Acta Biomed 2025; Vol. 96, N. 5: 17657 DOI: 10.23750/abm.v96i5.17657

Original article

MUC5AC expression as a predictive biomarker of omental metastasis in primary mucinous ovarian carcinoma

Desy Ekamadayani Ahmad[1], Rina Masadah[1], Berti Julian Nelwan[1], Upik Anderiani Miskad[1,2], Djumadi Achmad[1], Amalia Yamin[1,3], Suryani Tawali[4]

[1]Department of Pathology Anatomy, Faculty of Medicine, Hasanuddin University, Makassar, Indonesia; [2]Anatomical Pathology Laboratory, Hasanuddin University Hospital, Makassar, Indonesia; [3]Anatomical Pathology Laboratory, Wahidin Sudirohusodo Hospital, Makassar, Indonesia; [4]Department of Public Health, Faculty of Medicine, Hasanuddin University, Makassar, Indonesia

Abstract. *Background and aim:* Primary mucinous ovarian carcinoma is an uncommon epithelial ovarian cancer subtype with poor advanced prognosis. Identifying predictive biomarker of early metastatic spread is essential for improving staging and therapeutic strategies. Mucin 5AC (MUC5AC), a secretory glycoprotein, has been linked to tumor progression and epithelial–mesenchymal transition (EMT). This study aimed to evaluate the association between MUC5AC expression and omental metastasis in primary mucinous ovarian carcinoma. *Methods:* A cross-sectional study was conducted to semi-quantitatively analyze MUC5AC expression in 63 paraffin-embedded tissue samples of primary mucinous ovarian carcinoma. Immunohistochemical staining was performed using a rabbit polyclonal MUC5AC antibody. Expression levels were categorized as low or high based on intensity and distribution. A Chi-square test was used to assess the relationship between MUC5AC expression and omental metastasis. *Results:* The study included 63 cases of primary mucinous ovarian carcinoma, consisting of 37 (58.7%) with omental metastasis and 26 (41.3%) without metastasis. High MUC5AC expression was observed in 86.5% of metastatic cases and in 50.0% of non-metastatic cases. This difference was statistically significant (*P*-value 0.002 [≤0.05]). Patients with high MUC5AC expression had a 6.40 times higher likelihood of omental metastasis than those with low expression (95% CI: 1.89–21.5). *Conclusions:* High MUC5AC expression was significantly associated with omental metastasis in primary mucinous ovarian carcinoma, supporting its potential role as a predictive biomarker for metastatic risk stratification. (www.actabiomedica.it)

Key words: MUC5AC expression, mucinous ovarian carcinoma, omental metastasis, predictive biomarker

Introduction

Ovarian cancer is the sixth most prevalent malignancy in women worldwide and has a high fatality rate owing to delayed diagnosis and lack of early indications (1). Ovarian cancer is hard to detect because of peritoneal spread and ambiguous abdominal symptoms. Worldwide, 313,959 new ovarian cancer cases and 207,252 deaths occurred in 2020, indicating its poor prognosis (2). These figures underscore a mortality-to-incidence ratio that is substantially higher compared to breast or cervical cancer, reinforcing its status as one of the most lethal cancers affecting women in the region (3). A 5-year survival rate of over 90% is typical for early-stage mucinous ovarian cancer. Metastatic illness patients had a 12- to 30-month survival rate (4). Ovarian cancer has several histological subgroups with different molecular characteristics, clinical behavior, and therapeutic responsiveness (5). Pathogenic processes divide ovarian carcinoma into

two forms. Type I includes endometrioid, clear cell, seromucinous, Brenner, and low-grade serous carcinomas. (6) Undifferentiated, carcinosarcoma, and high-grade serous carcinoma are type II. Epithelial ovarian cancers account for 90%, with serous carcinoma being the most frequent subtype. Mucinous ovarian carcinoma, which accounts for 3%–5% of epithelial ovarian malignancies, is a unique clinical and molecular subpopulation that warrants additional study (3). Mucinous ovarian cancer closely mimics the gastrointestinal tract's mucin-producing epithelium and progresses from benign mucinous cystadenoma to borderline mucinous tumors to invasive carcinoma. KRAS mutations and PI3K/AKT pathway dysregulation commonly accompany this development (7). While early-stage mucinous ovarian carcinoma generally carries a favorable prognosis, with a five-year survival rate approaching 90%, the prognosis significantly worsens once metastasis occurs. Advanced-stage disease is often resistant to conventional therapy and associated with substantially reduced survival outcomes. In the FIGO staging system, omental involvement is categorized as stage III disease, which is associated with a significant drop in overall survival and a shift in treatment strategy (8). Therefore, biomarkers that correlate with omental spread may aid early prognostication and clinical decision-making. A major clinical challenge in mucinous ovarian carcinoma is its frequent presentation at advanced stages, often after peritoneal spread or distant metastasis has occurred (1). Although early-stage mucinous tumors tend to exhibit indolent behavior, advanced-stage disease is typically associated with poor therapeutic response and decreased overall survival, underscoring the need for accurate risk stratification. Conventional imaging and histopathological assessment often fail to distinguish aggressive from indolent tumors in the early stages. This highlights the urgent need for reliable biomarkers to predict metastatic potential and guide early therapeutic intervention. Tumor metastasis depends on epithelial-mesenchymal transition (EMT), in which epithelial cells lose their polarity and intercellular connections and develop mesenchymal motility and invasiveness (7,8). EMT drives ovarian cancer peritoneal spread and is connected to chemoresistance and recurrence. Mucin family proteins, notably Mucin 5AC (MUC5AC), promote EMT in epithelial malignancies, including gastrointestinal and respiratory tract tumors (11). Although MUC5AC's significance in ovarian cancer is unclear, its overexpression is postulated to facilitate EMT-mediated metastatic progression, thereby contributing to the aggressive clinical behavior observed in certain cases of mucinous ovarian carcinoma. MUC5AC is a member of the mucin superfamily and belongs to the category of secretory mucins (12). MUC5AC is a secretory mucin typically expressed in the epithelial linings of the stomach, tracheobronchial tree, and endocervix, where it serves to protect mucosal surfaces. It is generally absent in normal ovarian tissue. Abnormal expression has been seen in stomach, pancreatic, and colon cancers. MUC5AC increases tumor cell proliferation, invasion, and metastasis via integrin-mediated signaling, cytoskeletal reorganization, and extracellular matrix breakdown. Specifically, MUC5AC promotes tumor invasiveness through interaction with β4 integrin and subsequent activation of focal adhesion kinase (FAK), which triggers downstream pathways such as PI3K/AKT and MAPK/ERK. In addition, MUC5AC contributes to enhanced cell migration, immune evasion, and resistance to apoptosis, reflecting its multifactorial role in tumor progression (11). Recent studies have increasingly focused on the role of MUC5AC across various carcinomas. Its expression is more frequently observed in primary mucinous ovarian carcinomas than in metastatic gastrointestinal tumors, suggesting its potential utility as a tissue-specific diagnostic marker (13). MUC5AC is consistently expressed in mucinous ovarian neoplasms and has been shown to correlate with higher histological grade and poorer clinical outcomes, indicating possible diagnostic and prognostic significance (14). MUC5AC is also involved in epithelial-mesenchymal transition, extracellular matrix remodeling, and peritoneal implantation in ovarian cancer, supporting its position as a metastasis protein (15). Given its established involvement in tumor progression and metastasis in various epithelial malignancies, as well as its consistent expression in mucinous ovarian neoplasms, MUC5AC emerges as a promising biomarker for further investigation. However, limited studies have specifically evaluated its role in relation to metastatic behavior in mucinous ovarian carcinoma.

According to the FIGO staging system, omental metastasis corresponds to stage III disease, which is associated with significantly worse prognosis and altered treatment algorithms. Although MUC5AC expression has been previously studied as a diagnostic marker to distinguish primary from metastatic mucinous tumors, its prognostic significance—particularly in predicting omental dissemination in primary mucinous ovarian carcinoma—remains underexplored. To the best of our knowledge, this is one of the first studies to semi-quantitatively evaluate MUC5AC expression in relation to omental metastasis in strictly primary mucinous ovarian carcinoma. Given the clinical implications of omental involvement, identifying tissue-based predictive biomarker of metastatic risk may provide prognostic value. Accordingly, we examined the correlation between MUC5AC expression and omental metastasis in mucinous ovarian carcinoma.

Material and Methods

Study design

This cross-sectional study was conducted at Wahidin Sudirohusodo Hospital and Hasanuddin University Hospital in Makassar, Indonesia. Mucinous ovarian carcinoma patient tissue specimens were examined for MUC5AC expression at Department of Pathology Anatomy, Faculty of Medicine, Hasanuddin University. Tissue specimens from patients diagnosed with mucinous ovarian carcinoma were collected from January 2020 to September 2024. Inclusion criteria for this study were paraffin-embedded ovarian tumor tissue blocks accompanied by omental tissue, histopathologically diagnosed as mucinous ovarian carcinoma with or without omental metastasis. Ovarian tumor tissue and omental tissue were processed as separate paraffin-embedded blocks to ensure independent evaluation of the primary tumor and metastatic deposits. Exclusion criteria included tissue blocks with poor preservation, damaged sections, or inadequate material for immunohistochemical examination. All cases were reviewed independently by two anatomical pathologists. MUC5AC expression was semi-quantitatively assessed and recorded as numerical scores derived from immunohistochemical analysis.

Research procedures

Formalin-fixed paraffin-embedded (FFPE) blocks were used to create 3 μm tissue sections. After deparaffinization, the slides were immunostained with a rabbit polyclonal antibody specific for MUC5AC (Elabscience, Wuhan, China; catalog no. D-AB-10374L) at a dilution of 1:1200. The staining was evaluated under a light microscope at 200× magnification. Two anatomical pathologists, blinded to the patients' clinical data, independently assessed MUC5AC expression. Specifically, the percentage of positively stained tumor cell membrane and cytoplasm exhibiting a brown coloration was determined microscopically. This assessment was performed using a semi-quantitative scoring system adapted from Rico *et al.* (16). MUC5AC expression was categorized as negative without staining; weak with intensity +1 in ≤70% of tumor cells or intensity +2 in ≤30% of tumor cells; moderate with intensity +1 in >70%, intensity +2 in >30% but ≤70%, or intensity +3 in ≤30% of tumor cells; and strong with intensity +2 in >70% or intensity +3 in >30% of tumor cells. For statistical purposes, MUC5AC expression was divided into low expression (negative and weak) and high expression (moderate and strong) groups. Omental metastatic status was confirmed by the presence of tumor cell nests within the omentum based on hematoxylin and eosin (H&E) staining.

Statistical analysis

Data analysis was performed using SPSS 26.0 and the research patients' clinical and pathological features were summarized using descriptive statistics. MUC5AC expression and omental metastasis were examined using the Chi-square test. A *P*-value <0.05 indicated statistical significance. Figure 1 shows the research flow, including MUC5AC expression and omental metastasis.

Results

A total of 63 primary mucinous ovarian carcinoma patients were studied. These were 37 (58.7%) with omental metastasis and 26 (41.3%) without metastasis

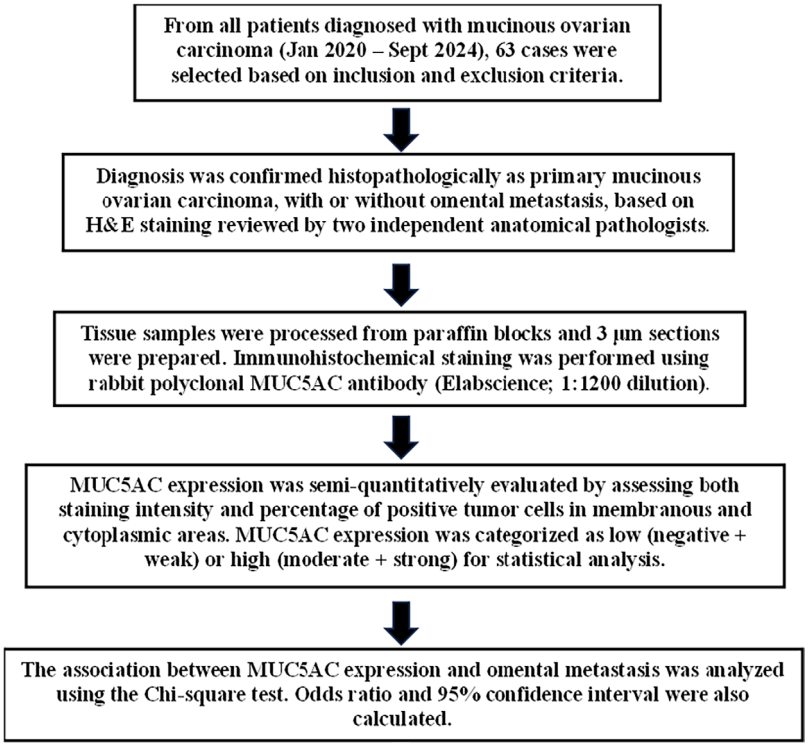

Figure 1. Study flow of MUC5AC expression and omental metastasis.

(Figure 2). The clinicopathological characteristics of the patients are shown in Table 1. The majority of patients were under 50 years of age (42 patients; 66.7%), with the remaining 21 (33.3%) aged 50 years or older. In terms of parity, most were multiparous (39 patients; 61.9%), followed by nulliparous (16 patients; 25.4%) and grand multiparous (8 patients; 12.7%).

MUC5AC expression was evaluated immunohistochemically and categorized into low and high expression groups. High MUC5AC expression was observed in 45 cases (71.4%), while low expression was found in 18 cases (28.6%). The distribution of staining intensity included strong expression (+3) in 25 cases, moderate (+2) in 20 cases, weak (+1) in 16 cases, and negative staining (score 0) in 2 cases. Both membranous and cytoplasm localization of MUC5AC was identified. Strong intensity appeared as dark brown, moderate as light brown, weak as faint brown, and negative cases showed no detectable staining (Figure 3).

As shown in Table 2, high MUC5AC expression was more frequently observed in patients with omental metastasis (32/37; 86.5%) compared to those without metastasis (13/26; 50.0%). Conversely, low expression was identified in only 5 metastatic cases (13.5%) and 13 non-metastatic cases (50.0%). Statistical analysis using the Chi-square test demonstrated a significant association between MUC5AC expression and metastasis status (P = 0.002 [≤ 0.05]). Patients with high MUC5AC expression had 6.40-fold higher odds of omental metastasis compared with those with low expression (95% CI: 1.89–21.5).

Discussion

In this study, a higher proportion of mucinous ovarian carcinoma patients with omental metastasis demonstrated high MUC5AC expression (32 out of 37 cases; 86.5%) compared to those without metastasis

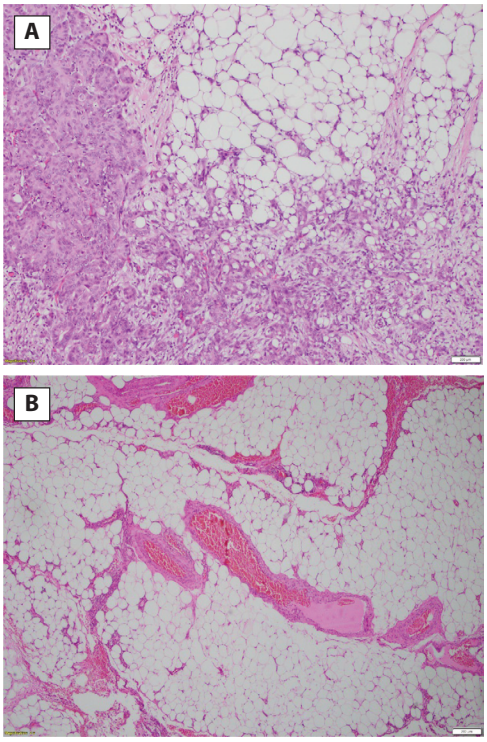

Figure 2. Omental Metastasis in Mucinous Ovarian Carcinoma. A: Omental metastasis showing tumor cell infiltration within adipose tissue; B: Omental tissue without metastatic infiltration. (H&E, 100x Magnification).

Table 1. Characteristic of patients

Characteristics	n	%
Age (years)		
< 50	42	66.7
≥ 50	21	33.3
Parity Status		
Nulliparous	16	25.4
Multiparous	39	61.9
Grand multiparous	8	12.7
Omental Metastasis		
Yes	37	58.7
No	26	41.3
MUC5AC Expression		
Low	18	28.6
High	45	71.4

(13 out of 26; 50.0%) which showed high expression. Conversely, low MUC5AC expression was observed in 5 metastatic cases (13.5%) and 13 non-metastatic cases (50.0%). Statistical analysis using the Chi-square test revealed a significant association between MUC5AC expression and omental metastasis (P = 0.002). This finding showed that a critical process in tumor metastasis, epithelial–mesenchymal transition (EMT), may be promoted by MUC5AC overexpression. Various ligands, including EGF, TGF-α, TNF-α, and interleukins, affect MUC5AC transcription in goblet and epithelial cells, activating downstream signaling pathways to increase MUC5AC expression (17). MUC5AC modulates β4- and α6-cadherins, triggering activation of the focal adhesion kinase (FAK) pathway—a major regulator of cell motility. This signaling promotes cytoskeletal remodeling and enhances cell migration. EMT also involves E-cadherin downregulation and N-cadherin upregulation (cadherin switching), leading to the loss of intercellular adhesion and acquisition of spindle-shaped, mesenchymal morphology. These changes enable tumor cells to detach and invade surrounding or distant tissues (18). Thus, MUC5AC expression contributes to tumor cell migration and adhesion, which are critical early steps in metastasis and vascular invasion (19). Research on primary mucinous ovarian carcinoma remains relatively limited. Despite fewer instances than the serous subtype, advanced-stage mucinous ovarian cancer has a greater fatality rate. This discrepancy emphasizes the therapeutic necessity to study its biochemical and molecular properties. While many studies have examined MUC5AC in other malignancies, its role in primary ovarian carcinoma, particularly the mucinous subtype, remains inadequately defined. In colorectal cancer, MUC5AC overexpression enhances invasion, motility, and apoptosis resistance via β-catenin and CD44 signaling (20). In pancreatic cancer, silencing MUC5AC reduces metastasis and tumor growth by suppressing the KLF4–Src–STAT3 axis (21). Additionally, MUC5AC-induced activation of the FAK pathway promotes EMT and invasive properties, supporting its oncogenic function (18). These mechanisms, shared across epithelial malignancies,

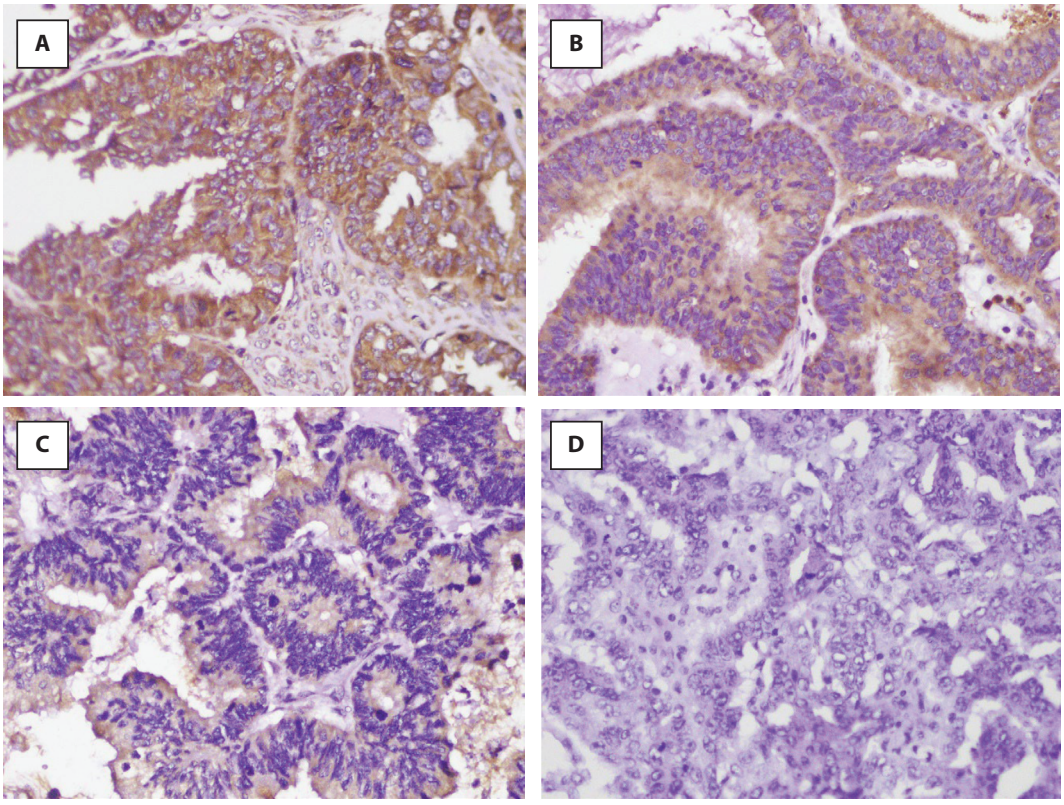

Figure 3. MUC5AC intensity in Mucinous Ovarian Carcinoma. A: Strong (+3); B: Moderate (+2); C: Weak (+1); D: Negative (0). (IHC, 200x Magnification).

Table 2. MUC5AC expression profile with omental metastasis status in mucinous ovarian carcinoma

MUC5AC Expression	Omental Metastasis Status		OR (CI 95%)	*P*-value
	Yes n (%)	No n (%)		
High	32 (86.5)	13 (50.0)	6.40 (1.89-21.5)	0.002*
Low	5 (13.5)	13 (50.0)		

Note: Chi Square test, Significant *P*-value if *P*<0.05

are relevant due to biological similarities with mucinous ovarian carcinoma (11). These findings support the role of MUC5AC in promoting invasive tumor behavior and underscore its potential as a prognostic biomarker for metastasis in primary mucinous ovarian carcinoma. In this study, the Chi-square test showed that patients with high MUC5AC expression were 6.4 times more likely to develop omental metastasis than those with low expression. Since FIGO stage III involves the omental metastasis, MUC5AC overexpression may be an early indicator of upstaging risk. Clinically, MUC5AC may be a valuable prognostic biomarker for identifying individuals at higher risk of metastatic spread. Although MUC5AC is often used to differentiate primary from metastatic mucinous tumors, its prognostic relevance in predicting metastasis in primary ovarian carcinoma remains limited. Our results demonstrate a strong association between high MUC5AC expression and omental metastasis, supporting its potential role in early risk stratification—particularly for peritoneal dissemination, which is often underrecognized in this subtype. In clinical practice, detecting high MUC5AC expression at the time of diagnosis may prompt heightened suspicion for occult omental metastasis. This could guide clinicians to perform more comprehensive surgical staging or initiate more aggressive initial treatment plans.

Early identification of high-risk cases may help prevent undertreatment and ultimately improve patient prognosis. Notably, this is the first semi-quantitative study correlating MUC5AC expression with omental metastasis using a defined scoring system in strictly primary cases. Although this study provides important preliminary evidence of the association between MUC5AC expression and omental metastasis, several limitations should be acknowledged. First, the cross-sectional design limits causal inference regarding the role of MUC5AC in metastatic progression. Second, external generalizability may be constrained by the absence of validation in an independent cohort. Third, the use of a single immunohistochemical biomarker may not fully capture the molecular complexity underlying metastasis. To strengthen these findings, future research should adopt prospective cohort designs, involve larger multi-center cohorts, and include additional biomarkers such as EMT or ovarian lineage markers. Furthermore, integrating MUC5AC expression into clinical risk models or molecular profiling platforms may enhance its prognostic utility in guiding personalized management strategies for mucinous ovarian carcinoma.

Conclusion

This study demonstrated a significant association between MUC5AC expression and omental metastasis in primary mucinous ovarian carcinoma. High MUC5AC expression was more frequently observed in patients with metastasis than in those without. These findings suggest that elevated MUC5AC expression may be associated with an increased risk of metastatic progression.

Ethic Approval: This study was approved by the institutional review board and conducted in accordance with the principles of the Declaration of Helsinki. Ethical clearance was obtained from the Health Research Ethics Committee, Faculty of Medicine, Hasanuddin University (protocol number UH24080630 and registry number 801/UN4.6.4.5.31/PP36/2024) on August 21, 2024.

Conflict of Interest: Each author declares that he or she has no commercial associations (e.g. consultancies, stock ownership, equity interest, patent/licensing arrangement etc.) that might pose a conflict of interest in connection with the submitted article.

Authors Contribution: DEA (Concept, Design, Resources, Materials, Data Collection and Processing, Analysis and Interpretation, Literature Search, Writing Manuscript), RM, BJN (Concept, Design, Supervision, Resources, Materials, Data Collection and Processing, Analysis, and Interpretation), and UAM, DA, AY, ST (Analysis and Interpretation, Supervision, Resources). All authors read and approved the final version of the manuscript.

Declaration on the Use of AI: Artificial intelligence tools (ChatGPT) were used only for grammar refinement and language editing during manuscript preparation. No AI tools were used to generate scientific content, analyze data, or draw conclusions. The authors take full responsibility for the integrity, accuracy, and originality of the entire scientific content of this manuscript.

Consent for Publication: All subjects have provided consent for publication.

Acknowledgments: We thank the Department of Pathology Anatomy, Faculty of Medicine, Hasanuddin University, and Wahidin Sudirohusodo Hospital, Makassar, Indonesia, for their assistance. We also extend our heartfelt thanks to all our mentors for their invaluable guidance throughout this study.

Funding: This research received no external funding.

Data Availability Statement: All the data are available from the corresponding author upon a reasonable request [DEA].

Abbreviations

MUC5AC: Mucin 5AC
EMT: Epithelial-mesenchymal transition
FIGO: Fédération Internationale de Gynécologie et d'Obstétrique (International Federation of Gynaecology and Obstetrics)
KRAS: Kirsten rat sarcoma virus
PI3K/AKT: Phosphatidylinositol-3 kinase/Protein kinase B
FAK: Focal adhesion kinase
MAPK/ERK: Mitogen-Activated Protein Kinase/Extracellular Signal-Regulated Kinase
FFPE: Formalin-fixed paraffin-embedded
H&E: Haematoxylin and Eosin
EGF: Epidermal Growth Factor
TGF-α: Transforming Growth Factor-alpha
TNF-α: Tumor Necrosis Factor-alpha

References

1. Wang Y, Liu L, Yu Y. Mucins and mucinous ovarian carcinoma: Development, differential diagnosis, and treatment. Heliyon. 2023;9(8):e19221. doi: 10.1016/j.heliyon.2023.e19221
2. Globocan Observatory WHO. Ovarian Cancer Incidence and Mortality. Int Agency Res Cancer GLOBOCAN. 2020;5–6. Available from: https://gco.iarc.fr/today/data/factsheets/cancers/25-Ovary-fact-sheet.pdf
3. Momenimovahed Z, Tiznobaik A, Taheri S, Salehiniya H. Ovarian cancer in the world: Epidemiology and risk factors. Int J Womens Health. 2019;11:287–99. doi: 10.2147/IJWH.S197604
4. Morice P, Gouy S, Leary A. Mucinous Ovarian Carcinoma. N Engl J Med. 2019;380(13):1256–66. doi: 10.1056/nejmra1813254
5. Kroeger PT, Drapkin R. Pathogenesis and heterogeneity of ovarian cancer. Curr Opin Obstet Gynecol. 2017;29(1):26–34. doi: 10.1097/GCO.0000000000000340
6. Budiana ING, Angelina M, Pemayun TGA. Ovarian cancer: Pathogenesis and current recommendations for prophylactic surgery. J Turkish-German Gynecol Assoc. 2019;20(1):47–54. doi: 10.4274/jtgga.galenos.2018.2018.0119
7. Koshiyama M, Matsumura N, Konishi I. Recent concepts of ovarian carcinogenesis: Type I and type II. Biomed Res Int. 2014;2014. doi: 10.1155/2014/934261
8. Javadi S, Ganeshan DM, Qayyum A, Iyer RB, Bhosale P. Ovarian cancer, the revised FIGO staging system, and the role of imaging. Am J Roentgenol. 2016;206(6):1351–60. doi: 10.2214/AJR.15.15199
9. Lengyel E. Ovarian cancer development and metastasis. Am J Pathol. 2010;177(3):1053–64. doi: 10.2353/ajpath.2010.100105
10. Yang Y, Yang Y, Yang J, Zhao X, Wei X. Tumor Microenvironment in Ovarian Cancer: Function and Therapeutic Strategy. Front Cell Dev Biol. 2020;8(August):1–30. doi: 10.3389/fcell.2020.00758
11. Rico SD, Mahnken M, Buscheck F, Dum D, Luebke AM, Kluth M. MUC5AC Expression in Various Tumor Types and Nonneoplastic Tissue - A Tissue Microarray Study on 10 399 Tissue Samples. Technol Cancer Res Treat. 2021;20:1–13. doi: 10.1177/15330338211043328
12. Kufe DW. Mucins in cancer: Function, prognosis and therapy. Nat Rev Cancer. 2009;9(12):874–85. doi: 10.1038/nrc2761
13. Kelemen LE, Köbel M. Mucinous carcinomas of the ovary and colorectum: Different organ, same dilemma. Lancet Oncol. 2011;12(11):1071–80. doi: 10.1016/S1470-2045(11)70058-4
14. Chelariu-Raicu A, Holley E, Mayr D, et al. A combination of immunohistochemical markers, MUC1, MUC5AC, PAX8 and growth pattern for characterization of mucinous neoplasm of the ovary. Int J Gynecol Cancer. 2022;662–8. doi: 10.1136/ijgc-2021-003104
15. Jun SY, Lee EJ, Kim S Il, An S. Tumor Microenvironment Prognostic Risk and Its Association with MUC5AC in Ampullary Carcinoma. Arch Pathol Lab Med. 2023;147(9):1060–74. doi: 10.5858/arpa.2022-0131-OA
16. Rico SD, Schmalfeldt B, Müller V, et al. MUC5AC expression is linked to mucinous/endometroid subtype, absence of nodal metastasis and mismatch repair deficiency in ovarian cancer. Pathol Res Pract. 2021;224(January). doi: 10.1016/j.prp.2021.153533
17. Krishn SR, Ganguly K, Kaur S, Batra SK. Ramifications of secreted mucin MUC5AC in malignant journey: A holistic view. Carcinogenesis. 2018;39(5):633–51. doi: 10.1093/carcin/bgy019
18. Marimuthu S, Rauth S, Ganguly K, et al. Mucins reprogram stemness, metabolism and promote chemoresistance during cancer progression. Cancer Metastasis Rev. 2021;40(2):575–88. doi: 10.1007/s10555-021-09959-1
19. Reynolds IS, Fichtner M, McNamara DA, Kay EW, Prehn JHM, Burke JP. Mucin glycoproteins block apoptosis; promote invasion, proliferation, and migration; and cause chemoresistance through diverse pathways in epithelial cancers. Cancer Metastasis Rev. 2019;38(1–2):237–57. doi: 10.1007/s10555-019-09781-w
20. Pothuraju R, Rachagani S, Krishn SR, et al. Molecular implications of MUC5AC-CD44 axis in colorectal cancer progression and chemoresistance. Mol Cancer. 2020;19(1):1–14. doi: 10.1186/s12943-020-01156-y
21. Ganguly K, Krishn SR, Rachagani S, et al. Secretory Mucin 5AC Promotes Neoplastic Progression by Augmenting KLF4-Mediated Pancreatic Cancer Cell Stemness. Cancer Res. 2021;81(1):91–102. doi: 10.1158/0008-5472.CAN-20-1293

Correspondence:
Received: 3 August 2025
Accepted: 3 September 2025
Desy Ekamadayani Ahmad, MD
Department of Pathology Anatomy, Faculty of Medicine, Hasanuddin University, Makassar, Indonesia, Jalan Perintis Kemerdekaan KM 11, 90245, Makassar, Indonesia
E-mail: desy.madayani@gmail.com
ORCID: 0009-0005-3491-8359