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# Selection in the Making: A Worldwide Survey of Haplotypic Diversity Around a Causative Mutation in Porcine *IGF2*

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ABSTRACT

Domestic species allow us to study dramatic evolutionary changes at an accelerated rate due to the effectiveness of modern breeding techniques and the availability of breeds that have undergone distinct selection pressures. We present a worldwide survey of haplotype variability around a known causative mutation in porcine gene *IGF2*, which increases lean content. We genotyped 34 SNPs spanning 27 kb in 237 domestic pigs and 162 wild boars. Although the selective process had wiped out variability for at least 27 kb in the haplotypes carrying the mutation, there was no indication of an overall reduction in genetic variability of international *vs.* European local breeds; there was also no evidence of a reduction in variability caused by domestication. The haplotype structure and a plot of Tajima's *D* against the frequency of the causative mutation across breeds suggested a temporal pattern, where each breed corresponded to a different selective stage. This was observed comparing the haplotype neighbor-joining (NJ) trees of breeds that have undergone increasing selection pressures for leanness, *e.g.*, European local breeds *vs.* Pietrain. These results anticipate that comparing current domestic breeds will decisively help to recover the genetic history of domestication and contemporary selective processes.

A major goal of current genetics research, in livestock as in plants or humans, is to identify the polymorphisms responsible for the variability in complex traits, *i.e.*, traits affected by the environment as well as by more than one locus. This endeavor has proved to be difficult. In livestock, despite the large number of chromosome regions associated with phenotypes of economic interest (QTL), very few causative polymorphisms have been convincingly identified. The number of published QTL amounts to hundreds in pigs (http://www.animalgenome.org/cgi-bin/QTLdb/SS/summary) (Rothschild *et al.* 2007), but <10 causative mutations have been reported so far in this species. A comparable picture exists in all species. To accelerate causative gene discovery, traditional QTL studies are usually pursued with gene or genomewide association studies. A complementary approach is to infer the action of selection at specific loci from their nucleotide variability, the so-called selection footprint. To date, several works have shown the usefulness of this approach in humans and in other species (*e.g.*, DuMont and Aquadro 2005; Nielsen *et al.* 2005; Wright *et al.* 2005; Caicedo *et al.* 2007). However, different genomewide scans have picked up different regions as affected by selection (see reviews for humans in Nielsen *et al.* 2007; Thornton *et al.* 2007). Possibly, one of the reasons for conflicting results is that disentangling selective from purely demographic forces is very challenging. One of the additional difficulties is that the target of selection cannot always be identified, even when the observed nucleotide variability pattern is not explained by demography alone and selection is the most plausible explanation.

Domestic plant and animal species offer underexploited genetic resources, which are extremely valuable to disentangle demographic from selective processes. Modern breeding and artificial selection techniques allow

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