

Polygenic scores for cancer: key points

- ◆ Cancer is a highly variable and complex disease, and each cancer has a variety of factors – e.g. genetics, environment – that contribute to its development. The genetic component of different cancers, and their subtypes, varies.
- ◆ Between a third and a half of cancer cases could be prevented if current knowledge about risk factors was translated into effective public health actions.
- ◆ Comprehensive risk prediction models (RPMs) that bring together information across a diverse range of factors can inform prevention strategies. The extent to which such models are used in clinical practice varies.
- ◆ Polygenic scores are considered a measure of genetic contribution to the risk of developing cancer. They are now being considered as a factor for risk prediction which could be used independently or as part of RPMs for cancer.
- ◆ Polygenic scores can improve risk prediction in some cancers and some clinical contexts, but the magnitude of the improvement varies between cancers.
- ◆ Any use of polygenic scores in cancer management will be specific to the cancer and the clinical context. This is not a one size fits all solution.
- ◆ Wider implementation of risk prediction using polygenic scores requires sufficient understanding of how they will affect clinical care, as well as wider infrastructure considerations for delivery.
- ◆ Continued effort is needed to gather the appropriate evidence for evaluation and demonstration of utility that would support implementation efforts.
- ◆ Premature implementation of polygenic scores in cancer risk estimation approaches could undermine these efforts, and risk loss of confidence in this potentially valuable area of population health improvement.

