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診斷子宮內膜癌的挑戰

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Diagnosing endometrial cancer can be a challenging task. Although it is one of the most common malignancies among women, its symptoms and diagnostic results often mimic other gynecological conditions, leading to misdiagnosis or delayed diagnosis. Patients may experience only mild vaginal bleeding or unusual discharge, may be interpreted as signs of irregular menstruation or other gynecological conditions. Therefore, early comprehensive gynecological examinations are crucial to avoid missing the diagnosis of endometrial cancer.

Another challenge in diagnosing endometrial cancer is the difficulty in interpreting gynecological examination results. Traditional methods such as endometrial sampling and tissue biopsy may not always establish a definitive diagnosis. In recent years, several new technologies such as liquid-based cytology and endoscopic biopsy have been developed to detect endometrial cancer, but their sensitivity and specificity require further research and evaluation.

Some endometrial cancers are caused by mutations in genes such as PTEN, while others are associated with the expression of estrogen and progesterone receptors. These differences may affect the biological characteristics of the disease and treatment response, highlighting the need for deeper understanding of these features to improve the diagnosis and treatment of endometrial cancer.

Recent advances in diagnostic technology have led to the development of novel techniques for diagnosing endometrial cancer. For example, the molecular biology and genetics of endometrial cancer are diverse. DNA methylation marker analysis of minimally- and non-invasive sample types could provide an easy-to-apply and patient-friendly alternative to determine cancer risk.

Ongoing research and exploration are needed to improve our understanding of the disease and to develop more effective diagnostic and treatment strategies.

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複雜性卵巢腫瘤之鑑別診斷

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The differential diagnosis of an adnexal mass includes benign and malignant gynecologic and non-gynecologic etiologies. In gynecologic origin adnexal mass, functional cyst, hemorrhagic cyst, endometrioma, tubo-ovarian abscess are common benign lesions. Other lesions with non-gynecologic etiologies, such as appendicitis or diverticulum abscess should be considered as well. The goal of evaluation is to differentiate between benign and more serious conditions, such as ovarian cancer.

Important considerations in arriving at the most probable diagnosis are the age of the patient, the history, the findings on physical examination and the results of radiologic and laboratory studies.

The patient's age is a crucial factor in determining the probable etiology of an adnexal or pelvic mass. There are different considerations of diagnosis in reproductive age women and post-menopausal women. History including last menstrual period, pregnant status or medication history can provide us the information of possible diagnosis. Physical examination helps us to detect infection sign; besides, in premenopausal women, the presence of a complex adnexal mass, cul-de-sac nodularity and shortened or tender uterosacral ligaments suggests endometriosis. These same findings in the postmenopausal patient may signify malignancy. An ultrasound examination is the most valuable diagnostic study in the evaluation of an adnexal mass. The size, shape, countour, consistency and doppler flow under sonogram of adnexal mass are important characteristic to differentiate benign or malignant lesion. Besides, other radiologic tools including magnetic resonance imaging (MRI) and computed tomography (CT) are also informative for differential diagnosis of complex adnexa mass.

Although it is difficult to have a precise differatial diagnosis sometimes, it is important to achieve the most probable diagnosis by thorough clinical examination pre-operatively to make the most adequate treatment plan.

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ChatGPT 在婦癌的應用

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ChatGPT 在女性癌症研究中有著巨大的潛力，該研究專注於檢測、治療和預防影響女性的癌症。乳癌是全球女性最常見的癌症類型，迫切需要改進診斷和治療選擇。

ChatGPT 可以協助分析和解讀複雜的醫學數據，包括乳腺 X 光攝影結果、基因檢測結果和患者病史。ChatGPT 還可以分析大數據集，以識別不同類型癌症的模式和風險因素，包括乳癌。

ChatGPT 可以幫助制定個人化治療計劃，基於患者獨特的病史、基因組和其他因素。這種方法可以改善治療結果並減少不良反應的風險。 ChatGPT 還可以用於改善患者溝通和參與度，向患者提供有關其診斷、治療選擇和預後的信息，以易於理解且適合其個人化需求的方式。

此外，ChatGPT 可以協助設計和實施臨床試驗，這對於測試新的癌症治療方法和改進現有治療方法至關重要。ChatGPT 可以協助招募患者、監測治療結果和分析試驗數據。

然而，在女性癌症研究中使用 ChatGPT 存在挑戰。主要的挑戰之一是確保患者數據的準確性和隱私性，以及 AI 在醫療保健中使用時所涉及的道德考慮。此外，ChatGPT 可能無法完全替代醫療保健專業人員的專業知識和經驗。

結論： ChatGPT 有潛力通過改進數據分析、個性化醫學、患者溝通和臨床試驗設計來徹底改變女性癌症研究。但是，必須仔細考慮其使用，以確保患者安全、隱私和道德考量。

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ChatGPT 在婦癌應用的可能性 II

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人工智慧（AI）已經深深地影響了醫學領域，包括生物化學、基因組學、藥物發現和影像分析等。AI 系統如 DeepMind 的 AlphaFold 開創了蛋白質摺疊預測的新範疇，其他 AI 系統助力無創癌症檢測和 CRISPR 基因編輯的進步。AI 正改變藥物發現的速度與效率，並找尋治療抗生素抗藥性細菌及各種疾病的新途徑。此外，AI 在婦產科領域也有重大突破，協助解讀胎兒監控數據，確定懷孕併發症，並降低早產風險。AI 強化的產前篩檢和影像分析技術有助於早期檢測胎兒異常和婦科癌症，進一步提升女性醫療保健的診斷精確度和治療效果。ChatGPT 是由 OpenAI 開發的大規模語言模型，融入了卓越的語言理解與文本生成能力，成為現今人工智慧領域的一項重要技術。其基礎技術來自於「Generative Pre-training Transformer」，簡稱 GPT。這項基於 Transformer 模型的語言生成技術，以其對大量文本數據的訓練與理解，突破了過去人工智慧對語言使用的局限。使用者與 ChatGPT 進行互動時，會發現它可以自如地生成各種形式的自然語言文本，無論是日常的對話、學術的文章，甚至是富含情感與意象的詩歌。因此，ChatGPT 不只在用戶與機器間的交流中提供自然且流暢的對話體驗，甚至有時能給使用者帶來驚喜的創意激發。

ChatGPT 的便利性與實用性，使其在推出後迅速積累了大量的用戶。而隨著人工智慧在各領域的廣泛應用，如何將 ChatGPT 引進醫學領域，特別是婦產科，已經成為近期的熱門討論主題。事實上，ChatGPT 的特性使它在醫療場景中有許多潛在的應用可能性。例如，醫生可以利用其語言生成能力，來撰寫醫療紀錄、電子郵件、病患照護報告，甚至是翻譯醫學文獻，大幅提高工作效率。然而，儘管 ChatGPT 具有許多優點，也存在一些使用時需注意的缺點。例如，其所能提供的知識範圍，僅到 2021 年 9 月為止，也就是說，對於該日期之後的新知，或是最新的醫學研究進展，ChatGPT 可能無法提供準確的信息。此外，有時 ChatGPT 可能會出現所謂的「幻覺」現象，也就是在無法回答用戶問題時，它可能會創造出不存在的回應來處理該問題。總結來說，ChatGPT 以其卓越的語言理解和文本生成能力，展現了人工智慧在語言處理上的潛力。不論是在日常對話、學術寫作或是創作詩歌等方面，都展現了令人驚奇的表現。這種強大的功能性，讓 ChatGPT 在推出後就獲得了大量的使用者支持。現在，這種對話型人工智慧在醫學領域的潛在應用，尤其是在婦產科，也已經成為一種重要的研究和討論議題。

醫學界對於 ChatGPT 的潛在應用情況充滿期待。它的語言理解和生成能力，讓它在許多場合上都可以大幅提升工作效率。比如說，在撰寫醫療紀錄、電子郵件、或者進行醫學翻譯上，都可以發揮出大量的潛力。然而，這並不意味著使用 ChatGPT 就無需擔心任何問題。例如，ChatGPT 的知識庫在 2021 年 9 月就已經停止更新，這意味著對於那之後的新知，它可能無法提供準確的資訊。此外，有時 ChatGPT 可能會出現「幻覺」，即在回答無法處理的問題時，可能會生成一些不存在的回應。因此，雖然 ChatGPT 在語言處理上具有很大的優勢，但在應用上還需要我們謹慎地思考和評估。這是一種我們必須認真面對的問題，因為只有這樣，我們才能確保這項人工智慧技術在醫學領域中的發揮出它最大的價值，並為人類的健康與福祉做出更大的貢獻。

這次我們的主題著重在探討 ChatGPT 在婦產科及婦癌科的可能應用。身為一名婦產科醫師，我將從使用者的角度介紹 ChatGPT 可能的潛力與實際應用，並提出在使用過程中需特別留意的議題。針對這種不斷進步與優化的新科技，如果我們能善加利用，必定能大幅提升我們的生活品質與效率。

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子宮內膜癌的分子分型-POLE 突變

POLE is a gene that encodes the catalytic subunit of DNA polymerase epsilon, which is essential for DNA replication and repair. Mutations in the POLE gene are linked with a distinctive subset of endometrial cancers and is categorized as the ultramutated phenotype in TCGA classification with the following characteristics:

1.Poor histological differentiation, significant pleomorphism and high mitotic index
2.Presence of tumor infiltrating lymphocytes
3.Expression of immune checkpoint proteins
4.High tumor mutation burden
5.Good prognosis after surgery
6.Potential response to immune checkpoint blockade therapy

Of 397 patients with endometrioid endometrial cancer treated between 2009 and 2013. Hot spot mutations in the exonuclease domain of DNA polymerase epsilon analyzed by Sanger sequencing were detected in 44 cases. A total of 46 hot spot mutations of POLE exonuclease domain were discovered in 44 patients (Table 2), in which two patients showed mutations in both exon 9 and 13. The most common POLE mutation spot was c.857C>G in exon 9, followed by c.1231G>C (exon 13), c.1231G>T (exon 13), and c.1366G>C (exon 14) (Table 2). Most mutations were in exon 9 (N = 25), followed by exon 13 (N = 15) and exon 14 (N = 5). No mutations were detected in exon 10 and 12.

Although metastatic lymph node was suspected in 6 of the 42 cases after comprehensive image staging, only two patients with histological lymph node metastasis noted. Except for one patient with stage IVB disease, there were no cancer-specific death among patients with POLEmut tumors.

The detailed clinical manifestation of these cases and their implication of molecular classification is to present in the conference.

■專題演講——婦癌

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子宮內膜癌的分子分型-異常 p53 表現

Molecular Subtypes of Endometrial Cancer - Abnormal p53 Expression

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The p53 gene is an essential tumor suppressor gene that regulates critical functions such as cell cycle control, DNA repair, and apoptosis in normal cells. The significance of p53 gene mutations in carcinogenesis lies in the loss of normal tumor suppressor functions, abnormal cell proliferation, anti-apoptotic capability, and impaired DNA repair, thereby promoting tumor formation and progression.

The diagnosis of p53 mutations in endometrial cancer typically involves molecular testing methods such as immunohistochemistry (IHC), DNA sequencing, next-generation sequencing (NGS), and PCR-based assays.

The prognosis of endometrial cancer with p53 mutation subtype varies and is generally associated with a poorer outcome compared to other subtypes. Endometrial cancer patients with p53 mutation subtype often exhibit aggressive tumor behavior and are more likely to have advanced-stage disease at the time of diagnosis. These tumors tend to be more invasive and have a higher propensity for metastasis. Furthermore, p53 mutations may confer resistance to certain treatment modalities, such as radiation therapy and certain chemotherapy drugs, leading to reduced treatment effectiveness. This can contribute to a higher risk of disease recurrence and poorer overall survival rates.

In this presentation, we will discuss the role of the p53 gene in cancer development, the importance of p53 gene mutations in endometrial cancer, methods for diagnosing p53 mutations, and how p53 mutations affect the prognosis of endometrial cancer. Additionally, we will explore adjuvant therapy options to enhance treatment outcomes for patients with endometrial cancer.

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HRD 的充分了解

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Poly (ADP-ribose) polymerase inhibitors (PARPi) showed promising activity in patients with BRCA1 or BRCA2 mutated (BRCAm) ovarian cancer. Based on the rationale of synthetic lethality, the response of PARPi is associated with defects in the homologous recombination repair (HRR) pathway and not limited in patients with BRCAm. To find the patients with defective HRR phenotype(HRD), different homologous recombination deficiency scoring systems(genomic instability scores(GIS)) were developed as a prognostic and predictive biomarker in the response of PARPi. We will discuss about (1) the technical considerations and proposed perspectives of diffent GIS and (2)the clinical validation and limitation in assessment of HRD in clinical setting.

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Assessment of Mismatch Repair Deficiency and Associated Clinicopathologic Significance

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Ensuring high-fidelity DNA replication is essential for maintaining genome stability in humans. DNA mismatch repair (MMR) targets replication errors by excising regions containing mismatched base(s) on the synthesized DNA strands. The MutS homolog proteins (MSH) MutSα (heterodimer of MSH2-MSH6) or MutSβ (MSH2-MSH3) detect, bind a mismatch and interact with MutL homolog proteins (MLH) (MutLα，MLH1 and PMS2). EXO1 nuclease then participates in the MMR process during mismatch excision. DNA gap filling by polymerase Pol δ or ε and ligation by DNA ligase I restore a corrected and intact DNA duplex.

Compromised MMR function by mutation or epigenetic silencing results in inherited cancer susceptibility (e.g. Lynch syndrome, LS). Amsterdam criteria and Bethesda guidelines were developed to identify suspected LS patients who should undergo molecular tests such as MSI-PCR testing. The majority of germline mutations in MMR genes in LS patients result in loss of stable protein, immunohistochemistry (IHC) analysis of the four major MMR proteins in tumors can provide a diagnostic clue.

The impairment of MMR results in genome-wide hypermutation and in the "microsatellite instability" (MSI) phenotype, occurrence of insertion– deletion mutations (indels) at short tandem repeat (microsatellite) loci. The MSI status of tumors was traditionally assessed by molecular testing of various MS panels such as Bethesda panel, pentaplex panel or by measuring MMR protein expression levels. Whole-genome sequencing (WGS) or whole-exome sequencing (WES) can seacrch for indels across various MS loci with statistical analysis integrating the instability signal to predict global MSI or MSS status for each tumor sample. A high burden of somatic mutations from MMR failures predicts response to immunotherapy. This session addresses issues around testing characteristic, test status concordance and provides recommendations as to the appropriate modality of testing.