PublisherInfo		
PublisherName	:	BioMed Central
PublisherLocation	:	London
PublisherImprintName	:	BioMed Central

ER variants in breast cancer

ArticleInfo		
ArticleID	:	3750
ArticleDOI	:	10.1186/bcr-2000-66713
ArticleCitationID	:	66713
ArticleSequenceNumber	:	22
ArticleCategory	:	Paper Report
ArticleFirstPage	:	1
ArticleLastPage	:	4
ArticleHistory	:	RegistrationDate : 2000–9–26 OnlineDate : 2000–9–26
ArticleCopyright	:	Current Science Ltd2000
ArticleGrants	:	
ArticleContext	:	1305833

Valerie Speirs,[Aff1]

Aff1 University of Leeds, UK

Keywords

Breast cancer, estrogen receptor variants, PCR

Introduction

ER is expressed in approximately 60% of all breast cancers. It is an independent prognostic factor upon which decisions on whether to give hormonal therapy are based. Two forms of ER are known to exist, the original ER, now renamed ERα, and the more recently discovered, ERβ. The ERα gene consists of eight exons from which splice variants can arise due to alternative processing. The relative frequency of such variants in breast cancer progression is, however, unclear.

Aims

To identify the frequency of occurrence of variant forms of ERα mRNA in breast cancer.

Comments

Estrogen receptor (ER)α variants have been described in normal breast as well as in tumours, with their role (if any) in carcinogenesis remaining unclear. The results of this study indicate that in breast cancer progression their role is relatively minor. However, the authors have not taken into account the second ER, ERβ. Splice variants for this receptor have been described in breast tumours and breast cancer cell lines (see Additional information). Studies aimed at understanding the importance of variants of both receptor subtypes are warranted.

Methods

Breast tumour samples (n = 110) and normal breast samples (n = 8) were used. Wild type ERα was determined by routine immunohistochemistry. cDNA was synthesised from total RNA and amplified by PCR using primers designed to detect specific regions of ERα. PCR products were cloned and sequenced using standard methods.

Results

Sequence analysis of PCR-amplified cDNAs confirmed the absence of point mutations or small deletions in both normal breast and tumour samples. Although most samples contained ERα variants at low levels, only two out of 118 samples, both ductal carcinomas, showed variant ERs comparable to the intensity of the full size product when amplified using primers located in exons 6 and 8. One tumour expressed a single variant form, which was node positive but wild type ERα was undetectable by immunohistochemistry or northern blot. The second sample, of unknown node status, showed normal wild-type ERα by immunohistochemistry and northern blot and contained at least five ERα variants. Four out of five were processing variants and three had not previously been described. The main variant contained deletions in exons 2-5.

Discussion

ERα variants occured at relatively low frequency in the panel of 118 breast tumours examined. This result suggests such variants play no major part in the development and progression of human breast cancer.

Additional information

Vladusic EA, Hornby AE, Guerra-Vladusic FK, Lupu R: **Expression of estrogen receptor β; mRNA variant in breast cancer.** *Cancer Res* 1998, **58**:210-214 (PubMed abstract).Fuqua SA, Schiff R, Parra I, Friedrichs WE, Su JL, McKee DD, Slentz-Kesler K, Moore LB, Wilson TM. Moore JT: **Expression of wild-type estrogen receptor β and variant isoforms in human breast cancer.** *Cancer Res* 1999, **59**:5425-5428 (PubMed abstract).

References

1. Anandappa SY, Sibson R, Platt-Higgins A, Winstanley JHR, Rudland PS, Barraclough R: Variant estrogen receptor α mRNAs in human breast cancer specimens. Int J Cancer. 2000, 88: 209-216.