■ Article

Genomic Variants Associated With Cancer-Related Fatigue: A Systematic Review

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Background: Cancer-related fatigue (CRF) is the most common stressful side effect caused by cancer and cancer treatments. Although CRF causes a significant burden to quality of life, no pharmacologic interventions are available because the mechanism remains unknown.

Objectives: This systematic review analyzed the genomic variants that have been found to be associated with CRF.

Methods: A search for peer-reviewed articles through PubMed, EBSCOhost, and DePaul WorldCat Libraries Worldwide yielded 16 published studies.

Findings: The majority of genomic variants demonstrated that the inflammatory and immune response pathways, including the neuro-proinflammatory cytokine pathway, have statistically significant associations with CRF. Additional genomic studies are still needed to validate the findings in this systematic review. The exact biologic underpinnings that contribute to the development of CRF remain unknown.

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The prevalence of fatigue experienced by patients with cancer during treatment ranges from 25%–99% (Bower et al., 2013). Healthcare providers are proactive about treating pain and related acute symptoms, and cancer-related fatigue (CRF) is a symptom that has been recognized for many years. However, a biologic-based intervention remains elusive because of a lack of systematic studies examining the biologic underpinnings of CRF. Researchers believe that the cancer itself and its treatment contribute to the development of CRF (Piper & Cella, 2010). The physiologic basis of molecular-genetic etiology of CRF is still unclear, and limited research has been done (Saligan & Kim, 2012). To develop treatments for CRF, accurately assessing and analyzing biologic biomarkers related to CRF is essential. Researchers on CRF are now using advanced technologies, such as genomics or proteomics, to accurately and reliably discover biomarkers that can explain the biologic mechanisms of CRF development.

CRF is associated with negative health outcomes and decreased health-related quality of life. Some of the health issues associated with CRF include sleep disturbance, impaired cognitive function, and increased rates of depression (Bower & Lamkin, 2013; Piper & Cella, 2010; Saligan et al., 2015). Biomarkers are characteristics that are objectively measured and evaluated as indicators of normal biologic processes, pathogenic processes, or pharmacologic responses to a therapeutic intervention (News-Medical.Net, 2016). Examples of biomarkers studied in CRF include inflammatory and metabolic cytokines or chemokines (e.g., interleukin-6, tumor necrosis alpha, cortisol, serotonin), but results are conflicting. Investigators are starting to examine the role of genomics, genomic variants, and other genomic biomarker changes associated with CRF to better understand the biologic mechanisms of this symptom and overcome some of the weaknesses of conventional biomarker tests. Nurses need to understand the significance of biomarkers and their biologic impact on CRF development to help design interventions based on the biologic mechanism of symptoms. In addition, advanced genomic technologies have the potential to uncover the downstream and/or upstream mechanisms that are at the root of CRF development and eventually provide new insights into the role of inflammatory and metabolic pathways