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REVIEW

Genetic and molecular criteria for the study of the most common hereditary cancers: A literature review

Criterios genéticos y moleculares para el estudio de los tipos de cánceres hereditarios más comunes: Una revisión bibliográfica

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ABSTRACT

Introduction: for centuries, cancer was interpreted as a divine punishment, and its treatment was based on rituals. However, the advancement of medicine led physicians to observe familial patterns, thus exploring potential genetic causes. Presently, genomics has unveiled the underlying complexity of cancer, offering new avenues for its prevention and treatment. This review focuses on hereditary cancers, proposing criteria for their study and genetic counseling, thereby providing a crucial guide for informed clinical decision-making.
Objective: this study aims to deepen the current understanding of the most prevalent hereditary cancers, with a specific focus on their genetic bases.
Method: in this review, a detailed analysis of the literature was conducted using Scopus, PubMed, Google Scholar, and other online sources, employing specific keywords supported by specialized thesauri. Thirty-eight references focused on hereditary cancers published between 2019 and 2024 were carefully selected.
Development: exploring the genetic bases of cancer involves addressing the cell cycle, genetic regulation, and crucial genes such as p53. Cancer predisposing genes are identified, and common hereditary syndromes, such as hereditary breast and ovarian cancer, hereditary non-polyposis colorectal cancer, and familial adenomatous polyposis, are described.
Conclusions: cancer, influenced by genetic factors, manifests in specific mutations such as BRCA1, BRCA2, MLH1, MSH2, MSH6, PMS2, and APC, increasing the risks of breast, ovarian, colorectal cancer, and familial adenomatous polyposis. The application of study criteria based on family history and genetic testing facilitates the identification of individuals and families prone to these mutations.

Keywords: Hereditary Cancer; Genetic Counseling; Genetic Predisposition; Genetic Diagnosis; Breast Cancer; Colorectal Cancer.

RESUMEN

Introducción: durante siglos, el cáncer fue interpretado como un castigo divino, y su tratamiento se basaba en rituales. Sin embargo, el avance de la medicina llevó a los médicos a observar patrones familiares, explorando así posibles causas genéticas. En la actualidad, la genómica ha desvelado la complejidad subyacente del cáncer, ofreciendo nuevas vías para su prevención y tratamiento. Esta revisión se centra en los cánceres hereditarios, proponiendo criterios para su estudio y asesoramiento genético, proporcionando así una guía crucial para la toma de decisiones clínicas informadas.
Objetivo: este estudio tiene como objetivo profundizar en el conocimiento actualizado de los cánceres hereditarios más prevalentes, con un enfoque específico en sus bases genéticas.

Método: en esta revisión se realizó un análisis detallado de la literatura utilizando Scopus, PubMed, Google Scholar y otras fuentes en línea, empleando palabras clave específicas respaldadas por tesauros especializados. Se seleccionaron cuidadosamente treinta y ocho referencias centradas en cánceres hereditarios, publicadas entre 2019 y 2024.
Desarrollo: explorar las bases genéticas del cáncer implica abordar el ciclo celular, la regulación genética y genes cruciales como el p53. Se identifican genes predisponentes al cáncer y se describen síndromes hereditarios comunes, como el cáncer de mama y ovario hereditario, el cáncer colorrectal hereditario no polipósico y la poliposis adenomatosa familiar.
Conclusiones: El cáncer, influenciado por factores genéticos, se manifiesta en mutaciones específicas como BRCA1, BRCA2, MLH1, MSH2, MSH6, PMS2 y APC, aumentando los riesgos de cáncer de mama, ovario, colorrectal y poliposis adenomatosa familiar. La aplicación de criterios de estudio basados en la historia familiar y pruebas genéticas facilita la identificación de individuos y familias propensas a estas mutaciones.

Palabras clave: Cáncer Hereditario; Asesoramiento Genético; Predisposición Genética; Diagnóstico Genético; Cáncer De Mama; Cáncer Colorrectal.

INTRODUCTION

For centuries, cancer has been part of human history. In ancient times, its occurrence was attributed to divine punishments, and treatments consisted of rituals and ancestral potions. Despite the religious beliefs of the era, physicians, upon observing entire families displaying similar illnesses, began to develop a scientific interpretation of cancer's etiology. They started to consider genetic factors in the onset of the disease.[1]

Currently, thanks to the revolution in medicine and genetics, it is known that cancer has a multifactorial etiology. Environmental factors, lifestyle, and genetics are all contributors to the onset of the disease. New techniques for manipulating genetic material have allowed for the identification of mutations associated with cancer susceptibility, which is crucial for prevention, detection, and treatment of a disease that, according to the UN, caused the deaths of 1,4 million people in the Americas by 2020.[2]

As genomics becomes increasingly integrated into clinical medicine, addressing hereditary cancers becomes crucial. This review not only aims to identify the most common hereditary cancers but also to provide clear criteria for conducting studies and genetic counseling. This establishes a solid foundation for informed clinical decision-making.[3]

When a genetic mutation that significantly increases the risk of cancer within a family is identified, the terminology of hereditary cancer syndrome is used. Alternative terms such as familial cancer syndrome or genetic cancer syndrome are also employed to describe this condition.[4]

The most common syndromes include: Hereditary Breast and Ovarian Cancer Syndrome, Hereditary Nonpolyposis Colorectal Cancer Syndrome (Lynch syndrome), Familial Adenomatous Polyposis, Multiple Endocrine Neoplasia (Type 1, Type 2), Cowden Syndrome, Li-Fraumeni Syndrome, Von Hippel-Lindau Disease, Hereditary Diffuse Gastric Cancer, and Hereditary Prostate Cancer.[4,5]

The underlying issue in this study lies in the urgent need to synthesize and critically analyze the vast body of knowledge regarding hereditary cancer. With this aim, this review aspires to become a fundamental resource for healthcare professionals and students alike, contributing to a deeper understanding of hereditary cancers and providing an essential guide for informed and strategic clinical decision-making. The objective of this work is to present a comprehensive and updated review of the most common hereditary cancers, highlighting their genetic foundations.

METHOD

The Materials and Methods in this article, an exhaustive literature review was conducted to analyze research on hereditary cancers. To gather diverse and updated information, various sources were employed, including Google Scholar and other specialized online sources. Careful selection of specific keywords such as "Hereditary cancer" and "Genetic diagnosis," supported by specialized thesauri, was chosen to ensure the accuracy of the search.

The selection of the 38 references was carried out meticulously, focusing on hereditary cancers from 2019 to 2024. Three key criteria were followed for this selection: relevance to the topic, inclusion of updated information, and the possibility of including up to three older documents (from 2009 and 2008) due to their valuable unique information.

The review process commenced on January 25, 2024, and concluded approximately three weeks later, around February 15, 2024. During this period, scientific literature was thoroughly explored to capture the latest developments in cancer genetics, ensuring the robustness and relevance of the selected sources. This rigorous approach supports the integrity and validity of the results obtained, thus providing a solid foundation for the

analysis and understanding of hereditary cancers.

DEVELOPMENT

Cancer, also referred to as tumorigenesis, is marked by the abnormal and unregulated proliferation of cells that infiltrate organs and tissues. It encompasses a spectrum of diseases with diverse causes, though its genetic underpinnings are incontrovertible. Rather than inheriting tumors themselves, individuals inherit a predisposition to develop cancer. Numerous cancers arise from inherited genomic variations passed down via germline cells (sperm and eggs). The onset of cancer results from a complex interplay between genetic susceptibilities and environmental influences.[5]

Currently, cancer is the leading cause of death in developed countries and the second leading cause in developing countries after cardiovascular diseases. Globally, it is estimated that there are 20 million cancer patients and 10 million deaths due to the same cause. In Ecuador, up to 2020, there were 29,273 new cases registered, of which 76,062 are prevalent, and 15,123 patients died. The most common cancers were breast, colon or rectum, prostate, stomach, and cervical cancers.[6]

Hereditary cancers refer to cancers that develop due to inherited genetic mutations or predispositions passed down through generations. These mutations increase the likelihood of developing certain types of cancer. Unlike sporadic cancers, which occur by chance or due to environmental factors, hereditary cancers often exhibit a familial pattern of occurrence.[6,7] Examples of hereditary cancers include: Hereditary Breast and Ovarian Cancer (HBOC): Caused by mutations in genes such as BRCA1 and BRCA2, which significantly increase the risk of breast and ovarian cancers; Lynch Syndrome (Hereditary Nonpolyposis Colorectal Cancer or HNPCC): Caused by mutations in DNA mismatch repair genes (e.g., MLH1, MSH2, MSH6, PMS2), leading to an increased risk of colorectal cancer and other cancers such as endometrial cancer; Familial Adenomatous Polyposis (FAP): Caused by mutations in the APC gene, leading to the development of numerous polyps in the colon and an increased risk of colorectal cancer and Hereditary Retinoblastoma: Caused by mutations in the RB1 gene, resulting in the development of tumors in the retina. Hereditary cancers account for 5 to 10 % of all diagnosed cancers and are prevalent in our environment, such as breast or ovarian cancer.[6,34] These cancers have a significant genetic basis and can be inherited through familial germline lines, underscoring the importance of early detection and genetic counseling.

Genes and Cellular Regulation

The cell cycle is a series of events in the life of a cell, involving its growth and division. For the majority of its duration, the cell undergoes interphase, during which it grows, duplicates its chromosomes, and prepares for division. Following interphase, it enters mitosis, giving rise to daughter cells that initiate new cell cycles. This process of duplication and generation of two cells is referred to as the cell cycle, which consists of the phases G1, S, G2, and M. The G1 phase is dedicated to preparation for division, the S phase replicates DNA, the G2 phase organizes genetic material, and the M phase is mitosis, where copies of the genetic material are distributed into the daughter cells. After the M phase, two cells are obtained, and the cell cycle restarts for each of them.[7]

Cell cycle regulation is essential to ensure proper cell division and proliferation, thereby avoiding the dysregulation that could lead to diseases such as cancer. The cell cycle, consisting of various phases, is finely regulated by the interaction of multiple genes.[8]

In this context, proto-oncogenes play a fundamental role in positively promoting the different stages of the cell cycle, allowing controlled cell growth and division. However, when these proto-oncogenes undergo pathogenic mutations, they transform into oncogenes, inappropriately activating growth signals and contributing to tumor development.[6,8]

On the one hand, tumor suppressor genes play an opposite role by negatively regulating the cell cycle. These genes act as brakes, inhibiting cell proliferation and preserving genomic integrity. Mutations in tumor suppressor genes can lead to loss of this inhibitory function, allowing uncontrolled cell division and promoting tumor formation.[6,8]

In contrast, when one allele of a tumor suppressor gene undergoes mutation, it acquires a recessive behavior, meaning the inhibitory function continues as long as cells have the normal allele. However, when oncogenes mutate, they exhibit dominant behavior, meaning they can induce tumor formation independently.[6,7]

The p53 gene is indispensable for cancer prevention as it acts as a tumor suppressor. However, it is estimated that 50 % of human tumors have mutations in the p53 gene.[7,8]

Genes predisposed to cancer

Cancer predisposition genes (CPGs) are those that contribute to cancer formation with varying levels of penetrance risk, whether high, moderate, or low, due to changes in the biological processes they are involved in. Penetrance of a mutation refers to the percentage of carrier individuals who exhibit symptoms of the

disease. In hereditary cancer (HC), it has been observed that alleles with higher penetrance are less common. Currently, around 100 CPGs with variable penetrance have been identified, classified according to the risk they pose for the development of malignant and benign tumors.[8]

These genes, which contribute to more than 50 hereditary tumor syndromes (HTS), can be transmitted in a dominant or recessive manner. In dominant inheritance, a single altered allele is sufficient to manifest the traits of the disease, inherited from one parent with a 50 % risk. On the other hand, in recessive inheritance, the affected individual has both alleles altered, both parents are carriers, and there is a 25 % risk of inheriting the mutation.[7,8]

Most common hereditary cancer syndromes

Based on the aforementioned, this article will focus on providing a detailed description of Hereditary Breast and Ovarian Cancer Syndrome, as well as Hereditary Nonpolyposis Colorectal Cancer Syndrome (Lynch syndrome). These syndromes are of great importance due to their frequency and clinical relevance.[9] In addition to exploring these syndromes in depth, the criteria for their study will be addressed, and the importance of genetic counseling in their clinical management will be discussed.

Molecular Aspects of Hereditary Predisposition to Breast Cancer

Hereditary breast cancer (HBC) accounts for approximately 5 % to 10 % of all cases of this pathology.[10,11] It is estimated that eight out of ten women are affected by this type of cancer, making it one of the leading causes of mortality in women.[12]

Hereditary breast cancer is characterized by the transmission of specific genetic mutations from one generation to another. Mutations in the BRCA1 and BRCA2 genes are recognized as the primary drivers of this predisposition and have been extensively studied. These mutations can increase the risk of developing breast cancer by up to 80 % over a lifetime. Consequently, early detection and genetic counseling are of vital importance, especially for women with family histories, particularly first-degree relatives.[13]

In contrast, the BRCA1 gene acts as a tumor suppressor gene with a crucial role in controlling cell growth and DNA repair.[14] On the other hand, the BRCA2 gene also functions as a tumor suppressor gene, playing an essential role in preventing the development of cancerous cells. Therefore, mutations or deletions in these genes can result in the loss of their function, meaning the organism's ability to repair DNA damage efficiently is affected, thereby increasing the risk of tumor formation.[15]

There are common mutations in the germline of the BRCA1 and BRCA2 genes. In the case of BRCA1, common mutations include 5382insC, 185delAG, 3819del5, and 4153delA, while for BRCA2 they are 4075delGT and 580del4.[16]

Study Criteria

The primary study criteria include:

Assessment of breast cancer risk focuses on recognizing family history, particularly in close relatives such as mothers, sisters, or daughters, as well as other first-degree relatives. A greater number of affected relatives and a closer kinship are associated with an increased risk of developing the disease.[17]

The risk also increases when the diagnosis occurs at early ages in family members, particularly before the age of 50, which suggests the possibility of an inherited genetic predisposition.[18]

The presence of related cancers, such as ovarian cancer, in the family can also be a study criterion since it is related to mutations in the same genes.[19] Additionally, hereditary breast cancer tends to present as bilateral tumors, affecting both breasts, at a higher rate than non-hereditary breast cancer.[20]

The detection of mutations in specific genes associated with hereditary breast cancer, such as BRCA1 and BRCA2, is positioned as an essential criterion. To confirm the presence of these mutations, genetic testing is employed, which may be recommended in individuals with family history of breast cancer or other risk factors.[21]

Molecular Aspects of Hereditary Predisposition to Ovarian Cancer

Ovarian cancer is one of the most common worldwide, ranking third in frequency among gynecological cancers. Its mortality rate exceeds 50 %, making it the most unfavorable prognosis, being three times more deadly than breast cancer.[22]

Approximately 25-30 % of ovarian cancer cases have a hereditary component, mostly linked to genetic alterations in the BRCA1 and BRCA2 genes.[23]

BRCA1, located on 17q21, encodes a multifunctional protein that safeguards genomic stability. BRCA2, on 13q12, is implicated in DNA repair. Both genes are expressed in breast and ovarian tissues, crucial for preventing chromosomal instability and suppressing tumor formation. Mutations in these genes are known to significantly increase susceptibility to ovarian cancer, resulting in carriers having a much higher risk than the general population.[24]

The BRIP1 gene, implicated in DNA replication and homologous recombination repair, has been associated with a potentially high risk of late-onset serous ovarian cancer. RAD51C and RAD51D, both involved in DNA repair, also harbor pathogenic variants that may increase the risk of ovarian cancer, with carriers typically diagnosed around the age of 60. These genes, especially RAD51C, are associated with high-grade serous adenocarcinomas in ovarian cancer.[24]

Patients who carry the BRCA1/2 genes have more positive survival outcomes compared to those who do not have these mutations, as these women typically undergo more detailed screening, facilitating diagnosis at earlier stages.[25]

The high mortality rate associated with this cancer is attributed to the silent growth of the tumor. Symptoms, typically nonspecific, tend to manifest in advanced stages, with the most common being back pain, fatigue, abdominal pain or bloating, constipation, or urinary symptoms, which often appear at least three months before diagnosis.[26]

Study Criteria

To develop an effective detection method, it is crucial to identify risk factors linked to the disease. These factors include age, mutations in the BRCA1 and BRCA2 genes, Lynch syndrome, family history of ovarian tumors, history of infertility, presence of endometriosis, smoking habit, use of intrauterine devices, use of oral contraceptives, prolonged breastfeeding for more than 12 months, and previous pregnancy experiences.[27]

Similarly, screening for ovarian cancer, through the use of tumor markers such as CA-125 and imaging techniques such as transvaginal ultrasound, can contribute to the early detection of the disease.[27]

Hereditary Non-Polyposis Colorectal Cancer without Microsatellite Instability

The term "familial colorectal cancer type X" (FCCTX) is used to refer to a group of families exhibiting a strong aggregation of hereditary non-polyposis colorectal cancer, whose genetic etiology is not fully understood. This designation is used despite the lack of knowledge about the underlying genetic basis.[1]

The most notable is the familial origin, which includes several criteria for diagnosis:

- One case of breast cancer diagnosed at 40 years of age or younger.
- Simultaneous diagnosis of breast and ovarian cancer in the same patient.
- Two or more cases of breast cancer, with one being bilateral or occurring in individuals under 50 years of age.
- One case of breast cancer in a woman under 50 years of age or bilateral, and another case of ovarian cancer in first or second-degree relatives.
- Three cases of cancer, with at least one case of ovarian cancer, in first or second-degree relatives.
- Two cases of ovarian cancer in first or second-degree relatives.
- One case of breast cancer in a man, along with at least one first or second-degree relative with breast or ovarian cancer.[28]

Lynch syndrome is a hereditary condition passed from parents to children that increases the risk of developing cancer. It is estimated that 1 in every 279 people in the general population has this syndrome. LS accounts for about 3 % of colorectal cancer (CRC) cases and 2 % of endometrial cancer (EC) cases. CRC is the most associated cancer type with LS and tends to occur on the right side of the colon. This type of cancer in individuals with LS is often poorly differentiated, with mucinous features or a medullary growth pattern. Additionally, there is abundant lymphocyte infiltration, a higher likelihood of synchronous or subsequent tumors, and a better prognosis in the absence of metastasis.[28,29]

Study Criteria

The guidelines from the European Society for Medical Oncology (ESMO), Molecular Oncology Committee (MOC), provide guidance and recommendations for Hereditary Non-Polyposis Colorectal Cancer without Microsatellite Instability (HNPCC-MSI). Although they all share fundamental criteria, they present notable differences.

The ESMO guideline[30] highlights several criteria for studying HNPCC-MSI. Emphasis is placed on diagnosing CCR without microsatellite instability (MSI) before the age of 50, as well as the presence of mucinous tumor and medullary carcinoma. Family history plays a crucial role, including the existence of a first-degree relative with CCR without MSI and two or more second-degree relatives with the same diagnosis. Additionally, the guideline considers the presence of adenomatous polyps and other criteria, such as the development of endometrial cancer in the family context.

On the other hand, the MOC guideline[31] reflects similar criteria, emphasizing the importance of age at diagnosis, histological characteristics, family history, and the presence of adenomatous polyps. The agreement between both guidelines extends to the recognition of the relevance of genetic counseling, genetic testing to identify mutations in DNA repair genes such as MLH1, MSH2, MSH6, and PMS2, as well as the need for regular monitoring for early detection of possible signs of cancer in at-risk individuals.

HNPCC is caused by germline mutations in the so-called "mismatch repair genes" (MMR), the most important of which for hereditary susceptibility to colorectal cancer (CRC) are hMLH1, hMSH2, hPMS1, hPMS2, and hMSH6. In most individuals with germline mutations in any of these genes, the tumor exhibits what we call "microsatellite instability" (MSI), which refers to the expansion or contraction of repetitive DNA sequences. This instability occurs due to the inability of the repair system to correct errors during DNA replication. The 5 most informative markers for the presence of MSI in CRC tumors are: BAT 25, BAT 26, D5S346, D2S123, D17S250. This panel is performed on patients who meet a series of criteria known as "Bethesda Criteria".[29]

The genes MLH1, MSH2, MSH6, and PMS2 encode proteins of the DNA mismatch repair (MMR) system that corrects errors that occur during DNA replication. Germline variants in MMR genes cause Lynch syndrome, characterized by an increased risk of colorectal, endometrial, stomach, and ovarian cancer at younger ages than in the general population.[32]

The Amsterdam I (1990) and Bethesda (1998) Criteria, which establish guidelines for diagnosing Lynch syndrome (LS), but clinical heterogeneity complicates identification. Amsterdam II (1998) was introduced to address limitations, requiring four criteria to be met (Table 1). In 2004, the Revised Bethesda Criteria expanded the guidelines. The sensitivity of Amsterdam II is 87 %, 62 %, 38 %, and 48 % for MLH1, MSH2, PMS2, and MSH6. The Revised Bethesda Criteria have >94 % sensitivity with 25 % specificity. "Familial Type X CRC" is suggested for cases meeting Amsterdam criteria without MMR mutations, indicating its predictive limitation (50 % and 20 %). 40 % of patients meeting Amsterdam criteria lack mutations.[33]

Table 1. Clinical Diagnostic Criteria

Amsterdam Minimum Criteria (1990)	Revised Amsterdam Criteria II (1998)
1. At least 3 cases of colorectal cancer in relatives (verified pathologically)	1. At least 3 relatives with an HNPCC-associated cancer (cancer of the colorectum, endometrium, small, bowel, ureter or renal pelvis)
2. One is a first degree relative of the other two	2-5. As for the minimum criteria
3. At least two successive generations should be affected	
4. One case of colorectal diagnosed before the age of 50 years old	
5. Familial adenomatous polyposis syndrome (FAP) should be excluded	

Source: Own elaboration according to the Manual of Clinical Oncology.[33,38]

Familial adenomatous polyposis

"Familial adenomatous polyposis is the second most common syndrome and occurs in 1 % of colorectal cancers".[34]

Familial adenomatous polyposis (FAP) is a hereditary syndrome in which hundreds or thousands of masses, known as polyps, form in the colon and rectum projecting into the intestinal lumen, with a higher prevalence in males. They are often asymptomatic; however, as the polyp grows in size, it is more likely to develop symptoms such as changes in bowel movements, abdominal pain, and the appearance of rectal bleeding, which is one of the warning signs for patients. Since it is mostly asymptomatic, it is usually incidentally discovered during endoscopy.[35]

This disease typically appears at a young age and carries a high risk of developing colorectal cancer if measures such as colectomy are not taken.

The genetic basis of familial adenomatous polyposis

This follows an autosomal dominant inheritance pattern. In the 1990s, the Adenomatous Polyposis Coli (APC) locus (5q21) was identified on chromosome 5 and deletions in this chromosomal region were found in patients with this condition.

"The APC gene has 21 exons, of which 15 are coding exons. It encodes a 2843-amino acid protein and is a tumor suppressor gene. The APC protein plays important roles in the Wnt signaling pathway and cellular processes such as neuronal differentiation, apoptosis, cell adhesion, and migration"[34, 35].

The Wnt/beta-catenin signaling pathway plays a crucial role in embryonic development, and following this, the most important pathway is the canonical pathway, in which APC plays significant functions.

APC, along with AXIN2 and GSK3-beta, forms the destruction complex of beta-catenin, marking it for subsequent destruction by the proteasome. If APC has a mutation, beta-catenin accumulates in the cytoplasm and enters the nucleus. Here, it forms a complex with T-cell factor (TCF), promoting the expression of various genes involved in cancer transformation and proliferation.[35]

The APC gene is a crucial negative regulator in the Wnt signaling pathway, playing a fundamental role in

the control of cell proliferation and differentiation. However, when this gene undergoes alterations, it leads to dysregulation of several cellular processes. This includes loss of cell adhesion, defects in cell cycle control, and impairment in base excision repair mechanisms. These changes result in chromosomal mis-segregation and instability.[35]

Study Criteria

There are a large number of studies and tests to detect abnormalities, such as molecular and genetic tests, among these techniques are "PCR, DNA sequencing, and comparative genomic hybridization on microarrays to detect amplifications and deletions." However, many of these tests are not accessible to everyone due to cost and standardization issues. Nevertheless, we will briefly explain three of them for educational purposes.[36]

1. Full gene sequencing: It is believed to be one of the best tests for detecting the disease; however, this depends on the severity of the condition.
2. Deletion/duplication analysis: It detects deletions or duplications of exons or the entire gene. The methodology of this test is quantitative real-time PCR and multiplex ligation-dependent probe amplification (MLPA).
3. Complete coding region analysis for mutation monitoring: It analyzes sequences in the messenger RNA and consists of two steps: "first, identifying alterations in the sequence, and second, sequencing directly on the region that showed alterations".[36]

Genetic counseling

According to the National Society of Genetic Counselors in the United States, cancer development is a process that addresses the medical, psychological and family implications of genetics in the disease, taking into account the personal or family history of cancer, indicative characteristics of hereditary cancer, and other risk factors. This multifaceted process involves professionals from various fields and is based on the principles of voluntariness, confidentiality, privacy, psychosocial care and informed decision-making. Cancer, like other scourges, is a disease that has multiple causes and many of them are still uncertain about their origin.

Therefore, building relationships, gathering information, verifying diagnoses, assessing risks and recurrences, obtaining informed consent and conducting psychosocial evaluations of the patient are all components of comprehensive genetic counseling. Everyone must take into account their race, origin and ethnicity.[37,38]

CONCLUSIONS

Cancer, a multifactorial disease, exhibits a clear genetic predisposition. Mutations in specific genes such as BRCA1 and BRCA2 are strongly associated with an increased risk of breast and ovarian cancer. Similarly, variants in genes responsible for DNA repair, such as MLH1, MSH2, MSH6, and PMS2, increase susceptibility to colorectal cancer and other types of cancer. Likewise, genetic abnormalities in the APC gene are directly related to familial adenomatous polyposis.

Study criteria, such as family history and age at diagnosis, along with the presence of specific tumors, will determine whether individuals or entire families should undergo molecular testing to detect specific genetic mutations related to these types of cancer. The implementation of these criteria and genetic testing will facilitate early detection and provide appropriate genetic counseling.

Genetic counseling plays a vital role in understanding and addressing the risks associated with hereditary cancer. Its proper implementation ensures accurate diagnoses, optimal treatment options, and prevents misinterpretations of genetic tests, thus ensuring effective disease management and avoiding costly and unnecessary tests.

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CONFLICT OF INTEREST

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