

These two meetings exposed considerable rancor among the ranks of prominent molecular biologists, but they also began the search for common ground, and laid the groundwork for a two-year succession of countless meetings that redefined the human genome project. The redefinition took place most conspicuously in a committee of the National Research Council (NRC).

In September, 1986, two projects were initiated to study the idea. The NRC, the largest operational arm of the National Academy of Sciences, approved a study. The NRC appointed a committee of extremely prestigious researchers chaired by Bruce Alberts of the University of California at San Francisco. This study committee vigorously debated the merits of a concerted scientific program, carrying out in microcosm the debate transpiring more broadly in the scientific community.

The NRC committee took a commonsense approach, looking at the scientific and technical steps that would be necessary to construct comprehensive maps of the human genome and to make sense of the resulting information. They started by bringing together those constructing various kinds of genetic maps in different organisms. The idea of a human genetic linkage map grew out of work in viruses, bacteria, yeast, and other organisms. The key insight grew from a 1978 inspiration shared between David Botstein, then at the Massachusetts Institute of Technology, and Ronald Davis of Stanford. In a discussion at Alta, Utah, they speculated that researchers could find natural DNA differences among individuals in families, most of which would not necessarily lead to clinically detected differences, to trace the inheritance of chromosome regions through those families.

Each person has a pair of each of the 22 nonsex chromosomes. (Women also have a pair of X chromosomes, while men have an X and a Y.) Botstein and Davis suggested that if detectable differences could be found for discrete chromosome regions, then one could figure out which of each parent's chromosome pair was inherited by each child. A map of such differences would enable geneticists to determine the approximate location of disease-associated and other genes,