Biogeoinformatics of livestock genomic resources

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In 2008, FAO and WAAP published a report on production environment descriptors for animal genetic resources. One of the main conclusions was that it was necessary to quickly systematize the recording of breeds' geographical coordinates worldwide in order to enable links to any kind of information available in other geo-referenced databases. Today we must recognize that this recommendation has hardly been applied and that even important projects on genomic resources did not take care of characterizing sampled animals with their precise location.

Indeed, livestock conservation tasks require complementary data on population and evolutionary genetics, on animal husbandry practices, but also data characterizing the socio-economic and environmental conditions of the regions where animals are bred. Only the integration of these different information levels is likely to facilitate and optimize the processes used to establish priorities in the conservation of livestock genetic resources.

In addition, in conjunction with molecular data the use of geographical coordinates enables the implementation of livestock landscape genomics to seek regions of the genome influencing the ability of animals to cope with environmental variations. This approach can be used to identify key traits involved in parasite resistance, to conserve the adaptive potential of local breeds, and even to increase adaptability in industrial breeds.

In both cases computer science and biogeoinformatics have a more important role than ever. New knowledge will be extracted from the present data tsunami – constituted by the advent of high throughput molecular data, new sources of high resolution environmental data, new sources of socio-economic data, etc. – only if innovative, transdisciplinary and efficient computing tools are developed.

But for biogeoinformatics can keep its promises, an important challenge for the livestock genomics resources community for the next decade remains to enforce the recording of geographical coordinates of any sampled animals as a standard rule.