



GENOME WATCH

Adapting to domesticity

Adam J. Reid

This month's Genome Watch highlights new insights into the impact of food production on the evolution of microorganisms.

The evolutionary success of *Homo sapiens* has had a great influence on microbial evolution. In addition to the parasites and symbionts with which we have co-evolved, we have affected microbial evolution artificially by domesticating certain species used in food production. Furthermore, we have exerted indirect selection on pathogens of domesticated crops and livestock. Understanding how these genomes have evolved is important for research into improving the efficiency of food production and to ensure food security. Recent papers in *Genome Research* explore the genomic impact of food production on the milk-souring bacterium *Lactococcus lactis*, used in cheese production, and the wheat pathogen *Mycosphaerella graminicola*.

The ancestor of dairy-dwelling *L. lactis* is thought to have lived on plants. To understand how this species might have evolved during domestication, researchers grew a plant strain in milk for 1,000 generations¹. This strain seemed to adapt to its new niche by increasing its ability to acidify milk and enhancing its biomass yields. The researchers then sought to identify which mutations the strain had accrued and whether these were similar to those observed in existing domesticated strains. In two out of three replicated experiments, two identical mutations were observed in evolving strains. One mutation restored the reading frame of a pseudogene, and the other seemed to increase the expression of an adjacent gene; both mutated genes were in an operon encoding an ABC-type oligopeptide transport system.



This operon was also upregulated in the reference domesticated strain, suggesting convergent evolution of these experimental strains with the domesticated one. The role of this operon in growth in milk is not understood, but this experiment suggests that it provides a selective advantage.

This study also highlights the fact that evolution may occur quickly during adaptation to a new niche. The authors observed that experimental strains underwent genome reduction or, in one case, developed a mutator phenotype (a much greater accumulation of mutations than other strains). Both processes allow rapid changes in genome sequence, through which an organism might adapt to a new niche. Adaptation through gene duplication and divergence would, for instance, take distinctly longer. Together, these findings help us to understand the genomic basis of niche adaptation in a domestic setting but also point the way towards an understanding of how to improve microorganisms for greater efficiency in food production.

Microorganism domestication has also occurred indirectly through the domestication of crops and livestock. Pathogens of domesticated crops have often co-evolved with their hosts, and understanding how they have done so should allow us to combat them and improve crop yields. A recent study focused on the ascomycete fungus *M. graminicola*, which is thought to have emerged 11,000 years ago, during the domestication of wheat and at the beginnings of human agriculture in general².

A population genomics approach was used to examine the forces shaping the evolution of this and 11 related grass pathogens. The authors analysed rates of mutation in different lineages and argue that, compared with wild species, *M. graminicola* has undergone a greater amount of adaptive evolution. In particular, they showed that secreted proteins (those most likely to interact with the host)

and genes involved in signal transduction have been subjected to positive selection. These findings suggest that while domesticated wheat was rapidly diverging from its ancestor by artificial selection, parasite genes involved in host–parasite interactions also evolved rapidly, allowing the parasite to co-evolve with its host.

Further analysis of evolutionary signatures in the pathogen genome identified a clear signal of purifying selection, a process by which deleterious alleles are removed from the population and which is more effective in large populations. This is in contrast to crop and livestock species, in which many deleterious mutations 'piggyback' on the strength of those conferring advantageous properties, such as increased yield, during domestication³. This indicates that the selective pressures faced by pathogens of domesticated species are different from those faced by the domesticated species themselves.

These papers explore the rapid evolution of species as they adapt to domestic niches, and begin to pick apart the pathways that such evolution takes. As food security is under the spotlight, we should look to use these approaches to improve the efficiency of food production both by better understanding the microorganisms that we use in its production and by fighting the relevant pathogens.

Adam J. Reid is at the Wellcome Trust Sanger Institute, Genome Campus, Hinxton, Cambridge CB10 1SA, UK.

e-mail: microbes@sanger.ac.uk

doi:10.1038/nrmicro2752

1. Bachmann, H. *et al.* Microbial domestication signatures of *Lactococcus lactis* can be reproduced by experimental evolution. *Genome Res.* **22**, 115–124 (2012).
2. Stukenbrock, E. H. *et al.* The making of a new pathogen: insights from comparative population genomics of the domesticated wheat pathogen *Mycosphaerella graminicola* and its wild sister species. *Genome Res.* **21**, 2157–2166 (2011).
3. Lu, J. *et al.* The accumulation of deleterious mutations in rice genomes: a hypothesis on the cost of domestication. *Trends Genet.* **22**, 126–131 (2006).

Competing interests statement

The author declares no competing financial interests.