apoio físico e emocional para o enfrentamento da doença. Transtornos de humor apresentam-se de maneira atípica em idosos, sendo difíceis de diagnosticar pelo processo de senescência, exigindo uma abordagem singular, principalmente quando associados aos quadros de câncer. Por se tratar de uma condição que não tem cura, os casos de suicídio são vistos como uma maneira de os pacientes tomarem o controle de suas próprias vidas, acabando com o sofrimento, impotência e incerteza. **Conclusão:** Conclui-se que o tratamento paliativo precoce facilita o enfrentamento da doença MM na esfera biopsicossocial, no entanto, é necessária a realização de mais estudos para melhor compreensão dos impactos.

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DESCRIÇÃO EPIDEMIOLÓGICA DAS MORTES POR MIELOMA MÚLTIPLO E NEOPLASIAS MALIGNAS DE PLASMÓCITOS NO BRASIL (2018-2022)

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Objetivo: Analisar a descrição epidemiológica das mortes por Mieloma Múltiplo e neoplasias malignas de plasmócitos (CID 10 – C90), entre os anos de 2018 a 2022, no Brasil, com o objetivo de compreender os principais fatores correlacionados a essa mortalidade. **Material e métodos:** Estudo epidemiológico, descritivo e retrospectivo, cuja fonte de dados foi o Sistema de Informações sobre Mortalidade - SIM, disponíveis na plataforma DATASUS. A seleção de dados foi realizada por meio do processo de tabulação com as principais variáveis epidemiológicas disponíveis (faixa etária, sexo e cor/raça), no período de janeiro de 2018 a dezembro de 2022. **Resultados:** No Brasil, houve um total de 17.640 mortes por Mieloma Múltiplo e neoplasias malignas de plasmócitos, no espaço temporal analisado. As mortes por ano apresentaram números próximos, entre 3.407 e 3.679. Além disso, a mortalidade concentrou-se majoritariamente em indivíduos com mais de 40 anos de idade (98,9%). A diferenciação com relação ao sexo apresentou-se pequena, sendo que 52% foram do sexo masculino e 48% do sexo feminino. Considerando indivíduos com 40 anos ou mais, o número de óbitos de mulheres superou o de homens na faixa etária de 80 anos ou mais, sendo que nos decênios anteriores a quantidade de mortes masculinas foi maior. Quanto ao aspecto cor/raça, houve destaque para a cor/raça branca (56,77%), seguida pela parda (31,17%) e preta (8,83%). **Discussão:** Diante da grande repercussão em números de mortalidade dessas neoplasias e as consequências do avanço da doença, o diagnóstico deve ser realizado o mais precoce possível. Isso é necessário porque, atualmente, raramente o diagnóstico é realizado antes dos 40 anos de idade e quanto mais postergado, pior será o prognóstico do paciente. Outro fator relevante é o número superior de mortes de mulheres com 80 anos ou mais, uma vez que é, conforme a literatura, um reflexo da maior expectativa de vida e associação aos cuidados em saúde do sexo feminino em relação ao sexo masculino. Cabe salientar que mulheres enfrentam efeitos das alterações hormonais a partir da menopausa, os quais tornam ainda mais significativos os prejuízos ocasionados pelo Mieloma Múltiplo e neoplasias malignas de plasmócitos em diferentes órgãos, destacando-se estruturas musculares e ósseas. Os resultados do aspecto cor/raça estão de acordo com estudos na população brasileira, em que a maioria das mortes foi de indivíduos brancos. **Conclusão:** Em face dessa descrição epidemiológica das mortes por Mieloma Múltiplo e neoplasias malignas de plasmócitos, é possível confirmar a concentração de óbitos a partir da meia-idade, em torno dos 45 anos, em uma população em que a transição demográfica reflete um maior número de indivíduos mais velhos. De modo geral, são necessários avanços nas formas de diagnóstico precoce e no tratamento, visando aumentar a sobrevida e melhorar o prognóstico dessas doenças, principalmente no que tange ao acesso e às necessidades de serviços de saúde por homens e mulheres.

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IMPACT OF MULTIPLE MYELOMA: REVEALING CLINICAL AND GENETIC ASPECTS

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Introduction: Multiple myeloma (MM) is a neoplastic disease of plasma cells, the second most prevalent hematological cancer in Brazil, characterized by infiltration of the bone marrow by differentiated B lymphocytes (plasma cells) and progressive destruction of bone tissue. The pathology arises from an asymptomatic pre-malignant disorder and involves multifactorial components that result in MM. **Objective:** This study addresses the impact of multiple myeloma (MM), focusing on essential clinical and genetic aspects to understand its pathogenesis and impact on public health. **Materials and methods:** This study critically reviewed current guidelines on diagnosis, risk stratification, and treatment of multiple myeloma (MM). Using databases such as PubMed, Scopus, and Google Scholar, articles published from 2020 to 2022 were selected, including systematic reviews, meta-analyses, observational studies, and relevant clinical trials. The focus was on advances in

molecular genetics. **Results:** Multiple myeloma (MM) begins from an asymptomatic precursor stage, relating complex genetic and microenvironmental changes that transform plasma cells into a malignant neoplasm. It was reported that its silencing suppressed cell proliferation and increased apoptosis by transcriptionally regulating the miRNA hsa-miR138-5p, targeting caspase-3, a potential target for the early diagnosis and treatment of MM. The KIAA1191 gene was associated with improved overall survival and progression-free survival. Furthermore, its high expression suppressed the proliferation and migration of MM cells and had a synergistic effect with bortezomib on the cells' proliferation capacity. Initial therapies include VRd or Dara-VRd, followed by autologous stem cell transplantation (ASCT) in suitable candidates. **Discussion:** The clinical findings of this study showed that clinical history and investigation of the initial symptoms are needed. Multiple myeloma is more common in men above 65 years. The main symptoms are bone pain, anemia, leukocyte dysfunction and renal function alterations. To confirm the diagnosis, some additional tests are needed for therapeutic planning, including prothrombin time, activated partial thromboplastin time, fibrinogen, d-dimer, total bilirubin and fractions, alkaline phosphatase, transaminases and gamma-gt. **Conclusion:** This research underscores the complexity of multiple myeloma (MM) and the importance of early diagnosis and personalized treatment, beginning from an asymptomatic precursor stage with genetic and microenvironmental changes that transform plasma cells into malignant neoplasms. Initially, the progression from monoclonal gammopathy of undetermined significance to latent MM is marked by increasing genetic instability, exacerbated in patients with high-risk chromosomal abnormalities. Additionally, the Twist1 protein and miRNA hsa-miR138-5p emerge as potential targets for early diagnosis and treatment. Moreover, the KIAA1191 gene is associated with improved overall and progression-free survival, especially when combined with bortezomib. Risk stratification, including del(17p) and p53 mutation, guides initial therapies such as VRd or Dara-VRd, followed by autologous stem cell transplantation (ASCT). Therefore, treatment personalization, based on biomarkers and risk stratification, is crucial for improving outcomes in MM, ensuring more effective and targeted disease management.

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MULTI-OMIC ANALYSIS OF MULTIPLE MYELOMA BY T(11;14) STATUS

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Aims: To characterize the genomic and transcriptomic profiles associated with t(11;14) status in NDMM and RRMM. **Methods:** The global, non-interventional MEDICI study (NCT04721002) enrolled pts aged ≥18 years who provided informed consent and had BM aspirates collected at diagnosis and/or relapse. In this analysis (data cutoff October 31, 2023), BM aspirates were subjected to plasma cell enrichment and next-generation RNA sequencing (RNAseq) followed by differential gene expression analysis. *P* values were corrected by the Benjamini and Hochberg method. **Results:** A total of 525 pts were included. Among 110 pts with t(11;14)-positive (NDMM, n = 56; RRMM, n = 54), the median age was 64.5 years (range, 38.0–89.0), 60.0% of pts were male, and 74.5% of pts were White. Among 376 pts with t(11;14)-negative (NDMM, n = 235; RRMM, n = 141), the median age was 67.0 years (range, 37.0–90.0), 54.0% of pts were male, and 75.8% of pts were White. ECOG performance status for pts with t(11;14)-positive vs t(11;14)-negative status was 0–1 in 72.7% vs 69.7%. ISS stages I, II, and III disease were present in 34.5%, 21.8%, and 23.6% of pts with t(11;14)-positive and 30.9%, 24.7%, and 25.0% of pts with t(11;14)-negative status, respectively. Of the 525 pts, 369 had samples subjected to RNAseq for whole transcriptome sequencing (WTS). Differential gene expression analysis showed overexpression of *CCND1* (encodes cyclin D1) in pts with t(11;14)-positive vs t(11;14)-negative status in both NDMM and RRMM, as expected. Evaluation of BCL-2 family genes revealed increased expression of the pro-apoptotic BH3 sensitizer *PMAIP1* (encodes NOXA) in pts with t(11;14)-positive vs t(11;14)-negative status with NDMM and RRMM. Comparison of differentially expressed genes among pts with t(11;14)-positive NDMM vs RRMM, showed that while *BCL2* (encodes BCL-2) expression was similar in both disease settings, *MCL1* (encodes MCL-1) and *BCL2A1* (encodes BFL-1) expression were significantly increased in RRMM. Overexpression of *MCL1* and *BCL2A1* have been shown to drive Ven resistance in hematologic malignancies. Whole-exome sequencing analysis will be presented at the meeting. **Discussion:** The selective, potent, oral BCL-2 inhibitor venetoclax (Ven) has demonstrated efficacy in patients (pts) with t(11;14)-positive relapsed/refractory MM (RRMM) and is currently being evaluated as biomarker-directed therapy in this population. Clinical trials estimate 15%–20% of pts with MM carry t(11;14); however, t(11;14)-positive MM prevalence has yet to be established in a real-world setting. Using BM aspirates from MEDICI, WTS and differential expression analysis of key apoptotic pathway genes showed significantly higher *PMAIP1* expression in t(11;14)-positive NDMM and RRMM. Comparison among pts with t(11;14)-positive showed increased *MCL1* and *BCL2A1* expression in RRMM; further evaluation may offer insights into acquired genomic heterogeneity in RRMM and guide optimal combinations with Ven. **Conclusion:** The pro-apoptotic BH3 sensitizer PMAIP1 (NOXA) was overexpressed in t(11;14)-positive vs t(11;14)-negative disease in both NDMM and RRMM. Although BCL2 (BCL-2) expression levels were similar, MCL1 (MCL-1) and BCL2A1