EVOLUTION OF TUMORS

The study of the evolution of a population goes through the analysis of changes in allele frequency over time. The term "evolution" has always been widely used in the context of tumors, but it often referred only to the successive stages and not to evolution in the Darwinian sense. Then, the possibility of analyzing the genome of a single cell opened the way for an evolutionary study of the tumor population in the strict Darwinian sense. The first work based on these new technologies was published 2011. The following year, a review specifically dedicated to Darwinian concepts in the evolution of tumors appeared. In fact, the famous sketch of the tree of life designed by Darwin in 1837 appears in this paper.
The variability of a population allows it to cope with a changing environment (adaptation through the selection of the fittest). From the tumor point of view, the changing environment can be chemotherapy. The authors say: "The inherently Darwinian character of cancer is the primary reason for this therapeutic failure" (i.e. of the evolutionary success of the cancer).
In a recent issue of Nature several articles from a collaborative study involving 2658 tumors, of 38 different types, have appeared. The title of one of these papers reads "*The evolutionary history of 2,658 cancers*". One of the most interesting observations concerns the fact that "driver" mutations (ones responsible for the tumor) can arise years, sometimes many years, before the tumor manifests itself clinically. Mutations in cancer-related genes, however, are not rare in normal people. The Nature paper elucidates that "*Early oncogenesis is characterized by mutations in a constrained set of driver genes, and specific copy number gains, such as trisomy 7 in glioblastoma and isochromosome 17q in medulloblastoma. The mutational spectrum changes significantly throughout tumour evolution in 40% of samples. A nearly fourfold diversification of driver genes and increased genomic instability are features of later stages*".