How to Cite:
Alhussain, A. H., Alquwayi, W. A., Alameer Alkuwaiti, Y. A., Almehainy, A. M., & Alkhathami, A. A. (2019). Applications of Cytogenetics and Cytogenomics Evaluation techniques in cancer diagnosis: A review. *International Journal of Health Sciences*, *3*(S1), 336–351.
https://doi.org/10.53730/ijhs.v3nS1.15214

Applications of Cytogenetics and Cytogenomics Evaluation techniques in cancer diagnosis: A review

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***Abstract*---Background:** Cytogenetics and cytogenomics have revolutionized cancer diagnosis by revealing the underlying genetic alterations that characterize malignancies. The identification of chromosomal rearrangements, mutations, and DNA dosage abnormalities in cancer cells has enhanced our understanding of cancer as a genomic disease, enabling the detection of residual disease and improving patient prognosis. **Aim:** This review aims to explore the application of cytogenetic and cytogenomic evaluation techniques in cancer diagnostics. **Methods:** Through a detailed examination of traditional cytogenetic methods like karyotyping and fluorescence in situ hybridization (FISH), along with advanced genomic tools such as next-generation sequencing (NGS) and single-cell technologies, the review highlights their respective contributions to precision oncology. **Findings:** It also discusses the challenges posed by tumor heterogeneity and the need for individualized treatment

International Journal of Health Sciences E-ISSN 2550-696X © 2019.
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Manuscript submitted: 9 Jan 2019, Manuscript revised: 18 Feb 2019, Accepted for publication: 10 March 2029

approaches. The integration of cytogenetic and cytogenomic techniques provides critical insights into cancer heterogeneity, clonal evolution, and the identification of therapeutic targets, facilitating early diagnosis, prognosis, and personalized treatment plans. **Conclusion:** The advancement of high-throughput technologies has further accelerated the discovery of novel biomarkers, enhancing the precision of cancer diagnosis and treatment strategies.

***Keywords*---**cytogenetics, cytogenomics, cancer diagnosis, karyotyping, fluorescence in situ hybridization, next-generation sequencing, tumor heterogeneity, precision oncology.

Introduction

Cytogenetics and genomics technologies have elucidated that cancer constitutes a genomic disease, leading to the clonal proliferation of cells that have accrued the most advantageous array of genetic anomalies, including point mutations, chromosomal rearrangements, DNA dosage abnormalities, and microsatellite alterations [1]. Certain chromosomal rearrangements are characteristic of specific malignancies, exemplified by the translocation between chromosomes 9 and 22 in chronic myeloid leukemia, commonly referred to as the 'Philadelphia chromosome,' which produces the BCR-ABL fusion protein [2]. Other chromosomal modifications arise from processes of malignant cellular transformation, such as isochromosomes 8q and 17q observed in carcinomas and trisomy 8 in acute myeloblastic leukemia [3]. The identification of distinct chromosomal and genetic alterations unique to malignant cells enhances cancer diagnosis and prognosis, also enabling the quantification of residual disease. Various types and sizes of chromosomal abnormalities are present in human cancers, and the products of these dysregulated genes and cellular pathways serve as specific targets for novel pharmacological interventions [4]. Furthermore, it is noteworthy that certain molecular changes critical in the initial stages of tumorigenesis may be lost or obscured by subsequent events or may no longer hold functional significance. Other alterations may be neutral or detrimental to the tumor yet persist in cells that exhibit sufficiently protumorigenic characteristics [1].

The emergence of high-throughput technologies facilitates the comprehensive characterization and sequencing of cancer genomes, allowing comparisons of genomic alterations not only between normal and tumor genomes but also across various patients and tumor types [5]. Next-generation sequencing (NGS) analyses illuminate tumor heterogeneity by sequencing spatially and temporally distinct tumor regions [6]. The accessibility of large-scale cytogenomic technologies, coupled with their declining costs, has significantly advanced human cancer research, leading to the identification of new mutations and gene fusions that contribute to the evolution of precision medicine and personalized treatment for cancer patients [7]. Consequently, advancements in tumor mutational analysis have paved the way for the development of innovative molecular targeted therapies, such as those targeting BRAF and NRAS mutations, which are the most frequently identified genetic alterations in cutaneous melanoma [8].

Additionally, NGS technology has enabled the identification of multiple mutations across different genes through the detection and analysis of circulating tumor cells (CTCs) and circulating tumor DNA (ctDNA), providing a minimally invasive or non-invasive approach for early cancer diagnosis and monitoring the genomic events that transpire during cancer progression as well as throughout and following cancer treatment [9]. This review discusses the significance of cytogenetics and cytogenomics analyses in human cancer for the identification of clinically applicable biomarkers that contribute to enhancing the precision of medical practices in oncology.

Technological Progress: From Cytogenetics to Cytogenomics Analysis

The integration of cytogenetic and molecular biology methods has significantly expanded opportunities in oncology and precision medicine for cancer patients. Currently, a blend of low-throughput and high-throughput technologies is employed in clinical genetics laboratories to detect deregulated cellular pathways, mutation patterns, noncoding RNAs, and protein expression profiles, which play a crucial role in early cancer diagnosis and predicting therapeutic responses. Cytogenetic techniques, which involve evaluating structural and numerical chromosomal aberrations, first identified the Philadelphia chromosome as a cancer-associated abnormality in 1960 [10], marking a pivotal moment in cancer cytogenetics. In the 1970s, conventional cytogenetics, also called karyotyping, underwent a transformation with the development of chromosomal banding techniques, allowing individual chromosomes to be distinguished by their unique banding patterns [11]. The 1980s saw the emergence of molecular cytogenetics, which enhanced conventional cytogenetics by enabling more precise detection of clinically relevant genetic abnormalities through observing specific DNA sequences in chromosomes and cancer cell nuclei [12]. Fluorescence in situ hybridization (FISH) became the primary method for molecular cytogenetic characterization of chromosomes, using fluorescently labeled DNA probes on metaphase chromosomes or interphase nuclei [13]. A major advantage of FISH in clinical settings is its ability to analyze chromosomal alterations in non-dividing cells, such as in cytological preparations and tissue sections. Variants of FISH, including multiplex FISH (M-FISH), spectral karyotyping (SKY), and comparative genomic hybridization (CGH), have simplified the interpretation of complex cancer karyotypes and are widely used in both research and clinical cancer detection [12]. FISH has significantly advanced the diagnosis and research of hematological malignancies and solid tumors [14], supplementing the information provided by G-banded karyotyping. FISH technology is now widely accepted in clinical practice due to progress in the availability and combination of DNA probes, improvements in probe labeling techniques, and advancements in optical microscopy [15]. FISH is commonly used for diagnosing breast cancer by detecting HER2 gene amplification, leukemia via BCR-ABL gene rearrangements, and non-small-cell lung carcinoma (NSCLC) through ALK-EML4 gene rearrangements [12]. Additionally, FISH-based cancer diagnostic panels, such as the UroVysion test (Abbott, USA) for bladder carcinoma screening, are utilized clinically [16].

In 1992, CGH was introduced as a genome-wide screening method using FISH technology. CGH involves co-hybridizing differentially labeled DNA from the sample under study and control DNA from a person with a normal karyotype

(46,XX or 46,XY) onto a reference human metaphase spread. Differences in fluorescence ratios reveal DNA content disparities between the control and the study sample [14,17]. CGH does not require prior knowledge of chromosomal alterations, as it is not a targeted technique for specific probes or panels, though it does require high-quality metaphase spreads. The development of DNA microarray technologies later provided high-resolution whole-genome analysis, opening new avenues for cancer cytogenomics. By replacing conventional metaphase spreads with DNA probes immobilized in an array format, these techniques revolutionized tumor genome understanding and expanded possibilities for clinical applications [18,19]. Genome-wide array-CGH initially utilized cDNA microarrays for gene expression profiling [20]. Today, genomic and gene expression profiling technologies enable simultaneous analysis of thousands of loci, offering substantial advantages in clinical settings [21].

While conventional and molecular cytogenetics identify recurrent chromosomal abnormalities and clonal evolution at the cellular level, cytogenomics technologies, such as array-CGH, single-nucleotide polymorphism (SNP) array, and next-generation sequencing (NGS), identify specific genomic coordinates and cancer-related genes with copy number alterations and mutations at the whole-genome level [22]. The early 21st century saw significant advances in Multiplex Ligation-dependent Probe Amplification (MLPA), array-CGH, and NGS technologies, propelling the field of personalized cancer genomics. These advances revealed specific genomic cancer signatures that classify tumors into subtypes with different behaviors and prognoses [23]. MLPA, a multiplex polymerase chain reaction-based method, detects copy number alterations and point mutations in a short hands-on time [24]. This technique targets specific MLPA probes, allowing nearly 50 genomic locations to be tested in a single reaction, making it a reliable and robust method for detecting diagnostic and prognostic genetic alterations [24,25,26]. NGS, also known as massive parallel sequencing, rapidly sequences large numbers of individual genomes. However, selecting clinically relevant oncological genomic data from the millions of genetic variations identified in tumors presents a challenge [27]. Despite this, improvements in sequencing chemistry, pipeline analysis, bioinformatics algorithms, data interpretation, and cost have made this technology applicable in clinical oncology [28]. NGS allows for whole-genome or exome analysis, as well as gene panels for screening cancer-associated genes and mutations with therapeutic implications, combining clinical applicability, cost-effectiveness, and ease of interpretation [28]. Various NGS platforms and approaches are available, and different initial input materials can be used, including genomic DNA (DNA-seq) and messenger or non-coding RNA (RNA-seq) [28]. RNA-seq has proven particularly valuable for identifying gene fusions in solid tumors, as cytogenetic techniques and clonal heterogeneity previously limited this [27]. Large consortia and clinical trials now use NGS technology to map mutation landscapes in various cancer types, demonstrating its diagnostic, prognostic, and therapeutic potential in individualized cancer treatments [28].

Recent advances in single-cell technologies and cytogenomic-based integrated analysis are reshaping cancer characterization and patient management. These techniques reveal tumor heterogeneity, clonal evolution, and cellular architecture [29]. Single-cell DNA and RNA sequencing methods have several translational

applications, including diagnostics, prognostics, targeted therapy, early detection, and non-invasive monitoring [30]. Although these methods can detect rare cancer cells, intratumor heterogeneity, and molecular alterations, challenges such as experimental time, cost, and result interpretation must be addressed before routine clinical use [31]. The initial step in single-cell sequencing experiments involves whole-genome or whole-transcriptome amplification to generate sufficient input material for NGS library construction. However, several technical challenges must be overcome in the amplification process, such as allelic dropout, amplification distortion, false positives, and coverage non-uniformity [30,32]. Single-cell RNA sequencing has been widely used to improve understanding of intratumor heterogeneity, clonal evolution, metastatic spread, and the immune landscape of cancer patients [33]. This high-throughput technology has enabled the detection and genomic characterization of circulating tumor cells (CTCs) and cell-free DNA, opening new possibilities for early cancer diagnosis and non-invasive disease monitoring using biofluids and exosomes [9].

Cytogenetic and Genomic Rearrangements in Cancer

The transformation of a normal cell into a malignant one is a complex process driven by the accumulation of genomic alterations. These changes allow cancer cells to sustain proliferative signaling, evade growth suppressors, resist apoptosis, and achieve several other "hallmarks of cancer" including enabling replicative immortality, inducing angiogenesis, and promoting invasion and metastasis . Genomic alterations can involve single-nucleotide variants (SNVs), copy number variants (CNVs), and various structural rearrangements like deletions, duplications, inversions, insertions, and translocations . These mutations typically disrupt tumor suppressor genes or activate proto-oncogenes, contributing to cancer progression .

Cytogenetic abnormalities, including specific numerical and structural changes, have been associated with particular types of cancer. Reciprocal translocations, amplifications, deletions, and insertions are among the most frequent chromosomal alterations found in various cancers . For example, translocations are common in hematological malignancies, whereas partial deletions and unbalanced translocations are prevalent in cancers of epithelial origin . Structural changes such as focal deletions of genes like *FHIT*, *WWOX*, and *PTPRD* have been identified in a range of primary tumors , while key cancer-related genes such as *TP53*, *RB1*, *EGFR*, and *KRAS* are often mutated in many cancer types . Although many somatic mutations drive cancer development, others, termed "passenger alterations," do not contribute to tumorigenesis . Multiple driver mutations typically coexist in tumors, with cancers like breast, colorectal, and prostate harboring five to seven such mutations . Additionally, some cancers may arise from exogenous DNA sources, such as viral DNA from human papillomavirus (HPV) or Epstein-Barr virus (EBV) . While somatic mutations in mitochondrial DNA have been linked to cancer, their role remains under investigation .

Heterogeneity in Cancer

Cancer exhibits both intertumoral and intratumoral heterogeneity, complicating diagnosis and treatment. Intratumor heterogeneity arises within a primary tumor

and can manifest in spatial and temporal forms. Spatial heterogeneity refers to the uneven distribution of genetically distinct subpopulations across different areas of the same tumor, while temporal heterogeneity describes changes in a tumor's genetic makeup over time [43]. Intertumor heterogeneity, on the other hand, refers to differences between tumors in different tissues or within the same tumor type in different individuals, influenced by factors like germline genetic variation, somatic mutations, and environmental influences [43].

Tumor heterogeneity poses a significant challenge to cancer diagnosis and management. This variation can arise from distinct subpopulations of cells that possess unique genomic alterations or through clonal evolution driven by selective pressure from treatments [44,45]. Intratumor heterogeneity is a major factor contributing to therapeutic failure and poor patient outcomes, especially in highly heterogeneous cancers like lung, melanoma, bladder, and head and neck cancers. These tumors often have a high mutation rate and numerous copy number alterations [47]. Heterogeneity within tumors may explain the varying biological behavior and clinical outcomes of seemingly similar tumors. As cancer is a heterogeneous disease, successful treatments need to target patient-specific cytogenomic alterations and take into account the tumor microenvironment [48]. However, measuring intratumor heterogeneity is challenging due to limited access to tumor samples, which often provide only a partial view of the disease [47].

The concept of tumor heterogeneity emerged when pathologists first observed differences in tumor cell morphology, and cytogenetic techniques like G-banding, SKY, and FISH provided evidence of genetic subclones within tumors [49]. With advances in deep sequencing technologies, the extent of intra- and intertumoral heterogeneity has been revealed in cancers such as glioblastoma [50], non-small cell lung cancer (NSCLC) [51], breast [53], prostate [54], and ovarian cancers [44]. However, the mechanisms behind this diversity and its effects on therapy resistance and clinical outcomes remain unclear [55]. Tumor heterogeneity also complicates the identification of molecular biomarkers, limiting their translation into clinical practice. Single-cell sequencing has emerged as a powerful tool, enabling the detailed characterization of individual cells within a tumor, which holds great promise for unraveling the complexities of tumor heterogeneity [43]. Cytogenomic multiplatform analyses of individual cancer cells offer a more comprehensive molecular classification of tumors, which can significantly improve cancer management and inform clinical decisions [45].

Biomarkers in Cancer

Early detection remains the gold standard in cancer control and prevention, particularly for identifying asymptomatic malignancies or potentially malignant lesions [56]. This is made possible by recognizing specific biomarkers, which are cancer-associated molecular alterations that can aid in diagnosis, prognosis, patient risk stratification, therapy prediction, and treatment monitoring. Understanding the molecular profile of each cancer type is crucial for establishing biomarkers that have clinical applications through genotype-phenotype correlation [57]. The recent advent of high-throughput technologies has facilitated extensive cytogenomic characterization of tumors, though challenges remain in translating these data into clinical practice [58]. The shift from a "one-size-fits-all"

approach to precision medicine has been transformative but complex. Many molecular biomarkers are already in clinical use, while others are undergoing investigation or clinical trial evaluations [58,60]. For instance, DNA copy-number alterations have been associated with prognosis in various cancers, including prostate [61], breast [62], gastric [63], and lymphoma [64]. Despite the numerous prognostic biomarkers documented in literature, only a few have been successfully translated into clinical practice, highlighting the complexity of cancer and the gap between laboratory discoveries and clinical applications [58].

Genomic biomarker implementation has faced challenges despite advancements in genome sequencing and high-throughput technologies [59]. For example, the overexpression or amplification of HER2 (ERBB2) predicts the response to monoclonal antibodies like trastuzumab and pertuzumab in breast cancer and guides treatment in esophagogastric adenocarcinoma [65,66]. Other clinically relevant predictive biomarkers include the BCR-ABL tyrosine kinase fusion gene in chronic myeloid leukemia [67], KRAS mutations in colorectal cancer [68], and KIT proto-oncogene mutations in gastrointestinal stromal tumors [69]. In non-small cell lung cancer (NSCLC), mutations in EGFR, KRAS, and other driver mutations such as ALK, BRAF, PIK3CA, AKT1, MAP2K1, and MET also serve as predictive biomarkers [70], as does the BRAF mutation in melanoma [71].

Significant progress in gene expression analysis has enhanced our understanding of the roles of altered genes in cancer development, enabling the customization of diagnostic and therapeutic approaches. In breast cancer, several gene expression signatures can predict patient prognosis, with Mammaprint being one of the first assays to forecast breast cancer recurrence post-chemotherapy [73,74]. Similarly, the Oncotype DX genomic prostate score estimates prostate cancer aggressiveness, recurrence after surgery, and metastasis potential based on gene expression analysis [72]. Although precision medicine is recognized as a key strategy for improving cancer outcomes, its clinical integration has been slow [59]. The search for cancer biomarkers continues, with a growing focus on standardizing genomic analyses to enhance accuracy and reliability in clinical applications [75]. A paradigm shift is occurring from analyzing targeted sequencing panels of selected mutations to employing genome-wide assays at multiple omics levels, necessitating developments in computational biology for data interpretation and phenotype correlation.

Liquid biopsy, which involves analyzing circulating cells and DNA/RNA in body fluids, is gaining attention as a non-invasive method for early tumor detection, monitoring cancer progression, and patient follow-up [9,76]. Although tissue biopsies often fail to capture the full genetic heterogeneity of tumors, liquid biopsies hold great promise for real-time insights. However, technical challenges and the lack of standardization in preanalytical and analytical processes have hindered their widespread clinical use [77]. In 2016, the FDA approved the first ctDNA-based diagnostic test (cobas EGFR Mutation Test v2) to guide the use of EGFR-tyrosine kinase inhibitors in NSCLC patients with specific EGFR mutations [77,78]. Additionally, the CellSearch® platform, which enumerates circulating tumor cells (CTCs), remains the only FDA-approved method for CTC analysis in metastatic breast, prostate, and colorectal cancers [79].

FDA approved Markers:

Several FDA-approved biomarkers are used in clinical practice to guide cancer diagnosis, prognosis, and treatment. These biomarkers help predict responses to targeted therapies or monitor disease progression. Below is a summary of some key FDA-approved biomarkers:

1. HER2 (ERBB2)

- **Cancer Type**: Breast cancer, Esophagogastric adenocarcinoma
- **Use**: HER2 overexpression or amplification guides the use of targeted therapies like **trastuzumab** (Herceptin) and **pertuzumab** (Perjeta).
- **FDA-Approved Test**: HER2 testing through immunohistochemistry (IHC) or fluorescence in situ hybridization (FISH).

2. BCR-ABL Fusion Gene

- **Cancer Type**: Chronic myeloid leukemia (CML)
- **Use**: BCR-ABL fusion gene, associated with the Philadelphia chromosome, directs the use of **tyrosine kinase inhibitors** such as **imatinib** (Gleevec).
- **FDA-Approved Test**: Quantitative PCR-based tests for detecting BCR-ABL transcripts.

3. KRAS Mutations

- **Cancer Type**: Colorectal cancer, Non-small cell lung cancer (NSCLC)
- **Use**: KRAS mutation testing is used to determine the efficacy of **EGFR-targeted therapies** like **cetuximab** and **panitumumab** in colorectal cancer. Patients with certain KRAS mutations are unlikely to benefit.
- **FDA-Approved Test**: Therascreen KRAS PCR kit.

4. EGFR Mutations

- **Cancer Type**: Non-small cell lung cancer (NSCLC)
- **Use**: EGFR mutations guide the use of **EGFR-tyrosine kinase inhibitors** (TKIs) such as **erlotinib** (Tarceva), **afatinib** (Gilotrif), and **osimertinib** (Tagrisso).
- **FDA-Approved Test**: **Cobas EGFR Mutation Test v2**, the first ctDNA-based test approved for liquid biopsy in NSCLC.

5. ALK Rearrangements

- **Cancer Type**: Non-small cell lung cancer (NSCLC)
- **Use**: ALK rearrangements indicate responsiveness to **ALK inhibitors** like **crizotinib** (Xalkori), **alectinib** (Alecensa), and **brigatinib** (Alunbrig).
- **FDA-Approved Test**: VENTANA ALK (D5F3) CDx Assay.

6. BRAF V600E Mutation

- **Cancer Type**: Melanoma, Colorectal cancer, NSCLC
- **Use**: BRAF mutations predict responsiveness to **BRAF inhibitors** such as **vemurafenib** (Zelboraf) and **dabrafenib** (Tafinlar).
- **FDA-Approved Test**: Therascreen BRAF V600E Mutation Test.

7. PD-L1 Expression

- **Cancer Type**: Various cancers, including NSCLC, melanoma, bladder cancer
- **Use**: PD-L1 expression is used to predict response to **immune checkpoint inhibitors** like **pembrolizumab** (Keytruda) and **nivolumab** (Opdivo).
- **FDA-Approved Test**: PD-L1 IHC assays (e.g., 22C3 pharmDx for pembrolizumab).

8. BRCA1/BRCA2 Mutations

- **Cancer Type**: Breast and ovarian cancers
- **Use**: BRCA1/BRCA2 mutations indicate susceptibility to **PARP inhibitors** like **olaparib** (Lynparza) and **rucaparib** (Rubraca).
- **FDA-Approved Test**: BRACAnalysis CDx.

9. MSI-H/dMMR (Microsatellite Instability-High/Deficient Mismatch Repair)

- **Cancer Type**: Colorectal cancer, endometrial cancer, and others
- **Use**: MSI-H/dMMR is used to identify patients who may benefit from immune checkpoint inhibitors like **pembrolizumab** (Keytruda).
- **FDA-Approved Test**: MSI testing by PCR or IHC.

10. NTRK Fusions

- **Cancer Type**: Multiple tumor types
- **Use**: NTRK fusions predict response to **TRK inhibitors** like **larotrectinib** (Vitrakvi) and **entrectinib** (Rozlytrek).
- **FDA-Approved Test**: FoundationOne CDx.

11. Circulating Tumor Cells (CTCs)

- **Cancer Type**: Metastatic breast, prostate, colorectal cancer
- **Use**: CTC enumeration through the **CellSearch® platform** is FDA-approved to monitor disease progression and response to treatment.
- **FDA-Approved Test**: CellSearch CTC Test.

Future Perspectives in Cancer Diagnosis and Treatment

The continuous advancements in high-throughput technologies are revolutionizing our understanding of molecular alterations, biological mechanisms, and the behavior of various cancer types. Notably, progress in cytogenetics and cytogenomics, combined with bioinformatics, holds promise for identifying specific molecular signatures that are linked to tumor initiation, progression, and effective therapeutic targets. Current advancements in genome-wide techniques have transformed the oncologic diagnostic landscape, enabling comprehensive approaches like gene expression profiling, array comparative genomic hybridization (array-CGH), single-nucleotide polymorphism (SNP) arrays, and next-generation sequencing (NGS). These methods facilitate the analysis of specific genes, entire genomes, or exomes, along with gene interactions and altered cancer pathways. Despite this potential, the translation of the large datasets generated by high-throughput technologies into clinically actionable biomarkers remains limited. While numerous candidate biomarkers have been identified, few are currently validated and implemented in routine clinical practice. Looking forward, significant advancements in cancer diagnosis and treatment are anticipated, largely driven by a deeper understanding of tumor biology and heterogeneity. By identifying multiple molecular alterations that underlie cancer development, the potential for personalized treatments will expand. Cancer research will continue to benefit from these technological improvements, especially in detecting targetable mutations and gene fusions. Additionally, the current capacity of high-throughput technologies to map the molecular landscape of tumors in a cost-effective manner presents great potential for precision medicine. However, challenges remain regarding data interpretation and the practical application of this knowledge in clinical settings. As high-throughput technologies become more cost-effective, clinicians will be increasingly empowered to tailor treatments to the molecular profiles of individual

tumors. Nevertheless, current practices often rely on analyzing small tumor samples, which may not provide a full understanding of tumor biology. Single-cell sequencing offers a promising solution by revealing tumor heterogeneity and identifying therapeutic resistance or sensitivity. Yet, its integration into routine clinical practice faces hurdles, such as methodological limitations and challenges in interpreting the data. To bridge these gaps, collaboration among multidisciplinary teams—including clinicians, geneticists, researchers, and bioinformaticians—will be essential. These teams will play a pivotal role in interpreting and validating molecular data, ultimately facilitating its successful application in clinical practice. As technology evolves, multi-omics integrative studies will be critical for validating new targeted therapies and ensuring that the right patients benefit from these treatments based on their tumor-specific genomic signatures.

Conclusion

The advancement of cytogenetics and cytogenomics has played a pivotal role in reshaping cancer diagnosis and treatment. Early techniques, such as karyotyping and fluorescence in situ hybridization (FISH), laid the foundation for identifying chromosomal aberrations associated with various malignancies. These methods allowed clinicians to diagnose cancers based on the detection of specific genetic markers, such as the Philadelphia chromosome in chronic myeloid leukemia. However, despite their efficacy, traditional cytogenetic methods have limitations in detecting complex genomic alterations and addressing tumor heterogeneity. The emergence of high-throughput technologies like next-generation sequencing (NGS) has overcome these limitations, offering more comprehensive insights into the genetic landscape of cancers. NGS enables the identification of multiple mutations, gene fusions, and structural rearrangements across the entire genome, allowing for a more precise classification of tumors. The ability to sequence tumor samples at different stages of progression has provided valuable insights into the clonal evolution of cancers, enhancing the development of personalized treatment strategies. Additionally, cytogenomic tools, including array comparative genomic hybridization (CGH) and single-cell sequencing, have expanded our ability to detect rare genomic events, such as circulating tumor cells (CTCs) and circulating tumor DNA (ctDNA), offering minimally invasive diagnostic methods. Despite these advancements, challenges remain, particularly in addressing tumor heterogeneity. Tumor cells within the same tumor or between patients may exhibit significant genetic diversity, complicating treatment and leading to therapeutic resistance. As cancer research continues to progress, the integration of cytogenomic data into clinical practice will be critical in overcoming these challenges and developing more effective, individualized therapies. The ongoing refinement of genomic technologies promises to further enhance cancer diagnostics, providing deeper insights into tumor biology and guiding precision oncology approaches. Ultimately, the fusion of cytogenetics and cytogenomics continues to push the boundaries of cancer diagnosis, enabling early detection and more personalized treatment options for patients.

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تطبيقات تقنيات تقييم علم الوراثة الخلوية والجينومية في تشخيص السرطان - مقال مراجعة

الملخص:
الخلفية: أحدث علم الوراثة الخلوية والجينومية ثورة في تشخيص السرطان من خلال كشف التغيرات الجينية الأساسية التي تميز الأورام الخبيثة. أدى التعرف على إعادة ترتيب الكروموسومات، الطفرات، والتشوهات في الجرعات الوراثية في الخلايا السرطانية إلى تعزيز فهمنا للسرطان كمرض جيني، مما يمكن من اكتشاف المرض المتبقي وتحسين توقعات المرضى.
الهدف: تهدف هذه المراجعة إلى استكشاف تطبيق تقنيات التقييم الوراثي الخلوي والجينومي في تشخيص السرطان.
الطرق: من خلال فحص تفصيلي للطرق الوراثية الخلوية التقليدية مثل التصنيف الكروموسومي وتقنية التهجين الموضعي الفلوري(FISH) ، إلى جانب الأدوات الجينومية المتقدمة مثل تسلسل الجيل القادم (NGS) والتقنيات الخلوية الفردية، تسلط المراجعة الضوء على مساهماتها في الأورام الدقيقة.
النتائج: تناقش المراجعة أيضًا التحديات التي تفرضها تغايرية الأورام والحاجة إلى نهج علاجي مخصص لكل حالة. يتيح دمج تقنيات علم الوراثة الخلوية والجينومية رؤى هامة حول تغايرية السرطان، وتطور الاستنساخ، وتحديد الأهداف العلاجية، مما يسهل التشخيص المبكر، التنبؤ بالمآل، وخطط العلاج الشخصية.
الخاتمة: أدت التقنيات المتقدمة ذات الإنتاجية العالية إلى تسريع اكتشاف العلامات الحيوية الجديدة، مما يعزز دقة تشخيص السرطان واستراتيجيات العلاج.
الكلمات المفتاحية: علم الوراثة الخلوية، علم الوراثة الجينومية، تشخيص السرطان، التصنيف الكروموسومي، التهجين الموضعي الفلوري، تسلسل الجيل القادم، تغايرية الورم، الأورام الدقيقة.