

# Human Radiosensitivity

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**Abstract**—Over the past few decades, there has been increasing recognition that the characterization of health effects following radiation exposure should extend beyond traditional assessment by epidemiologic methods to incorporate biological evaluation of differences in susceptibility between individuals. The idea of individual sensitivity to radiation in humans has long been supported by data from patients with certain rare hereditary conditions. However, these cancer susceptibility syndromes affect only a small proportion of the general population. More relevant to the majority of the population is the idea that some part of the genetic contribution defining radiation susceptibility may follow a polygenic model, which predicts elevated risk resulting from the inheritance of several low penetrance risk alleles. Here, we review current evidence from population-based studies of radiation-related risk in susceptible groups, including data from the candidate gene approach, genome-wide association studies, and tumor sequencing. While these studies are faced with several challenges (including the need for large sample sizes, high-quality exposure assessment and meaningful replication sets), results of recent studies indicate that the integrated assessment of radiation exposure and genetic and epigenetic alterations may lead to a more nuanced characterization of radiation-related risk.