

Genetic Maps: Do We Still Need Them?

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Abstract:

In 1987 the first genetic map containing all of the human chromosomes was published (Donis-Keller et al. 1997). This genetic map which was generated using 21 CEPH families consisted of 403 markers of which the majority were RFLP markers. The early 1990s saw the advent of second generation genetic maps consisting mainly of microsatellite markers (Weissenbach et al. 1992; Broman et al. 1998). The majority of these markers were genotyped in only 8 CEPH families which provided at most 184 informative meioses. Recently new microsatellite (Kong et al. 2002) and SNP genetic linkage maps were published (Matise et al. 2002). Some of the topics which will be addressed in this presentation include: What is the accuracy of genetic maps? What strategies can be used to ensure that markers selected for fine mapping are correctly ordered? How many meioses are necessary accurately estimate genetic map distances? With the arrival of sequence-based physical map and soon to be constructed genome wide HapMaps are genetic maps still beneficial for gene mapping?