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Correction

Expression of Homeobox-containing Genes in Primary and Metastatic Colorectal Cancer—This paper was published in *The European Journal of Cancer*, Vol 29A, No. 6, pp. 887–893. Unfortunately, the abbreviation HOX was misued in several places in The Introduction; this has now been amended and a corrected version of The Introduction follows.

INTRODUCTION

COLORECTAL CARCINOMAS rank high among the most frequent human malignancies. Such tumours may arise from benign adenomatous polyps, which later progress to adenocarcinomas through several mutational steps [1]. Some of these events have been better understood through the identification of the genes 'Familial Adenomatous Polyposis' (FAP) and 'Deleted in Colorectal Cancer' (DCC) involved in colon tumorigenesis [2–3]. The overall biological characteristics of colorectal cancers, and of neoplastic tissues in general, result from accumulated genetic alterations rather than from the order in which these events occur with respect to one another [1]. Even though several important genes have been identified, other events, which remain to be elucidated, may well take place during the progression of colon cancer.

Homeobox genes are a family of genes containing a common 183-nucleotide sequence. The homeobox encodes a 61 amino acid domain, the homeodomain (HD), which includes a helix-turn-helix motif responsible for the DNA binding ability of homeobox-containing proteins [4]. On the basis of structural similarities and direct evidence that *Drosophila* homeodomain proteins are capable of binding DNA sequences and modulating transcriptional activity, it is generally accepted that homeodomain proteins are transcriptional regulators [5]. The homeobox was originally discovered in genes controlling *Drosophila* development [6] and has subsequently been isolated in other, evolutionarily distant species, such as nematodes and vertebrates [7]. Different homeobox gene families have evolved which encode homeodomain of different types or classes. Among these HD the *Drosophila antennapaedia* (Antp) homeodomain defines one consensus sequence referred to as class I HD [4]. Mammalian class I homeobox (HOX) genes are clustered in restricted regions of the genome (HOX loci) on four distinct chromosomes that presumably evolved by duplication of a primordial gene cluster [8]. A striking finding is that the order of genes within each cluster is also highly conserved throughout evolution, suggesting that the physical organisation of HOX genes may be essential for their expression [10]. HOX genes are expressed during embryogenesis in a tissue-specific and frequently stage-related fashion [11]. Expression of individual HOX genes has been detected in normal adult tissues [8–12].

A possible association between genes that control transcription and those involved in the oncogenic process has been postulated on the basis of several independent observations. Constitutive expression of the HOX-2.4 gene may entail oncogenic consequences in mice [13]. Mice homozygous for a null mutation in the HOX-1.5 and HOX-1.6 genes show major morphological abnormalities [14–15]. The growth factor activin activates homeobox gene expression in developing Xenopus embryos [16]. The coordinate regulation of HOX genes may play an important role in human haemopoietic differentiation [17]. HOX gene expression appears to be altered in renal cancer compared to normal human kidney tissues [12].

In line with the above association between HOX genes, development and oncogenesis, our aim has been to determine whether the physical organisation of HOX genes might be a part of a regulatory network involved in the control of such processes. We have thus analysed the expression of a panel of 38 HOX genes in adult human tissues originating from normal intestinal mucosa or liver parenchyma from colorectal carcinoma biopsy samples and liver metastases from colorectal cancers. We have identified HOX genes (HOX1J, HOX2F) whose expression remains unaltered during progression of colorectal tumours. We interpret this result as an intestinal-specific expression which may suggest the involvement of the corresponding homeoproteins in organ-specific functions. Expression of other HOX genes (HOX2C, HOX4F), however, is altered in primary and metastatic colorectal cancer suggesting the possible implication of these transcriptional regulators in colon tumorigenesis.