
Rice and bean molecular marker data base

Marcelo Narciso,
Raquel Mello,

The information, when organized and accessible, increases the possibility of generating knowledge, expand its application beyond the purposes for which it was first produced. The use of data bases and informatics tools is critical to the safe storage of the huge amount molecular data generated daily in biotechnology laboratories. An important class of data generated daily is the molecular markers (SSR, SNP, etc.). Molecular markers have been used as tools in the identification and discrimination genotypes in the analysis of genetic diversity in the construction of genetic maps and QTL mapping, among other applications. Thus, efforts have been made in identifying molecular markers and characterization of genotypes and populations using these markers. However, the results not always are available to the entire local community of researchers or the general public. Often the non-incorporation of genotypic information in the routine of programs is given by the absence of a data base where the information can be stored in a structured way, allowing easy recovery and application data. As data does not have a common space for storage, often these data are distributed in digital files on computers for individual use. However, other potential users such as breeders and researchers of genetic resources, have no access to them. This work has the aim to develop a data base of molecular markers of bean and rice, which allow storage of structured access and genotypic characteristics of populations and retrieval of this information through a search engine as well as to obtain output format html or csv file (comma separated value), which is easily read by Excel or Calc spreadsheet, and make data available for various purposes of analysis. Browser for rice genome and genes of bean (GMOD GBrowser)and data for input to FlapJack system to visualize genes are other functions that these system offers.