

Mark Twain once said,...

... "A thing long expected takes the form of the unexpected when at last it comes." Apparently, one of these "things" has recently turned out to be the human genome.

Wherever you look, new results about the human genome have mostly been described in comparative degrees. Typical phrases are, for example, "... contains more of...", "... is more variable than...", "... occur more frequently...", "... at a higher rate...", "... less stable...", "... more abundant..."

However, to what is the human genome constantly being compared? To any other genome? Rarely. In the majority of cases these comparisons simply refer to any more or less obscure expectations that have been floating around in advance. Indicative, for example, are expressions like "... than has (previously) been thought / expected / realised / estimated / imagined."

Examples? Okay, here we go:

► Only a couple of weeks ago the editors and news staff of *Science* presented the new insights into the high diversity between individual human genomes as their "Breakthrough of the Year 2007". "In 2007," they wrote, "advances on several fronts drove home for the first time how much DNA differs from person to person." One of these fronts has been the unexpected high number and variability of single nucleotide polymorphisms (SNPs) throughout the human genome. Another front was, as *Science* Editor-in-Chief, Donald Kennedy, wrote, that

"more extensive structural variations, such as additions, deletions, repeat sequences and stretches of 'backwards' DNA, turn out to be more prevalent than had been recognised".

► The December issue of *Genome Research* (vol. 17(12): 1723-1730) contained a paper by US computational biologists on the identification of potentially imprinted genes by algorithms developed from machine learning techniques. The study revealed four times as many imprinted genes as had previously been identified. Needless to say, the authors subsequently predict an even higher number of imprinted genes are still hidden in the genome than was previously estimated.

► In January, a paper appeared in *Nature Genetics* (vol. 40(1): 90-95) in which researchers from the Wellcome Trust Sanger Institute in Cambridge described results from experiments on the *de novo* rate of deletions, duplications, inversions and translocations in sperm cells. Their conclusion being that "Genomic disorders occur more frequently than previously thought."

► In the February issue of *Genome Research*, a team from the Johns Hopkins University in Baltimore will present a paper claiming that the portion of regulatory DNA in the human genome may be more abundant than we realise (epub ahead of print Dec. 10). The corresponding press release headline read, "More regulatory DNA than previously thought."

► Two months earlier, California-based scientists stated from results obtained from a comparative genomics search that there were "more gene losses in the human genome than previously recognised" (*PLoS Comput Biol* 14;3(12): e247). Moreover, they concluded that in particular the loss of some long-established genes might have significantly contributed to human evolution.

► Also in December, US anthropologists described findings from SNP analyses leading to the conclusion that the evolution of the human genome has recently accelerated at an unexpectedly fast rate (*Proc Natl Acad Sci USA* 104(52): 20753-8). In the past 5,000 years, the authors claimed, positive selection has occurred at a rate 100 times faster than in any other period of human evolution. This was in complete contrast to the long-held view that human evolution had instead slowed to a crawl or even stopped in modern humans.

Why were our expectations, estimations, views and concepts so very different to what the new data has obviously now revealed? One point certainly is that they were based on less comprehensive results from prior experiments which had been obtained by less powerful technology.

Be that as it may, perhaps one should view this topic from a different and possibly more interesting angle. Had none of these expectations already existed (and had they not finally turned out to be so far off the mark), would all the new data still have caused such a stir? Just another example of how the putative significance of scientific results is strongly dependent on what was "previously expected."

The Editors

