More Information on Know-how

About CSIR-Institute of genomics & Integrative Biology (IGIB)

CSIR-Institute of Genomics & Integrative Biology (IGIB) is a premier Institute of Council of Scientific and Industrial Research (CSIR), engaged in research of national importance in the areas of genomics, molecular medicine, bioinformatics, proteomics and environmental biotechnology, with mission "To translate concepts developed in basic biological research to commercially viable technologies for health care".

More details about IGIB's research & development activities are available at IGIB website : www.igib.res.in

About Know-How on HLA typing kits

Major Histocompatibility complex (MHC) plays a key role in acceptance or rejection of a transplant. Organ transplants, like Kidney and bone marrow transplants in humans require matching for the MHC of man i.e. Human leucocyte antigen system (HLA). For bone marrow transplants, very stringent matching for HLA is required which can be met by doing sequence based HLA typing. Methods for doing sequence based typing have been around for a while, but have been slow, expensive and tedious. However, with the advent of next generation sequencing, multiple samples can be sequenced and typed in a short span of time, which is the current requirement as many bone marrow registries are coming up. For theses registries, there is a need to develop affordable, indigenous sequence based HLA typing kits since the imported ones cost US $ 300-400 per sample. Currently HLA typing is being done either by using sequence specific primers or Luminex based kits, however, these are not high resolution methods. As a result, tissue matching for transplantation may not be correct, so there is a need to develop a sequence based typing method which will be accurate.

CSIR-IGIB, with its expertise in the field or HLA and NGS, is looking for partners to develop an indigenous, cost effective. high resolution as well as high throughput next generation sequencing based HLA typing kits with ability of multiplexing and functional interpretation of sequence data to decipher the HLA alleles.