Precision medicine in gynecological cancer (Review)

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Abstract. The advent of personalized and precision medicine has revolutionized oncology and treatment of gynecological cancer. These innovative approaches tailor treatments to individual patient profiles beyond genetic markers considering environmental and lifestyle factors, thereby optimizing therapeutic efficacy and minimizing adverse effects. Precision medicine uses advanced genomic technologies such as next-generation sequencing to perform comprehensive tumor profiling. This allows identification of distinct genetic mutations, expression patterns and signaling pathway alterations, revealing the complex molecular landscape of gynecological cancer such as ovarian, cervical and uterine cancer. A major challenge in treating these cancers is their inherent molecular heterogeneity, which can influence tumor behavior, therapy response and prognosis. Precision medicine aims to overcome this by identifying biomarkers and molecular drivers for targeted therapy selection. For example, the identification of breast cancer (BRCA) gene mutations in ovarian cancer has guided the use of poly (ADP-ribose) polymerase inhibitors, leading to more effective treatments with fewer side effects. Similar targeted therapies and immunotherapies have also been developed for cervical and uterine cancer, marking progress toward personalized care. Future directions in gynecological oncology emphasize the importance of molecular profiling and development of targeted therapies. By understanding the unique molecular features of each patient, clinicians can select the most effective personalized treatment strategies to improve patient outcomes and quality of life.

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Contents

1. Introduction

The landscape of cancer treatment and research has undergone notable transformation, with the emergence of personalized and precision medicine as groundbreaking approaches in the management of various types of cancer, including those affecting gynecological organs. These approaches mark a departure from the traditional one-size-fits-all strategy, paving the way for more targeted, efficient and effective interventions (1). In gynecological cancer, encompassing ovarian, cervical, uterine, vaginal and vulvar cancer, precision medicine may improve outcomes, decrease side effects and enhance patient quality of life (2).

Personalized medicine, often used interchangeably with precision medicine, involves customization of medical therapy according to the unique attributes of each patient. It extends beyond focusing on genetic profiles, encompassing a wide array of patient-specific factors, including environmental influences, lifestyle and unique disease pathways. The holistic approach of personalized medicine, which views the patient as an integral part of the treatment equation, optimizes therapeutic decisions and practices for individual patients (3).

Precision medicine emphasizes the incorporation of genetic, environmental and lifestyle information into the diagnosis, treatment and prevention of disease. This approach relies on advanced technologies and the analysis of large

datasets to identify which therapies will be beneficial for patients depending on their genetic and molecular profiling (4). The goal is to select optimal therapies and interventions for patients, minimizing unnecessary treatments and focusing on those most likely to benefit the patient (5).

The present review aims to provide a comprehensive overview of the advances in precision medicine within the context of gynecological cancers, focusing on the challenges posed by tumor heterogeneity, the role of genetic alterations, and the development of targeted therapies. By discussing the current state of precision oncology and its future directions, the present study seeks to highlight the potential for improving patient outcomes through personalized treatment approaches.

2. Tumor heterogeneity in gynecological malignancy

Tumor heterogeneity, a hallmark of cancer, presents challenges in the diagnosis, treatment and management of gynecological malignancies. Heterogeneity manifests at multiple levels, including histological subtype, molecular profile and clinical behavior within gynecological cancers such as ovarian, cervical and uterine cancers (6).

Histological and molecular heterogeneity. Gynecological cancers, particularly ovarian cancer, exhibit substantial histological diversity. For example, ovarian cancer includes subtypes such as high-grade serous (HGS), endometrioid, clear cell and mucinous carcinoma, each with distinct genetic alterations, clinical presentations and responses to therapy (7). Molecular heterogeneity further complicates this landscape as tumors of the same histological subtype may show diverse genetic mutations, gene expression patterns and signaling pathway alterations (8). Advances in genomic technologies, including next-generation sequencing (NGS), enable comprehensive tumor profiling, revealing the complex molecular underpinnings and identifying potential therapeutic targets and biomarkers (8).

Functional and epigenetic heterogeneity. In addition to genetic variations, epigenetic modifications such as DNA methylation and histone modification contribute to tumor heterogeneity by regulating gene expression and cell phenotypes, leading to treatment resistance and phenotypical diversity (9). Phenotypical heterogeneity is also evident in varying cell morphology, proliferation rate and drug sensitivity, complicating treatment strategies (10). Moreover, functional heterogeneity arises from differences in cell metabolism, signaling pathway activation and immune microenvironment interactions, all of which influence tumor aggressiveness and therapeutic resistance (11-15).

3. Challenges in current treatment approaches and future directions

Despite advancements in understanding gynecological cancer and developing targeted therapy, challenges persist, particularly regarding tumor heterogeneity, treatment resistance and disparities in access to innovative treatments (16).

Treatment resistance and recurrence. A major challenge is the high rate of recurrence and development of treatment resistance, especially in advanced-stage gynecological cancer. Even with initial therapeutic success, many patients experience disease progression and become resistant to standard treatments, leading to poor long-term outcomes (16). This resistance often results from the tumor molecular heterogeneity, which necessitates alternative therapeutic strategies and development of novel targeted agents to overcome these resistance mechanisms (17).

Lack of predictive biomarkers. Another significant hurdle is the scarcity of reliable predictive biomarkers for selecting optimal treatment strategies. Although biomarkers such as breast cancer (BRCA) gene mutations in ovarian cancer have been validated for targeted therapy, many patients lack actionable mutations, limiting their treatment options (17). The identification and validation of robust biomarkers that accurately predict treatment response and guide therapeutic decisions is key (18).

Disparities in access to treatment. Disparities in access to genomic testing, targeted therapy and clinical trials are particularly pronounced among populations of developing countries. Limited access to precision medicine exacerbates disparities in outcomes and survival rates between demographic groups (18). Efforts to improve access to innovative therapy and clinical trials for all patients, regardless of socioeconomic status or geographical location, are essential for reducing these disparities (18).

Data interpretation and integration. The integration of multi-omic data and the development of computational algorithms for data analysis present opportunities and challenges. While genomic technology has enabled comprehensive molecular characterization of tumors, interpreting complex genomic data and translating research findings into clinical practice is challenging. Standardization of molecular profiling assays, data sharing initiatives and collaboration across research institutions are necessary to accelerate progress and ensure effective implementation of precision medicine (19).

4. Drivers of genetic alterations in gynecological cancer

A complex interplay of genetic alterations drives gynecological cancer, contributing to tumorigenesis, disease progression and treatment resistance. Understanding the key driver mutations and signaling pathways involved in gynecological malignancy is key for developing targeted therapy and personalized treatment strategies.

In ovarian cancer, HGS carcinoma (HGSC), the most common and aggressive subtype, is characterized by frequent mutations in genes involved in DNA repair pathways, such as BRCA1 and BRCA2 (20). These mutations impair homologous recombination-mediated DNA repair, leading to genomic instability and increased susceptibility to DNA-damaging agents such as platinum-based chemotherapy and poly (ADP-ribose) polymerase (PARP) inhibitors (21). Other recurrent genetic alterations in HGSC include mutations in TP53, which occur in nearly all cases, as well as alterations in genes involved in the PI3K/AKT/mTOR pathway, such as phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic

subunit α (PIK3CA) and PTEN (22). Targeted therapy directed against these genetic aberrations hold promise for improving outcomes in patients with ovarian cancer.

In endometrial cancer, the most common type of uterine cancer, molecular profiling studies have identified distinct genomic subtypes with different etiologies, clinical behavior and treatment responses (22-24). For example, 20-30% of endometrial cancer cases harbor mutations in the PTEN tumor suppressor gene, leading to dysregulated PI3K/AKT/mTOR signaling and aberrant cell proliferation (23). Other recurrent genetic alterations in endometrial cancer include mutations in PIK3CA, Catenin Beta 1 and TP53 genes, as well as microsatellite instability (MSI) and DNA mismatch repair (MMR) deficiency (24). These molecular alterations serve as potential therapeutic targets and predictive biomarkers for targeted therapy and immunotherapy in endometrial cancer.

High-risk human papilloma virus (HPV) types, particularly HPV16 and HPV18, which encode viral oncoproteins that promote cell transformation and oncogenesis, primarily drive cervical cancer (25). Integration of HPV DNA into the host genome disrupts cellular tumor suppressor pathways, such as the retinoblastoma and p53 pathways, leading to uncontrolled cell proliferation and tumor formation (26). In addition to HPV infection, cervical cancer may harbor genetic alterations in genes such as PIK3CA, PTEN and TP53, which contribute to tumor progression and treatment resistance (27). Targeting HPV-associated pathways and associated genetic alterations holds potential for improving outcomes in patients with cervical cancer.

Vulvar and vaginal cancers are relatively rare gynecological malignancies that are often associated with HPV infection, similar to cervical cancer (28). However, vulvar squamous cell carcinoma may also arise in the absence of HPV infection, with mutations in genes such as TP53, PIK3CA and fibroblast growth factor receptor 3 (FGFR3) implicated in tumorigenesis (28). In vaginal cancer, HPV infection is a common risk factor, particularly in younger patients, with mutations in TP53 and PIK3CA identified in a subset of cases (29). Targeted therapy directed against HPV-related pathways and genetic alterations offers potential avenues for improving outcomes in patients with vulvar and vaginal cancer.

5. PARP inhibitors, BRCA and homologous recombination deficiency (HRD) in gynecological cancer

PARP inhibitors exploit synthetic lethality, in which the simultaneous inhibition of two DNA repair pathways leads to cell death, to selectively target cancer cells with defects in HR-mediated DNA repair (21).

BRCA1 and BRCA2 are tumor suppressor genes involved in the repair of double-stranded DNA breaks via the HR repair pathway. Mutations in BRCA1 or BRCA2 impair this DNA repair mechanism, leading to genomic instability and increased susceptibility to DNA-damaging agents, such as platinum-based chemotherapy and PARP inhibitors (30). PARP inhibitors, such as olaparib, niraparib and rucaparib, block activity of PARP enzymes, preventing the repair of single-stranded DNA breaks and leading to accumulation of double-stranded DNA breaks in BRCA-mutated cancer cells. This synthetic lethality results in cancer cell death, sparing normal cells with intact HR repair pathways (31).

In addition to BRCA mutations, HRD, a measure of genomic instability and impaired DNA repair, is a predictive biomarker for response to PARP inhibitors in gynecological cancer (32). HRD can result from genetic alterations, including mutations in other DNA repair genes (such as RAD51 Paralog C and D), genomic rearrangement and chromosomal abnormality. Tumors with HRD are more reliant on alternative DNA repair mechanisms, such as PARP-mediated base excision repair, making them susceptible to PARP inhibition (32).

Clinical trials have demonstrated the efficacy of PARP inhibitors in the treatment of gynecological cancer, including ovarian, fallopian tube and primary peritoneal cancer (33,34). The SOLO-1 trial investigated the use of olaparib as maintenance therapy in patients with newly diagnosed advanced ovarian cancer and BRCA mutation (33). The study showed a significant improvement in progression-free survival (PFS) with olaparib compared with placebo, leading to its approval as a first-line maintenance therapy in this population (33). Similarly, the NOVA trial demonstrated the efficacy of niraparib as maintenance therapy in patients with recurrent ovarian cancer, regardless of BRCA mutation status (34). These findings have transformed the treatment landscape for gynecological cancer, offering new therapeutic options and improving outcomes for patients with BRCA mutations or HRD.

However, challenges remain in the clinical implementation of PARP inhibitors, including development of resistance mechanisms, optimal patient selection criteria and the identification of predictive biomarkers beyond BRCA mutations and HRD. Resistance to PARP inhibitors can arise through various mechanisms, such as restoration of HR repair, upregulation of alternative DNA repair pathways or acquisition of secondary mutations in PARP or other DNA repair genes (35).

6. Role of PD-L1 in gynecological cancer

Tumor and immune cells express programmed death-ligand 1 (PD-L1), a cell surface protein that serves a critical role in regulating the immune response and promoting immune evasion in gynecological cancer. PD-L1 interacts with its receptor, programmed cell death protein 1 (PD-1), on T cells, leading to T cell exhaustion and inhibition of antitumor immune responses (36). Immunotherapies, such as immune checkpoint inhibitors, target the PD-1/PD-L1 axis, a major immune checkpoint pathway for the treatment of gynecological cancer (37).

In ovarian cancer, PD-L1 expression is associated with aggressive disease characteristics, immune infiltration and poor prognosis (38). PD-L1 blockade enhances antitumor immune response and inhibits tumor growth in ovarian cancer models, providing rationale for clinical evaluation of immune checkpoint inhibitors in this disease (39). Clinical trials investigating PD-1/PD-L1 inhibitors, either as monotherapy or in combination with other agents, have shown promising results in patients with recurrent or refractory ovarian cancer, leading to their approval for this indication (40,41).

Similarly, PD-L1 expression has been reported in endometrial cancer, particularly in tumors with aggressive histological subtypes, high tumor grade and advanced-stage disease (42). The presence of PD-L1-positive immune cells in the tumor microenvironment is associated with immune evasion and

treatment resistance in endometrial cancer (43). Clinical trials evaluating efficacy of PD-1/PD-L1 inhibitors in endometrial cancer have shown encouraging responses in patients with high microsatellite instability (MSI-H) or MMR-deficient (dMMR) tumors (43). These findings have led to the approval of PD-1/PD-L1 inhibitors for treatment of advanced or metastatic endometrial cancer refractory to standard therapy (44).

Chronic inflammation and HPV infection in cervical cancer upregulate PD-L1 expression, which contributes to immune suppression and tumor immune escape. High PD-L1 expression in cervical cancer is associated with advanced-stage disease, lymph node metastasis and decreased survival outcomes (45). A clinical trial investigating immune checkpoint inhibitors targeting the PD-1/PD-L1 axis in cervical cancer has demonstrated durable responses and prolonged survival in patients with advanced or recurrent disease (46). These findings support use of PD-1/PD-L1 inhibitors as a treatment option for patients with advanced or metastatic cervical cancer.

Researchers have reported PD-L1 expression in a subset of vulvar and vaginal cancer, which is associated with immune evasion and treatment resistance (47). Clinical trials evaluating immune checkpoint inhibitors in vulvar and vaginal cancer are ongoing, with preliminary results showing promising antitumor activity and manageable safety profiles (48,49). To elucidate the role of the PD-1/PD-L1 axis in these rare gynecological malignancies and optimize treatment strategies, further research is necessary.

7. Clinical trials

Clinical trials serve a pivotal role in advancing the field of gynecological oncology by evaluating novel therapeutic strategies, validating predictive biomarkers and improving patient outcomes. Data from recent clinical trials has provided valuable insight into the efficacy and safety of emerging treatments and biomarker-driven therapy for gynecological cancers (50,51).

In ovarian cancer, several landmark clinical trials have evaluated the role of targeted therapy and immunotherapies in improving outcomes for patients with advanced or recurrent disease (33,52). SOLO-1 trial showcased the efficacy of olaparib as a maintenance treatment in newly diagnosed patients with advanced ovarian cancer and BRCA mutation, resulting in a notable enhancement in PFS compared with a placebo (33). Similarly, the PAOLA-1 trial investigated the combination of olaparib and bevacizumab as first-line maintenance therapy in patients with advanced ovarian cancer, showing a significant improvement in PFS in the overall population and patients with HRD (52). These findings have led to approval of olaparib and olaparib + bevacizumab as maintenance therapies in this population (33,52).

In endometrial cancer, KEYNOTE-146 trial evaluated the efficacy of pembrolizumab, a PD-1 inhibitor, in patients with advanced or recurrent disease refractory to standard therapy (53). The study demonstrated encouraging antitumor activity with pembrolizumab, particularly in patients with MSI-H or dMMR tumors, leading to its approval as a treatment option in this population (53). Similarly, the JAVELIN Solid Tumor Trial investigated the efficacy of avelumab, another PD-L1 inhibitor, in patients with advanced or recurrent endometrial cancer, showing promising responses and manageable safety profiles in these patients (54).

In cervical cancer, the KEYNOTE-158 trial evaluated the efficacy of pembrolizumab in patients with advanced or recurrent disease refractory to standard therapy (55). The study demonstrated durable responses and prolonged survival with pembrolizumab in a subset of patients with PD-L1-positive tumors, leading to its approval as a treatment option in this population (56).

Furthermore, metastatic endometrial tumors after progression in first-line platinum-based chemotherapy are treated with combination of immunotherapy and tyrosine kinase inhibitors pembrolizumab and lenvatinib based on results of phase III trial KEYNOTE-158 (56). The use of this combination is universal and does not require expression of specific biomarkers. Additionally, the GOG-240 trial investigated addition of the immune checkpoint inhibitor ipilimumab to standard chemotherapy in patients with recurrent or metastatic cervical cancer, showing improved overall survival compared with chemotherapy-alone (57).

In vulvar and vaginal cancers, clinical trials evaluating targeted therapies and immunotherapy are relatively limited due to the rarity of these malignancies. However, ongoing studies are investigating the role of immune checkpoint inhibitors, such as pembrolizumab and nivolumab, in patients with advanced or recurrent disease, with preliminary results showing promising antitumor activity and manageable safety profiles (58,59).

8. Real-world studies

Zhao *et al* (60) investigated the efficacy and safety of niraparib as a first-line maintenance treatment for patients with advanced ovarian cancer in a real-world setting across multiple centers in China. The findings revealed that niraparib provided significant PFS benefits, with PFS rates of 87.4, 75.9 and 63.6% at 6, 12 and 18 months, respectively. Factors such as age <65 years, BRCA mutation and successful cytoreductive surgery (R0 status) are associated with prolonged PFS. Additionally, starting niraparib at a 200 mg dose was effective and had manageable safety, with the most common severe adverse events being hematological, including decreased platelet and white blood cell counts. The study concluded that niraparib is a valuable and safe option for maintenance therapy in patients with advanced ovarian cancer, particularly when using an individualized starting dose strategy.

A retrospective cohort study in the USA evaluated the tolerability of PARP inhibitors (olaparib, niraparib and rucaparib) in patients with advanced ovarian cancer (61). The study included 824 patients and analyzed clinical events of interest such as anemia, neutropenia and nausea. The findings indicated that while PARP inhibitors are effective as maintenance therapy, they have a significant side-effect profile, which varies depending on the PARP inhibitor used. The aforementioned study highlights the importance of monitoring and managing adverse effects in real-world clinical settings (61).

Another real-world study (62) focused on treatment patterns following disease progression in patients with epithelial ovarian cancer who received PARP inhibitor maintenance therapy. The aforementioned study examined subsequent

therapies and outcomes, providing valuable data on how patients fare following disease progression while receiving PARP inhibitors. The results emphasized the importance of tailoring post-progression treatment based on individual patient profiles and previous responses to therapy (62).

Huepenbecker *et al* (63) aimed to describe the real-world usage of immune checkpoint inhibitors in patients with advanced or recurrent endometrial cancer. The aforementioned study analyzed data from a nationwide electronic health record-derived database, focusing on patients who received systemic treatment between January 2014 and November 2020, followed until May 2021. The study included 326 patients who received their first immune checkpoint inhibitors during this period, with usage increasing significantly over time. Pembrolizumab was the most common immune checkpoint inhibitor, often combined with lenvatinib. Immune checkpoint inhibitors were administered as first-, second- or later lines of therapy, with median time to next treatment being longer when immune checkpoint inhibitors were given earlier. The study found regional and stage-associated differences in immune checkpoint inhibitor usage, and ~1/3 of patients received subsequent treatments after immune checkpoint inhibitors, with no significant difference in demographic or clinical characteristics based on post-immune checkpoint inhibitor treatment type. The findings highlight the growing role of immune checkpoint inhibitors across various treatment lines in this population (63).

Passarelli *et al* (23) presented a case report of a 51-year-old patient with advanced endometrioid endometrial cancer harboring a PIK3CA mutation who showed an exceptional response to alpelisib, a PI3K α-selective inhibitor. Despite multiple prior treatments, including surgery, chemotherapy and hormone therapy, the disease progressed until alpelisib was introduced. Upon starting alpelisib, the patient experienced significant clinical and radiological improvements, with a notable decrease in tumor size and levels of tumor markers. This case highlights the potential of precision medicine in treating advanced gynecological cancers by targeting specific molecular alterations such as PIK3CA mutations. The aforementioned study emphasizes the importance of genomic profiling in guiding treatment decisions and suggests that alpelisib may be a promising option for patients with similar molecular profiles (23).

9. Role of multiple targeted mutations in gynecological cancer

Gynecological cancer often harbors multiple genetic mutations and molecular alterations that contribute to tumor heterogeneity, treatment resistance and disease progression (64). Understanding the interplay between these targeted mutations is key for optimizing treatment strategies and improving outcomes for patients with gynecological malignancy.

In ovarian cancer, HGSC, the most common subtype, is characterized by extensive genomic alterations, including mutations in tumor suppressor genes (such as TP53 and BRCA1/2) and oncogenes (such as PIK3CA and KRAS) (65). The presence of multiple targeted mutations in HGSC underscores the complexity of the disease and need for personalized treatment approaches. For example, patients with concurrent mutations in BRCA1/2 and HRD may benefit from PARP inhibitors, whereas those with mutations in PIK3CA or KRAS may respond to targeted therapy against the PI3K/AKT/mTOR or MAPK signaling pathways, respectively (66). Comprehensive molecular profiling of tumors is key for identifying actionable mutations and selecting tailored treatment regimens based on the genetic makeup of each patient.

Endometrial cancer is characterized by distinct molecular subtypes with different genetic alterations and clinical behavior. The Cancer Genome Atlas has identified four molecular subtypes of endometrial cancer, including DNA polymerase epsilon ultramutated, MSI and copy number-low and -high, each with unique genomic features and prognostic implications (22). Patients with MSI-high tumors, characterized by mutations in DNA MMR genes [such as DNA mismatch repair protein (MLH1) and MSH2], may benefit from immune checkpoint inhibitors due to increased tumor mutational burden and enhanced antitumor immune responses (44). Conversely, patients with copy number-high tumors, characterized by amplifications in oncogenes such as Cyclin E1 (CCNE1) and MYC, may respond to targeted therapy directed against these genetic alterations (20). Integrating molecular subtype classification with targeted mutation profiling enables identification of personalized treatment strategies tailored to the molecular characteristics of each endometrial cancer subtype.

Persistent infection with high-risk HPV types, particularly HPV16 and HPV18, drives cervical cancer by encoding viral oncoproteins that promote cell transformation and oncogenesis (67). In addition to HPV infection, cervical cancer may harbor mutations in genes such as PIK3CA, PTEN and TP53, which contribute to tumor progression and treatment resistance (22). Patients with concurrent HPV infection and targeted mutations may exhibit distinct clinical behavior and treatment responses, highlighting the importance of comprehensive molecular profiling in guiding treatment decisions for cervical cancer.

Vulvar and vaginal cancers are relatively rare gynecological malignancies that are less well-characterized than other types of gynecological cancer at the molecular level. However, mutations in genes such as TP53, PIK3CA and FGFR3 in a subset of tumors suggest potential therapeutic targets for these diseases (28). Additionally, HPV infection is associated with a subset of vulvar and vaginal cancers, particularly in younger patients, further highlighting the role of viral oncogenesis in these malignancies (68).

10. Challenges and limitations in clinical implementation of precision medicine in gynecological cancer

The clinical implementation of precision medicine in gynecological cancer, while promising, faces several challenges. These include issues associated with access to advanced genomic testing, cost and the necessity for interdisciplinary collaboration between healthcare providers.

Access to advanced genomic testing. NGS and other molecular profiling techniques are key components of precision medicine. These technologies enable the identification of specific genetic mutations and biomarkers to guide targeted therapy. However, the availability of advanced diagnostic tools is not

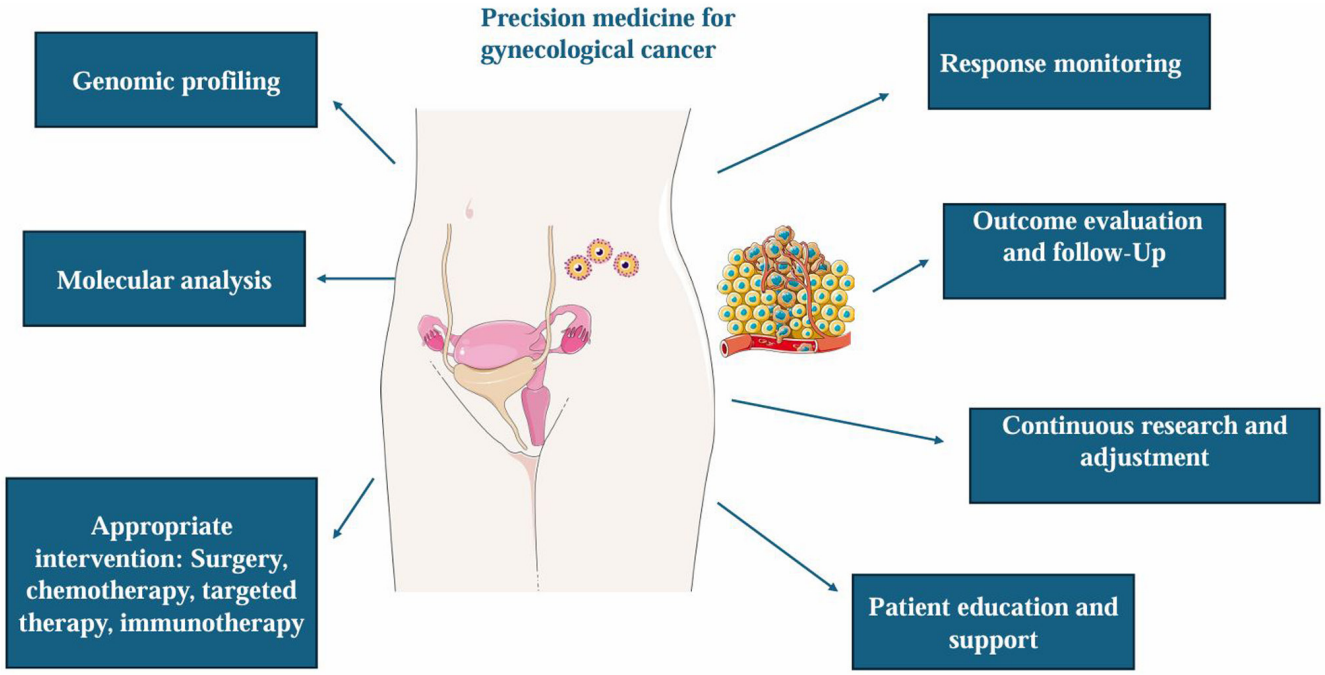

Figure 1. Schematic illustration of precision medicine for gynecological cancer. The personalized treatment begins with genomic profiling and molecular analysis to identify cancer-specific mutations, followed by tailored interventions such as surgery, chemotherapy, targeted therapy, or immunotherapy. Response monitoring ensures continuous tracking of treatment efficacy, while outcome evaluation and follow-up assess long-term results. The process includes continuous research to refine treatment approaches and emphasizes patient education and support, ensuring a comprehensive, individualized care plan for optimal outcomes. Image adapted from smart.servier.com/(accessed on 10 December 2024; Servier, licenced under a Creative Commons Attribution 3.0 Unported Licence).

uniform across healthcare facilities. In low-resource settings, the lack of infrastructure and expertise required to perform comprehensive genomic analysis limits the adoption of precision medicine. Moreover, even in well-resourced settings, there can be notable disparities in access based on geographical location, with urban centers typically having more advanced diagnostic facilities compared with rural areas (1).

Cost. The high cost of genomic testing and targeted therapies can be prohibitive for patients. For example, NGS, while providing comprehensive genomic information, is expensive and its costs are often not fully covered by insurance policies. This financial burden can limit patient access to precision medicine approaches. Additionally, targeted therapy, which is developed based on specific genetic mutations identified by genomic testing, tends to be more expensive than conventional treatment. The high cost of these therapies can strain healthcare budgets and make them inaccessible. Efforts to reduce the cost of genomic testing and targeted therapy and to increase insurance coverage for these services are essential to make precision medicine more accessible (3).

Interdisciplinary collaboration. The successful implementation of precision medicine requires interdisciplinary collaboration between various healthcare providers, including oncologists, geneticists, pathologists and bioinformaticians. This collaborative approach is necessary to interpret complex genomic data accurately and integrate this information into clinical decision-making effectively. However, fostering such interdisciplinary collaboration can be challenging. It requires effective communication and coordination between diverse healthcare professionals, which can be difficult to achieve in practice. Additionally, there is need for ongoing education and training for healthcare providers to keep up with rapid advancements in genomic technology and precision medicine approaches (4).

Data interpretation and standardization. Another challenge lies in the interpretation and standardization of genomic data. The vast amount of data generated by genomic testing requires sophisticated bioinformatics tools and expertise to analyze and interpret. Variability in data interpretation and lack of standardized protocols can lead to inconsistent clinical recommendations. Therefore, establishing standardized guidelines and protocols for genomic data interpretation is key to ensure reliable and actionable insights from genomic testing (19).

Ethical and privacy concerns. The collection and storage of genomic data raise issues of patient privacy and data security. Ensuring that genetic information is protected from unauthorized access and misuse is key. Additionally, ethical considerations regarding use of genetic information, such as potential discrimination based on genetic risk factors, need to be addressed through robust regulatory frameworks (5).

Fig. 1 provides a schematic illustration of precision medicine in gynecological cancer.

11. Conclusion

The transition towards personalized and precision medicine in gynecological oncology signifies a key shift from conventional treatment paradigms, offering new potential for improved

patient outcomes. Through the utilization of advanced genomic technology, such as NGS, clinicians can now unravel the complex molecular landscape of cancers affecting the gynecological organs. This detailed molecular profiling facilitates identification of unique genetic mutations and signaling pathways, enabling selection of targeted therapies tailored to the individual characteristics of each tumor.

The inherent molecular heterogeneity of gynecological cancers, presenting a notable challenge in treatment, is addressed by the ability of precision medicine to identify and target specific biomarkers and molecular drivers. Successes in ovarian, cervical and uterine cancer treatments, notably through the use of PARP inhibitors in BRCA-mutated ovarian cancer, exemplify the potential of precision medicine to enhance treatment efficacy while minimizing adverse effects. Focus on molecular profiling and development of novel targeted therapies may further refine treatment strategies to optimize outcomes and quality of life for patients with gynecological cancer. This underscores the shift towards more personalized care but also highlights potential for groundbreaking treatments in future.

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Authors' contributions

AAF and ML conceptualized the study. AAF, ML, MAD, and VEG wrote the manuscript. ML and MAD analyzed the data and provided critical revisions. All have read and approved the final version of the manuscript. Data authentication is not applicable.

Ethics approval and consent to participate

Not applicable.

Patient consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

Use of artificial intelligence tools

Chat GPT was used to improve the readability and language of the manuscript; authors revised and edited the content produced by the AI tool as necessary, taking full responsibility for the ultimate content of the present manuscript.

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