Erratum

The editors and publishers regret that in Volume 4, issue 4 of *European Review* there was an error in the article 'The human genome project and its impact in medicine' by Hamish S. Scott and E. Antonarakis. The caption to Figure 2 is printed correctly below. We apologize for this unfortunate mistake.

Figure 2. Schematic representation of how the different goals of the human genome project relate to each other and with human disease. The linkage map is represented with DNA polymorphic markers shown as flags along the entire genome with the distance between adjacent markers measured in centimorgans. The striped box represents a human phenotype which maps between the 3rd and 4th polymorphic markers. The physical map is represented as ordered arrays of cloned human DNA generated by determination of the STSs (filled circles) content of each clone. The gene responsible for the phenotype (striped box) must be encoded within the 3rd clone. Gene identification (genes are indicated as grey boxes) can be achieved by using the cloned DNA fragments for exon trapping, DNA selection and/or eventually sequencing. ESTs that may map to the same region may provide candidate genes. Identification of the gene actually involved in the phenotype, indicated above the striped box, is finally confirmed by sequence analysis and mutation detection. The sequence map of the entire genome is the final goal of the present HGP. The determination of the function of the encoded proteins will be one of the challenging post-HGP goals. The study of the genomics of model organisms will contribute greatly to the elucidation of these functions. The various phases of the HGP are aided by the clinical material and medicine in turn is benefiting from genomic information. Appropriate families and patient samples contribute to the mapping of disease phenotypes and indentification of mutations is a definitive proof of disease involvement for some genes. Mutations and phenotypes advance the understanding of protein function. The linkage and sequence maps are of use in diagnosis of hereditary disorders, traits, risk factors and predispositions. Discovery and elucidation of gene and protein function also benefit disease diagnosis, intervention and treatment.

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