

Report on BRIDGE Program (BR140203)

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I had the opportunity to visit two research teams during this BRIDGE program:

- National Institute of Genetics, Mishima, team of Dr. Toshihiko Shiroishi.
- University of Hokkaido, Sapporo, team of Pr. Hitoshi Suzuki.

In both institutions I gave a seminar entitled: "Sex chromosome introgression in mice and hares: possible dual consequences of sex-linked transmission and genetic conflicts". The seminar described my latest research, including unpublished work, and introduced my future research plans and major centers of interest, around which the discussions of potential future collaborations could build. In both institutions I had meetings with all members of the teams, during which we thoroughly discussed our latest findings and future research plans. This was an important step to increase awareness of each other's projects, perspectives, human and material resources. Only based on such awareness could we concretely determine areas and conditions of potential future interaction.

There are clear common interests, which are to use the house mouse as a model in evolutionary biology, and more precisely to understand the processes of genomic divergence that lead to adaptation and also to reproductive isolation resulting from genomic incompatibilities (and thus to speciation). As a framework for such an approach, we also need to describe the history of the differentiation and exchanges between populations and subspecies.

Nowadays such questions must be addressed using recently developed high throughput genomic sequencing technologies, which represent a great revolution. However this needs important budgets to acquire the data and skills to analyze them, but can be a motivation to attempt joining efforts.

We can summarize the present situation as we analyzed it as follows:

- The Japanese partners had started developing a genome-wide approach by sequencing the genomes of some wild-derived strains that they maintain. In that frame they have developed some tools to make such data available. However cost prohibited extending this project to large population samples.
- I am now developing a genomic approach on relatively large population samples of the different subspecies. Rather than being genome-wide, the approach is targeted to a subset of the genome to be made more affordable.

We could identify two aspects amenable to potential complementarities and collaborations between our teams:

- One concerns the targeted re-sequencing mentioned above. Dr. Shiroishi is studying the misregulation of gene expression in hybrids between mouse subspecies, and looking for the genetic causes of such divergence of expression control. It would certainly be of great interest to include such causative genomic regions in the re-sequencing experiment in order to characterize their mode of evolution and the influence of natural selection.

- A second aspect concerns complimentary sampling. Sampling wild mice from vast geographic regions such as whole Eurasia is a huge task, and some regions are difficult to access because of remoteness or political instability. Both partners have made large efforts over the years to collect representative samples of most regions in Eurasia. Our samplings are clearly complementary, the French sample being especially dense in the Middle East, and the Japanese sample in Asia.

Concerning the former point, it however appeared that the idea was a bit premature since we would need to wait for candidate genomic regions to be better identified. However this remains an interesting possibility for the future, although it may be difficult to have present funding for the experiment coincide with the discovery of the candidate genomic regions. However the possibility is kept in mind in the perspective of future fund raising attempts.

Concerning sample sharing, we identified one question that must be solved first. It concerns the application of the Nagoya protocol – Convention on Biological Diversity, which is now entering into application. Most of the samples in our collections come from countries other than France and Japan, and their use will need us to comply with the rules imposed by the Nagoya protocol. It is not yet clear how long this might take and even for which samples it will be possible. Ideally however, the use of the different collections should be coordinated and cooperative.

To summarise:

- The program was essential to acquire awareness of the possibilities and wills for future collaborations.
- Some common interests and complementarities clearly came out.
- We clearly identified the conditions under which collaborations and cooperation could be launched, and will do our best to meet these conditions. We would not have reached such a point without the BRIDGE program.