

# Genes associated with aggressive breast cancer

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Researchers at the University of Gothenburg, Sweden, have for the first time identified 12 genes that could be associated with aggressive breast tumours. The discovery could result in more reliable prognoses and better treatment strategies for patients.

The results, published in the journal *Clinical Cancer Research*, are based on analyses of breast tumours from 97 female [breast cancer](#) patients. Half of these patients died within eight years of diagnosis, while the remainder survived for more than eight years.

Breast tumours consist of a heterogeneous mix of [tumour cells](#) which are markedly different in terms of their genes (DNA) and biological properties. The researchers used microarray techniques to study the overall picture of the tumours by measuring the amount of DNA and gene products (RNA) in each tumour. This enabled them to investigate the relationship between genetic changes and clinical parameters such as tumour properties and response to treatment.

"We've managed to identify 12 genes whose expression is associated with an aggressive form of breast cancer," says Toshima Parris, a PhD student at the Department of Oncology. "These 12 genes were much more prominent in patients who died within eight years than in those who survived."

Three of these 12 gene products were represented in much higher levels in aggressive breast tumours than in less aggressive tumours, whereas the

nine remaining genes were found in lower levels in aggressive tumours.

These findings suggest that the activity of these genes could have an effect on tumour progression by impacting cell growth, motility and development. According to Parris, it may one day be possible to test for these markers in blood samples containing circulating tumour cells and/or tumour tissue from [breast cancer patients](#) in order to ascertain whether the patient may benefit from a particular treatment or drug to counteract this change in the genes' activity.

"We hope that diagnostics focusing on these [genes](#) at an early stage will result in more reliable prognoses, which could lead to more effective treatment regimens for patients with aggressive tumours," says Parris.

Provided by University of Gothenburg

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