Using a Genomics Taxonomy

Facilitating patient care safety and quality
in the era of precision oncology

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Oncology nurses need to be competent in the ever-expanding application of genomics in cancer care, and understanding foundational terms is necessary. A landscape analysis of Oncology Nursing Society (ONS) materials, a literature review, and expert opinion revealed inconsistencies and varying use of genomic terms, some of which are outdated. In response, the ONS Genomics Taxonomy was built to address inaccuracies and discrepancies in terms and to be an accessible resource for oncology nurses. The taxonomy is a living document that is updated to reflect evolving science and evidence and serves to diminish confusion, improve genomic literacy, and assist oncology nurses in providing safe genomic care.

AT A GLANCE

- Advancements have transformed cancer care from genetics into genomics, necessitating changes in terminology used by professionals to avoid confusion and reflect the current state of the evidence.
- Patients and families rely on nurses to explain genomic terminology and concepts in ways that can be easily understood, which is facilitated by a taxonomy.
- Oncology nursing education programs should use consistent, accurate, and current terminology when providing education on genomic concepts.

Genomics is fundamental to cancer care and foundational to oncology nursing practice. However, practicing oncology nurses' knowledge of genomics is limited, and few oncology nurses have learned genomic content during educational preparation (Aiello, 2017). Expanding implications for germline genetic testing (Giri et al., 2020), as well as the rapid influx of biomarkers, biomarker testing with new technologies, and targeted therapies into cancer care, necessitate use of accurate and consistent terminology reflecting current evidence. Understanding these foundational terms and concepts is critical to reduce errors and confusion in practice and increase quality of care. The many quality and safety implications to genomics-based oncology care include incorrect or no somatic and/or germline testing performed when indicated; missed or incorrect genetic professional referrals; test result misinterpretation, leading to incorrect or absent interventions and/or therapies; and patient and family confusion—all of which result in missed opportunities for cancer prevention and effective cancer treatment.

Terminology is transitioning in cancer care from genetics into genomics as technology and science evolve and evidence-based testing applications expand. Genomics, the entire genome of any organism (including humans), is an expansion of genetics, which refers to a specific gene, such as *BRCA1* (National Human Genome Research Institute, 2020b). The focus on genomics is largely the result of rapid advances in technology, with substantial reduction in costs. The benchmark, now largely achieved, has been the ability to sequence an entire genome for $1,000 (National Human Genome Research Institute, 2020a). This was a cost considered within range of other healthcare tests that would make it feasible to translate genomics into practice to improve health outcomes.

As a result, patients with cancer receive increasing amounts of individualized genomic information about their disease through germline and somatic biomarker testing. The varied and inconsistent use of terms is a definite obstacle to effective patient–clinician communication and, ultimately, to optimal patient care (Martin et al., 2020). Oncology nurses play an essential role in leading the patient and family through the complex matrix of tests, results, and therapy plans. The development and adoption of a standard taxonomy improves communication among healthcare professionals, helps nurses educate patients and their families, diminishes confusion and the risk for error, and reflects the current state of the evidence.

Genomics Through a Quality and Safety Lens

The risk for error because of lack of genomic literacy is best illustrated by a case study