Networking in Human Genetics and Genomics Research in Asia-Pacific Region: Experience in HUGO Pan-Asian SNP Initiative

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Background and Purpose

Scientific collaborations among Asian countries are not so frequent in previous years. Usually, multinational scientific researches were lead by western countries and Asian countries rarely took leading roles. Such situation is slowly changing, as Asian economy booms and as each country increases the support for the scientific research.

Completion of Human genome sequencing opened a big opportunity for both basic science and medicine. Humans are similar but also different in each other. Human genome sequence can provide a quantitative major for such similarities and diversities. The study of human genome diversity gives the clue to the diversity of the susceptibility to disease or of the efficacy of medicines. It also can tell about our history, how we migrated and mixed

Asia-Pacific branch of Human Genome Organization (HUGO-AP) has pursued to set up Human diversity project with the regional initiative. HUGO Pan-Asian SNP Initiative is the fruits of such effort and now generating significant results. I will present the setting of this 11 country effort, how they networked and some of the results generated by this integrated effort of Asian-Pacific countries.

Results and Conclusions

In order to setup Asia based Genome Project, HUGO-AP tried several attempt under the guidance of Dr. Sakaki who was president of HUGO-AP at that time. First serious attempt was made around 2000. At that time there was no local Genome project in the region except in China who joined Human Genome Sequencing Project. The natural next target at that time is SNP based disease gene hunting. Although Japanese researchers promised to provide technology and fund, it did not stimulate the researchers in the region to join the program.

By the end of 2002, many countries in the region started their genome related research. Big program were started or expanded in Taiwan, Korea, Singapore China and Japan. Thus, many researchers in the region showed interest in doing the collaborative research. Although the most people and funding bodies were interested in the disease related research, it soon became apparent that the conflict of the interests was too high among the interested parties. HUGO-AP eventually gave-up to form join projects on medical related subjects. We decided to focus more on the basic aspect of population genetics. We needed a certain amount of data in order to give impact on such area and the cost of such amount was not funded for basic research at that time.

By 2004 the cost of SNP typing was dramatically reduced due to the chip-based SNP typing. Also, at that time, the infra-structure for typing and analysis was set in many countries in the region. Thus, the cost of conducting the research became less because we needed only samples and chips for typing, not extra machines or personnel. With the support of Affymetrix, we could trim the cost father and many groups could participate the project this time. Under leadership of Dr. Liu in Singapore, we formed HUGO Pan-Asian SNP consortium. This consortium operated very democratically every group had one vote and the consensus was sought as much as possible.

We collected 1,953 Pan Asian samples from 73 populations plus 4 HapMap populations, encompassing most of the major linguistic groups in Pan Asia region. We used Affymetrix 100,000K SNP array to analyse the ethnic differences. We used 58,960 SNPs on 22 autosomes and X chromosome for the comparison. Analysis in this scale using the regional samples were only possible by this group.

We are now preparing for the publication of the result and also for the next project. Interestingly, many groups in and out of Asia-Pacific region are interested in joining. These groups include the countries in South America and Meddle East. The infrastructure for the genome research is rapidly improving in these countries lately. As the Asian countries in early 2000s, they are very excited to make their international joint project in genomics area. Although this movement are some what slowed by the recent economic crisis, we think the trend will continue as did in the Asian region.