allergen exposure on the expression of well-characterized phenotypes associated with the various types of atopic diseases. Segregation analyses of appropriate families should be performed to determine the best fitting genetic models. Linkage studies should be undertaken using these models and, also, by analysing the proportions of the alleles shared in common by affected members of the pedigrees. Highly informative polymorphic microsatellite markers, evenly spaced throughout the human genome, 10–20 cM apart, should be utilized for linkage studies in a systematic manner. A new collaborative project to investigate the genetic basis of asthma, the most disabling of the diseases commonly associated with atopy, has begun in the United States and in other countries. These studies may soon reveal the molecular genetic basis of these most common, yet still enigmatic, chronic diseases. □

Correction

In her editorial *Breast cancer genes: how many, where and who are they?* (*Nature Genetics* **2**, 89–90), M.-C. King inadvertently omitted a reference to a personal communication from B. Weber *et al.* in citing Mfd188 (D17S579) as a flanking marker for the breast cancer gene BRAC1 on chromosome 17q21.