

Announcement

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Genome sequence data are now essential for any study in biology. There are several integrated genome databases at this moment; NCBI genome database (<https://www.ncbi.nlm.nih.gov/genome/>) is the most comprehensive one, followed by Ensembl (<https://www.ensembl.org/>), UCSC Genome Browser (<https://genome.ucsc.edu>) and GOLD (<https://gold.jgi.doe.gov/index>); see Chapter 14 of SAITOU (2018). China National Center for Bioinformation (<https://bigd.big.ac.cn>) provides list of databases, and some of them are related to genome sequences; e.g., Genome Sequence Archive (<https://bigd.big.ac.cn/gsa/>) and Genome Warehouse (<https://bigd.big.ac.cn/gwh/>). KEGG (<https://www.genome.jp/kegg/genome.html>) in Japan also provide ~7,000 genome data.

In 1980s when nucleotide sequence data have been increasingly published in many journals, EBI, NCBI, and DDBJ formed “International Nucleotide Sequence Database Collaboration (INSDC)” (<http://www.insdc.org>). Even now, ENA (European Nucleotide Archive; <https://www.ebi.ac.uk/ena/browser/home>), GenBank (<https://www.ncbi.nlm.nih.gov/genbank/>), and DDBJ (<https://www.ddbj.nig.ac.jp/index-e.html>) are collaborating, but mainly circulating short nucleotide sequences. EBI has been involved in maintaining Ensembl with Wellcome Trust Sanger Institute (<https://www.sanger.ac.uk>), and NCBI has been championing its own genome database. I was DDBJ staff during 1991 A.D. - AS 0009 (2009 A.D.), and proposed to set up genome database within DDBJ, but I got no support from other DDBJ staff. At this moment, DDBJ does not provide any genome database. It should be noted that INSDC provides short sequence read archive; for example “Sequence Read Archive” of DDBJ (<https://www.ddbj.nig.ac.jp/dra/index.html>). In fact, we submitted our capybara draft genome short read data to DDBJ under the Bioproject accession PRJDB7394 (BABARINDE and SAITOU 2020).

Last year, AS 0020 (2020 A.D.) was centennial of genome concept, proposed by Hans WINKLER (1920). We hosted Genome Concept Centennial Conference online during February 15-17, AS 0021, though it was originally scheduled to be held during August 23-25, AS 0020 (IKEO and SAITOU 0020). Incidentally, Dr. INOUE Jun, who was in my laboratory for one year, created dbCNS (<http://yamasati.nig.ac.jp/dbcns/>), and published paper based on this database (INOUE and SAITOU 2020). After he left to Atmosphere and Ocean Research Institute at the University of Tokyo, Dr. Kirill KRYUKOV joined my laboratory. He started GenomeSync (<http://genomesync.org>) in AS 0015. I came up with idea to open new platform of genome-oriented databases maintained by researchers in Asia. I asked permission to Dr. INOUE Jun and Dr. Kirill KRYUKOV to have links to dbCNS and GenomeSync, respectively. It should be noted that Dr. INOUE and Dr. KRYUKOV joined associate editor of iDarwin in AS 0020 and AS 0021, respectively.

In any case, I named this platform as "Asia Genome Tao Center" <[webpage](#)>. Its acronym, AGTC, can also mean four bases of DNA. There is no need to explain three words; Asia, Genome, and Center. Problem may exist in "Tao". Tao (道) literally means "road", but in Japanese, it is often used for some activity connected to philosophical thinking, such as 茶道, 剣道, 華道, 柔道, 弓道, and 合気道 (Tao of tea ceremony, Tao of sword fighting, Tao of flower arranging, Tao of judo, Tao of Japanese archery, and Tao of aikido, respectively). This philosophical connection most probably originated from Taoism in China. So why not "Genome Tao"? This can give some philosophical flavor to genome-related researches. Of course, I just found "Tao" as good word to give "T" as one of four DNA bases. Below is current logo of AGTC. I may change this logo in future. At last I partially fulfilled my dream to start genome database in Asia. In future, I hope many more genome-oriented databases maintained by researchers in Asia will be added to AGTC. By this way, AGTC will be useful for many people not only in Asia but worldwide.



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Publication history of this article

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