,15,22-24]. The average age of patients with ovarian metastases is 55 years [24]. Because of the histopathological similarity between PMOTs and gastrointestinal/appendiceal tumors, some authors suggest a modified classification, which includes low-grade or high-grade mucinous neoplasm and mucinous adenocarcinoma, intestinal type [12,25]. The differentiation between PMOTs and metastases is mainly based on histopathological examination with the use of immunohistochemical (IHC) markers [9]. Histologically, mucinous carcinomas are categorized into cystic and colloid type, based on intracellular or extracellular mucin localization. A large amount (>50%) of intracellular mucin in at least 90% of tumor cells is characteristic of ovarian and pancreatic cystic mucinous carcinomas, whereas colloid carcinomas deriving from the gastrointestinal tract, lung, breast or skin contain abundant extracellular mucin, accounting for at least 50% of tumor volume [15,26]. The investigation of IHC markers is a complementary procedure for the histopathological examination, although the levels of markers overlap in primary and secondary mucinous ovarian tumors [3,4]. The typical IHC profile for MOC is CK7(+), CK20 and CDX2(+/-), PAX8(+/-), and SATB2(-). The positivity of PAX8 strongly suggests ovarian origin [15,27-31]. The characteristic histopathological features of PMOTs are shown in Table 1.

Table 1. Abbreviated classification of primary mucinous neoplasms of the ovary [2,12,15,16,20,21,25,32-34]

Feature	Benign	Borderline	Carcinoma
Histological subtypes	Mucinous cystadenoma Mucinous adenofibroma With focal epithelial proliferation	With microinvasion With microinvasive carcinoma With mural nodule	With expansile invasion With infiltrative expansion With mural nodules
Age	50 years old	45 years old	<40 years old
Histopathological characteristics	Cysts and gland lined by a single layer of gastrointestinal or Müllerian-type mucinous epithelium Possibility of uncommon incidence of goblet cells, neuroendocrine or Paneth cells	Multiloculated Variably-sized cysts with at least 10% of the total tumor area demonstrating epithelial stratification with small papillae or tufts	Expansile growth: architecturally complex and confluent, well-formed glands with round, convex outer outlines, absent or minimal stroma, which does not surround individual glands entirely Infiltrative growth: glands with irregular contours, possibility of stromal desmoplasia

Molecular relation between benign, borderline and malignant ovarian mucinous tumors

The most frequent molecular alterations in all PMOTs are *KRAS* mutation and *CDKN2A* inactivation [1,2,6,7]. It is indicated that, in most cases, mucinous carcinomas develop from mucinous borderline tumors, and sporadically from mature cystic teratomas or Brenner tumors with gastrointestinal type cells [6,9,35,36]. Recent studies are not unanimous in determining the particular changes in molecular features

between benign, borderline and malignant mucinous tumors [8]. Some sources suggest that benign tumors exhibit either *KRAS* mutation or *CDKN2A* inactivation, while borderline tumors are more likely to have both, with additional copy number variations. In MOC, copy number alterations (especially amplification of 9p13.3) and *TP53* mutations are even more likely to appear [6,35,36]. One study has revealed that the prevalence of *KRAS*, *BRAF* and/or *CDKN2A* mutations in mucinous borderline tumors and MOCs totals 95% and 91%, respectively [1]. It is believed that the frequency of *TP53* pathogenic variants and whole genomic copy number variations are key drivers of malignancy [1,37]. Other studies suggest that the increased number of *KRAS* mutations is the strongest predictor of unequivocal malignancy in ovarian mucinous neoplasms [2,38]. Moreover, the less common *BRAF* mutations also seem to appear more frequently in carcinomas than in benign or borderline mucinous tumors [39]. A recent study reveals that *HER2* overexpression or amplification is observed more often in MOC than in borderline mucinous tumors (35,3% and 5,3%, respectively), and this correlation might play a role in differential diagnosis [8]. On the other hand, the absence of *KRAS* or *HER2* mutations in mucinous carcinomas might suggest that they originated from less frequent precursors, such as like mature cystic teratomas [40].

Generally, the most common molecular alterations in MOC include *KRAS* (40-76%) or *HER2* amplification (15-35%), *CDKN2A* (33-76%) and *TP53* (52-75%) mutations, as well as copy number alterations, which are much more prevalent in MOC than in their non-carcinomatous counterparts. One such example of copy number alteration is amplification of 9p13, which is usually seen in tumors with both *KRAS* and *TP53* mutations. Among the genes less frequently altered in MOC are *RNF43*, *BRAF* (0-9%), *PIK3CA* (6%) and *ARID1A* (8-12%) [1,2,6,8,12,15,27,39,41,42]. There is still limited data available to compare molecular features between infiltrative and expansile MOC. One study suggests that *HER2* overexpression or amplification is more common in expansile MOC than in infiltrative MOC, but the difference is not statistically significant [8].

Differences between mucinous ovarian neoplasms and other tumor types

MOTs show different molecular mutations than other subtypes of EONs. Epithelial ovarian cancer (EOC) is histologically divided into serous (high-grade (71% of all EOCs) and low-grade (4,1%)), endometrioid (8,3%), clear-cell (9,5%), and mucinous EOC [43]. However, there is another dualistic classification, which divides EOC into type I (low-grade) carcinoma and type II (high-grade) carcinoma [7]. Type I EOCs account for 25% of the total and include low-grade serous EOC, low-grade endometrioid EOC, mucinous EOC, and clear-cell EOC, meanwhile type II account for 75% of all EOC and include high-grade serous EOC, high-grade endometrioid EOC, undifferentiated carcinoma and carcinosarcoma [7]. Generally, in type II EOCs, *TP53* mutation is the most frequent (>95%), followed by *BRCA1* or *BRCA2* mutation, which is found in 30-50% of all type II EOCs [5-7,44]. The most common mutations in low-grade serous EOC are *BRAF* (8-38%) and *KRAS*

(19-25%), while other genes, such as *NRAS* (8%), *EIFAX* (15%) or *USP9X* (11%), are less often involved [5-7,45]. Mutations most characteristic of clear-cell carcinoma include *ARID1A* (40-75%), *PIK3CA* (40-50%), *PPP2R1A* (10-20%), *KRAS* (5-20%) and *TERT* (15%); *HER2* amplification, on the other hand, appears in 15% of all cases [5,6,46-49]. In turn, endometrioid carcinomas usually exhibit mutations in genes *CTNNB1* (30-50%), *PIK3CA* (15-45%), *ARID1A* (30-40%), *PTEN* (20-45%), *KRAS* (10-40%) and *TP53* (10-25%) [5,6,50,51]. In borderline endometrioid tumors, the incidence of *CTNNB1* mutations is exceptionally high and amounts to 90% [6]. The most frequent mutations in histological subtypes of MOCs are listed in Table 2.

Table 2. Comparison of the most common molecular alterations in the most significant subtypes of epithelial ovarian carcinomas [5-7]

Subtype of EOC	Endometrioid EOC	Clear-cell EOC	Mucinous EOC	Low-grade serous EOC	High-grade serous EOC
The most common mutations	<i>CTNNB1</i> , <i>PIK3CA</i> , <i>ARID1A</i> , <i>PTEN</i> , <i>KRAS</i> , <i>TP53</i> genes	<i>PIK3CA</i> , <i>ARID1A</i> , <i>KRAS</i> , <i>PPP2R1A</i> , <i>TERT</i> promoter genes	<i>KRAS</i> , <i>TP53</i> , <i>RNF43</i> , <i>ARID1A</i> , <i>BRAF</i> , <i>PIK3CA</i> , <i>CDKN2A</i> genes	<i>KRAS</i> , <i>BRAF</i> , <i>NRAS</i> , <i>USP9X</i> , <i>EIF1AX</i> genes	<i>TP53</i> , <i>BRCA1</i> , <i>BRCA2</i> genes

The molecular findings might be helpful in differentiating between PMOTs and metastatic mucinous tumors involving the ovary. For instance, *APC* inactivating mutations are more frequent in colorectal metastases than in primary MOCs (71% vs 4%, respectively) [52]. Another study shows that *TP53* and *KRAS* mutations are more common in primary MOCs than gastric metastases, meanwhile *APC*, *PIK3CA* and *FBXW7* are more common in colorectal (CRC) metastases than in primary MOCs [11,15,26,41]. In contrast, the prevalence of *KRAS* mutations in MOCs and mucinous CRC metastases is similar (33-46% vs 31-48%, respectively), while *BRAF* mutations in MOCs (0-9%) are significantly lower than in mucinous CRC metastases (15-27%). Moreover, *HER2* amplification appears in 18-35% of all MOCs, as compared to <1% in mucinous CRC metastases and only 2% in non-mucinous CRC metastases [11,15,26]. Furthermore, metastases derived from HPV-associated endocervical adenocarcinoma do not typically include *TP53* mutations, unlike MOC. Although the *TP53*, *KRAS*, and *CDKN2A* alterations overlap in gastric-type endocervical adenocarcinoma and MOC, the presence of *STK11* mutations is more indicative of the first one [53,54].

Molecular alterations in targeted therapy and prognosis

The management of PMOTs depends on the histopathological subtype and the size of the tumor. Generally, in the case of benign mucinous tumors, complete surgical resection is sufficient and recurrence is not observed [2]. 90% of all mucinous borderline tumors are diagnosed in stage I and only 10% are associated with extra-ovarian spread. In young patients, resection of primary borderline tumor with fertility preservation is recommended and relapse is uncommon. Postoperative therapy is dedicated to patients with serous borderline tumors and invasive implants [17]. In early-stage MOC, staging procedure including peritoneal washing for cytology, hysterectomy, bilateral salpingo-oophorectomy, pelvic and para-aortic lymphadenectomy,

omentectomy, and multiple peritoneal biopsies, is the gold standard. In advanced MOC, cytoreductive surgery with complete removal of all measurable disease is recommended [11,15,22,34,55]. The advanced stage of the disease requires platinum-based chemotherapy, although MOC has lower response than other types of EOC and is suspected to be platinum-resistant [7,11,23,37].

The rarity of advanced-stage MOC and its chemoresistance make proper management exceptionally difficult. Targeted therapy puts a new light on the treatment of the disease, although the available data is limited [15,56]. Amplification of *ERBB2* (26,7%) and *BRAF* mutation (9%) have been proven to be good targets for such therapy. Genetic alterations that are currently being examined as potential targets in clinical trials include: *KRAS/NRAS* mutations (66%), *TP53* missense mutation (49%), *RNF43* mutation (11%), *ARID1A* mutation (10%) and *PIK3CA/PTEN* mutation (9%) [56,57]. In non-mucinous type EOC, poly-adenosine diphosphate-ribose polymerase inhibitors (PARPis) turned out to be a milestone. However, they have no role in the treatment of MOCs as these tumors are not associated with *BRCA* mutations or homologous recombinant deficiency [15]. Bevacizumab, a vascular endothelial growth factor (VEGF) inhibitor, is found to improve progression-free survival (PFS) in EOC in the primary setting and in the platinum-sensitive and platinum-resistant recurrence settings. Moreover, the adjuvant therapy with bevacizumab has been demonstrated to increase overall survival in sub-optimally cytoreduced EOC and in metastatic colorectal carcinoma [58-63]. Cetuximab, EGFR monoclonal antibody, seems to be efficient in *KRAS* wild-type cases of CRC metastases and ovarian cancer. However, the results of cetuximab both as a single therapy or in combination with standard chemotherapy in ovarian cancer without specification of *KRAS* status were disappointing [15,64-66]. Limited studies suggest that anti-HER2 therapy with trastuzumab in MOC with *HER2* amplification might be sufficient, although more data is needed [6,15,56,67]. Moreover, *PLK1* inhibitors, dual *RAS/RAF* inhibitors and *MEK* inhibitors are suggested to be efficient in treatment of MOC, although there are currently no published studies evaluating such therapies in pre-clinical models [56].

Benign mucinous ovarian tumors, borderline mucinous ovarian tumors, and early-stage MOC have an excellent prognosis (>90% of 5-year OS), however, survival in metastatic disease ranges between 12 and 30 months (15,37,68). Moreover, infiltrative MOC has a significantly poorer PFS than expansile MOC (65,6% vs 94,7%), while the difference in OS was similar (90% vs 88,9%, respectively) (16). It is clearly evident that high copy number aberration burden is associated with poorer prognosis in MOC [1,6].


CONCLUSIONS


Molecular features in mucinous ovarian tumors are believed to help understand the origin and taxonomy of these rare neoplasms. They are not only prognostic factors, but also useful diagnostic tools in differentiating between PMOTs and other subtypes of EONs and mucinous metastases involving the ovary. Because surgical

management and adjuvant chemotherapy might be insufficient in the advanced disease, the possibilities within targeted therapies associated with molecular aberrations should be intensively investigated.

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