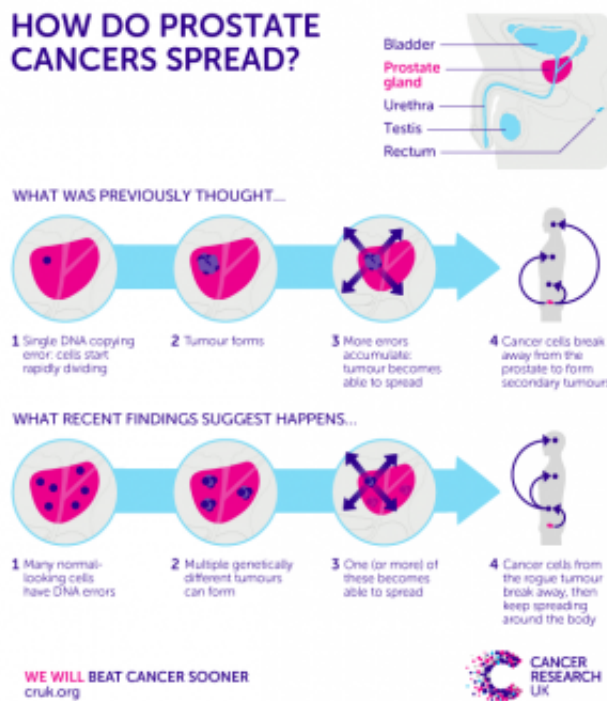


Drilling down to genetic root of prostate tumor development

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This infographic shows how prostate cancer spreads. Credit: Cancer Research UK

Scientists have revealed the root of prostate cancers in individual men, discovering that despite huge genetic variety between tumours they also share common gene faults - insight that could offer new treatment hopes, according to research published in *Nature* today (Wednesday).

In a landmark paper, Cancer Research UK funded scientists alongside an international team of researchers read all of the DNA in tumour samples from 10 men with prostate cancer. This allowed them to map a 'family tree' of the changes happening at a genetic level as the disease spreads, forms new tumours, and becomes resistant to treatment.

They also revealed more detail about how prostate cancer spreads, showing that the group of cells that first spread from the prostate carry on travelling around the body, forming more secondary tumours.

The research is part of the International Cancer Genome Consortium (ICGC) - a global project using the latest gene-sequencing technology to reveal the genetic changes driving the disease.

The ICGC Prostate Cancer UK group - funded by Cancer Research UK, the Dallaglio Foundation, the Wellcome Trust, the Academy of Finland and others - is examining how the disease evolves in patients to help develop approaches for personalised medicine, tailored to the genetic makeup of each person's cancer.

The team has already revealed a huge amount of genetic diversity between [cancer cells](#) taken from different sites within each man's prostate.

And this new study shows that, despite the diversity, [prostate cancer cells](#) that break free from the tumour and spread share common genetic faults unique to the individual patient.

Study author Ros Eeles, professor of oncogenetics at The Institute of Cancer Research, London, and honorary consultant at The Royal Marsden NHS Foundation Trust, said: "We gained a much broader view of prostate cancer by studying both the original cancer and the cells that had spread to other parts of the body in these men. And we found that all

of the cells that had broken free shared a common ancestor cell in the prostate.

"The common faults we found in each man could potentially offer new targets for treatment. But we found that, once cancer cells have spread, they continue to evolve genetically, so choosing the most effective treatments will remain a key challenge."

Professor Steven Bova, based at the University of Tampere, Finland, and head of ICGC prostate cancer UK metastatic studies, said: "The diversity we've found suggests multiple biopsies might be needed to identify the 'trunk' of the cancer's tree of mutations - we need treatments that target these core weaknesses to destroy all cancer cells in a clean sweep, rather than trimming the branches. We must also study more patients to learn how to apply these findings to develop more personalised treatments for people with the disease."

Dr Ultan McDermott, senior author at the Wellcome Trust Sanger Institute, said: "In the phylogenetic trees that our data have produced, we see that most of the oncogenic mutations are shared clonally by all the tumour sites in each patient. This common genetic heritage is a potential achilles heel of the metastases, however, many of these shared mutations are in tumour suppressor genes and our approach to therapeutically targeting these needs to be prioritised."

"It takes a while before a tumour develops the ability to metastasise but once it does the patient's prognosis changes significantly. We have to zoom in on this crucial junction and gather more data on the impact different therapies have on prostate cancer's evolution and spread."

Nearly 42,000 men are diagnosed with prostate cancer each year in the UK, making it the most common cancer in men and the third most common cancer overall. There are more than 10,800 deaths from the

disease every year in the UK.

Professor Peter Johnson, chief clinician at Cancer Research UK, said: "The thing we fear most about cancer is how it can spread around the body - this is what causes 90 per cent of all cancer deaths. We have to find out how cancer cells change as they do this, and how they become resistant to our treatments. This research using whole genome sequencing lets us look right into the molecular core of cancer, and reveals the secrets of how cancer cells change and evolve as they grow. By getting to grips with this detail, we can start to work out how to treat [prostate cancer](#) better in the future."

More information: Gundem et al. The Evolutionary History of Lethal Metastatic Prostate Cancer. *Nature*. [DOI: 10.1038/nature14347](https://doi.org/10.1038/nature14347)

Provided by Cancer Research UK

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