



Editorial

Foreword

Over the last few thousand years, humans have caused a rapid evolution and ultimately profound genetic changes within species they have elected to meet their needs. They domesticated them. Agriculture and animal husbandry have been “devised” little by little, allowing human communities to organize themselves, settle down, grow, and settle in new and more convenient areas.

In turn, accompanying a change in human lifestyle from hunting to animal husbandry and gathering to cultivation, human diets have also changed and Man himself has genetically evolved. These developments took place in a changing environment as evidenced by such travel range of plant species that are sensitive to climate variations. Crops and livestock have conquered new territories, species have been transported from one continent to another and they have adapted themselves to new environments.

Domestication and migration are the cause of what makes our everyday diet, our environment and our culture. Mankind, domesticated species, agriculture and livestock are interdependent in an ecosystem built in this way.

The traces of this history of the world are found in archaeological sites but also in the genomes of living forms involved. With the tremendous technological advances in recent years on DNA sequencing, the genomes are accessible in every detail. Since DNA is a stable enough molecule, levies on small fragments of skeleton or fossil pollen bring us information on new and sometimes surprising developments in domestic species and humans.

The following papers presented in this Special Issue exemplify this history.

Neolithisation was a pivotal change in the historical trajectories of humanity and the biosphere and transformations in many aspects of lifestyles, social structures, land use and diet can be illustrated through the Neolithisation in Europe.

Dog proto-domestication started during the Upper Paleolithic period well before any other animal or plant domestication. The real domestication process, which can be traced with different tools, dated around 14,000 BC led, in the historical period, to a wide range of morphologic and behavioral diversity.

As opposed to this early dog domestication, the most ancient domesticated chickens were found about 2500

years BC. Comparative genome sequencing between *Gallus gallus* and domestic chickens distributed among traditional populations, standardized breeds and highly selected lines allows to identify 21 selective sweeps during domestication and subsequent selection.

In between, cattle, sheep and goats were domesticated about 10,000 years ago, spread out of the domestication centers in Europe, Asia, and Africa during the next few thousands years, and gave many populations locally adapted.

As regards to plant domestication, recent palaeogenomic data demonstrate that whole genome duplications have provided a motor for the evolutionary success of cereals over the last 50 to 70 millions years.

In the same way, polyploidisation events facilitated wheat domestication creating genetic bottlenecks, which excluded potentially adaptive alleles we could need in the future.

The example of maize introductions in southern and northern Europe, which were followed by an extreme diversification and adaptation to long days and low temperatures of temperate climates, illustrates the capacity of biological evolution in a relatively short period.

This rapid evolution is particularly true in the case of yeasts, used at least since 7000 BC, where human selection has driven population differentiation according to the food process (wine, beer, bread) leading to the unconscious creation of new species by polyploidization and interspecific hybridization.

In contrast to these observed changes over thousands of years, sometimes invasive species migration, facilitated by the considerable development of intercontinental trade and by the amazing plasticity of life, occur at an unprecedented rate. Invasion biology and agriculture are intimately related and the reconstruction of invasion routes point to a scenario in which an invasive population is the source of other invasive populations.

Man has changed his environment and he eliminated or significantly downsized some species. Based on sound genetic characterization, urgent conservation measures must be taken to avoid an irremediable loss of farm animal genetic resources, integrating economical, sociological, and political parameters. The history of domestication

shows that the ecosystem developed by humans, like any ecosystem, is constantly evolving. We will need both to preserve its ability to adapt and allow it to host and operate effectively and judiciously new domestic forms.

Advances in life sciences and technology offer the appropriate and expected answers in the management of genetic resources provided the existence of residual diversity in present stocks. Therefore, a process aiming at constant and random enrichment of the existing diversity in domesticated plants, animals, and microorganisms, and giving a major and renewed place to men's imagination and innovation in life and agricultural sciences is compulsory.

The French Society of Agriculture was created in 1761 by the King Louis XV who named it "Société d'Agriculture de la Généralité de Paris". On February 23, 1915, it became "l'Académie d'Agriculture de France". In order to commemorate the 250th anniversary of the French Academy of Agriculture, a public meeting on palaeogenomics and domestications entitled "On the trail of domestications and migrations in agriculture" was held on March 22, 2011

at the Institute of France (Paris), jointly organized by the French Academy of Agriculture (www.academie-agriculture.fr/) and the French Academy of Sciences (www.academie-sciences.fr/).

We are grateful to all colleagues from these two academies for their constant support and their invaluable contribution to the success of the organization of this meeting and of this special issue.

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