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# Convergence in domesticated fungi used for cheese and dry-cured meat maturation: beneficial traits, genomic mechanisms and degeneration

Jeanne Ropars<sup>1</sup> and Tatiana Giraud<sup>1</sup>

<sup>1</sup> Ecologie Systématique Evolution, IDEEV, Bâtiment 680, 12 route RD128, 91190 Gif-sur-Yvette, France

Corresponding author: [tatiana.giraud@universite-paris-saclay.fr](mailto:tatiana.giraud@universite-paris-saclay.fr)

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**Short title:** Convergence in domesticated cheese and salami fungi

## Highlights

- Distant fungal lineages have been domesticated for cheese-or salami-making
- Multiple independent domestication events occurred within fungal species
- Parallel adaptation events in cheese and salami fungi led to phenotypic convergence
- Phenotypic convergence occurred by similar mechanisms of genomic adaptation
- Adaptation occurred via horizontal gene transfer, gene loss and amino-acid change

## Abstract

Humans have domesticated genetically distant fungi for similar uses, the fermentation of lipid-rich and sugar-rich food to generate attractive aspect, odor and aroma, and to improve shelf life and product safety. Multiple independent domestication events also occurred within species. We review recent evidence of phenotypic convergence during the domestication of fungi for making cheese (*Saccharomyces cerevisiae*, *Penicillium roqueforti*, *P. camemberti*, *Geotrichum candidum*) and for dry-cured-meat making (*P. nalgiovense* and *P. salami*). Convergence following adaptation to similar ecological niches involved colony aspect (fluffiness and color), lipolysis, proteolysis, volatile compound production and competitive ability against food spoilers. We review evidence for convergence in genetic diversity loss in domesticated populations and in the degeneration of unused traits, such as toxin production and sexual reproduction. Phenotypic convergence sometimes occurred by similar mechanisms of genomic adaptation, in particular horizontal gene transfers and loss of genes.

# Introduction

Domesticated organisms represent good models for studying diversification and adaptation [1–8]. Indeed, the strong and recent selection by humans often leave footprints of adaptation in genomes that are easier to detect than those left by natural selection, and traits under selection are often known. Studying domestication is not only an academic exercise as domesticated organisms have great applied importance. Studies on domesticated organisms have shed light on the genomic processes involved in adaptation, including horizontal gene transfers, hybridization, gene gains and losses, expansions of some gene families, transposable element insertions and changes in regulatory networks [9–13].

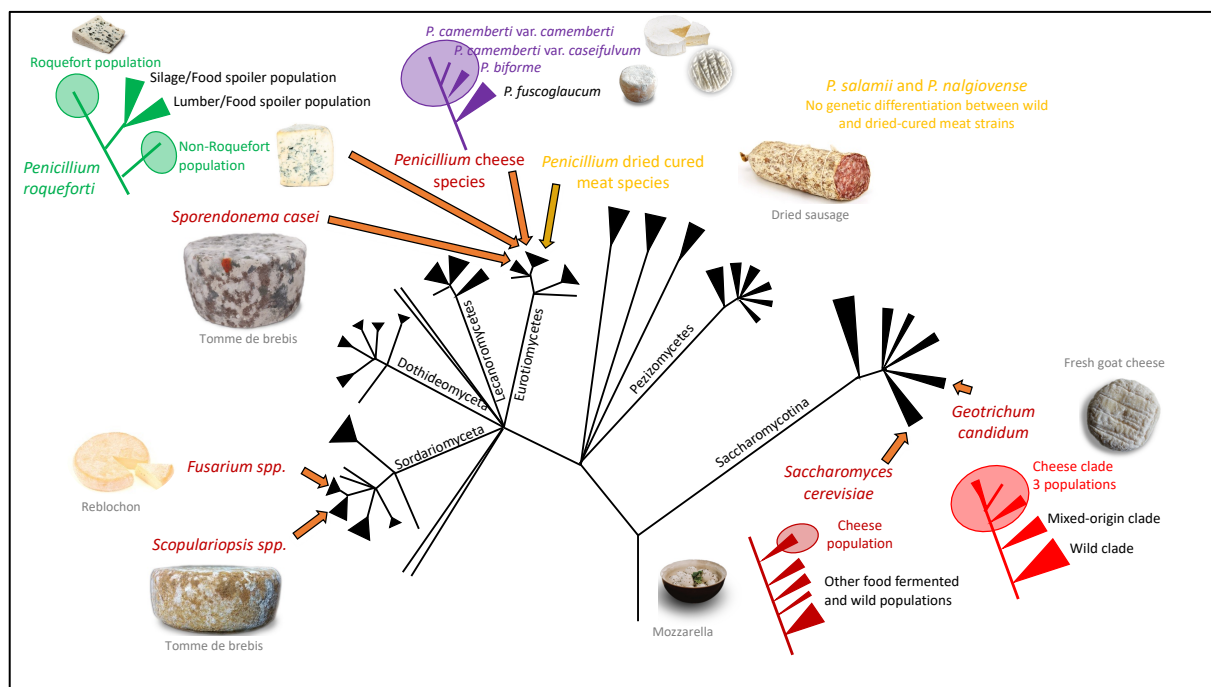
Humans have sometimes domesticated distant lineages for similar uses. This represents an ideal model in which to study parallel adaptation, i.e., independent adaptation events to the same ecological niche in several species or populations, at both the phenotypic and genomic levels. In sheep and goat for example, convergent genomic signatures of domestication involve genes controlling nervous system, immunity and productivity traits, while different genomic regions were found to be responsible for other phenotypic similarities, thus corresponding to phenotypic convergence through different genomic changes [14]. Domesticated crops also present multiple convergent phenotypic traits, including the loss of seed shattering, minimization of seed dormancy and increases in seed size and number. Most of these convergent events have involved different genomic changes [15,16]; exceptions include seed shattering loss, which shares the same genetic basis, involving the *Sh1* locus, in sorghum, rice, maize and foxtail millet [17–19].

Domestication has not only led to beneficial changes but also often to degeneration and loss of genetic diversity. Traits essential in wild environments but unused in domesticated organisms have often degenerated due to relaxed selection. In addition, the strong selection during domestication has led to bottlenecks, i.e. loss of genetic diversity compared to ancestral wild populations, in domesticated animals (e.g. dog and horses) [20,21] and annual plants (e.g. rice) [22]. Such bottlenecks led to the loss of some interesting traits, for example reductions in defense against moths in apples [23], and to the accumulation of deleterious mutations, e.g., in dogs, horses, rice [20,24].

In addition to animals (e.g. dog, chicken) and plants (maize, tomato), humans have also domesticated several fungi for fermenting food (e.g. bread, beer, wine, cheese), for producing secondary metabolites used in pharmaceuticals (e.g. penicillin) and for their nutritional and gustatory values (e.g. button and shiitake mushrooms). Fungi constitute tractable experimental models [10] with their small and compact genomes, making them ideal for exploring genomic footprints of adaptation. The domestication of the yeast *Saccharomyces cerevisiae*, used to make bread, beer and wine has been extensively studied [25–34]. Only more recently the domestication of filamentous fungi which are used for fermenting food has begun to be studied [35]. For example, *Penicillium camemberti* is inoculated for the ripening of soft

cheeses [36] and *P. roqueforti* for blue cheeses [37], whereas *P. salamii* and *P. nalgiovense* are used for dry-cured meat production [38].

Furthermore, humans have domesticated genetically distant filamentous fungi for similar uses, i.e. the fermentation of lipid- and sugar-rich food, to generate attractive appearance, odor and aroma, and to improve shelf life and product safety (Figure 1). This creates an ideal opportunity for studying the repeatability of evolution, by providing several recent independent replicates of adaptation to the same ecological niche under strong selection. Many fungi are used for cheese ripening, i.e., *S. cerevisiae*, *Geotrichum candidum*, *P. camemberti*, *P. roqueforti*, and for dry-cured meat production, i.e. *P. salamii*, *P. nalgiovense* and *P. biforme*, thus constituting particularly attractive model systems for studying parallel adaptation. Indeed, the multiple phylogenetically distant fungal species thriving in cheese and dry-cured meat ecological niches provide exciting “natural experiments” of recent similar selection and unique opportunities to assess the repeatability of evolution.



**Figure 1:** Cheese fungi are models for studying parallel adaptation because several phylogenetically distant lineages thrive in the same ecological niche and cheese adaptation is the result of strong and recent selection (<8000 years ago). Phylogenetic tree of Ascomycota modified from Lifemap (<http://lifemap.univ-lyon1.fr/>). Cheese species are indicated by orange arrows and names of cheese species are in dark red; *Penicillium* dried cured meat species are in light orange and shown on the tree by a light orange arrow. For each studied cheese species, a schematic tree is shown to display their population structure and the genetic differentiation between wild and cheese strains. As there is no genetic differentiation between dried-cured meat and wild strains of both *P. salamii* and *P. nalgiovense* species, no schematic tree is displayed.

Here we review recent evidence of phenotypic convergence during domestication of fungi for cheese-making and dry-cured-meat production, which occurred by similar mechanisms of genomic adaptation. We also review recent evidence of convergence in the degeneration of unused traits and loss of genetic diversity. We focus on the following species as recent studies

have elucidated their domestication history as well as their phenotypic and genomic adaptation and degeneration processes: *Penicillium roqueforti* is inoculated for making blue cheeses, and occurs as a common spoilage agent in food (e.g. on bread and fruits) and in other environments, such as silage and lumber. *Penicillium biforme* occurs on cheese crusts such as Tommes or fresh goat cheeses, and is also inoculated for making dry-cured meat. Its sister species, *P. camemberti*, is the result of the selection of a single white mutant at the end of the XIXth century, whose clonal lineage has ever since been inoculated for soft cheeses production like Brie and Camembert, and is not present in environments other than cheese. Although *P. camemberti* and *P. roqueforti* belong to the same genus, they are phylogenetically as distant as humans and spider monkeys [39,40]. *Geotrichum candidum*, which is phylogenetically even more distant, is also inoculated for cheese-making, e.g. for the production of semi-hard, mold-ripened, smeared soft cheeses, fresh goat and ewe cheeses, and occurs naturally in raw milk and other environments such as hay or soil; this is a dimorphic fungus, able to grow either as a yeast or a filamentous form. *Saccharomyces cerevisiae* is used for fermenting many foods and beverages, e.g. beer, wine, bread and cheese. The two very distant species *P. salami* and *P. nalgiovense* are used for dry-cured meat production.

## History of domestication: multiple independent domestication events and diversification into multiple varieties

Phenotypic and genetic differentiation between strains collected in cheese and in other environments have been detected in *P. roqueforti*, *G. candidum* and *S. cerevisiae* [25,37,41] and their demographic history of domestication could be inferred. In *P. roqueforti*, two distinct populations have been domesticated independently, one occurring only in cheeses in the protected designation of origin (PDO) Roquefort, the other population being inoculated in all the other blue cheeses worldwide [37]. *Penicillium camemberti* is the result of a stepwise domestication: the cheese-specific *P. biforme* lineage has first differentiated from the wild *P. fuscoglaucum* lineage, then the *P. camemberti* lineage differentiated from the *P. biforme* lineage, and then two varieties with contrasted phenotypes became differentiated in the *P. camemberti* lineage, i.e., var. *camemberti* and var. *caseifulvum*, found in different types of soft cheese [36]. In *G. candidum*, domestication has also occurred in several steps, the cheese clade being subdivided into three differentiated cheese populations displaying contrasting phenotypes [41]. In *S. cerevisiae*, the cheese population is genetically and phenotypically differentiated from populations domesticated for other usages [25].

Two *Penicillium* fungi are used for dry-cured meat production, *P. nalgiovense* and *P. salami*, that are also phylogenetically very distant to each other [38]. In contrast to cheese fungi, no genetic subdivision was found within each of these species, between strains from dry-cured meat and other environments, although phenotypic differentiation was found (see below).

## Phenotypic convergence in beneficial traits for food making

Recent studies have revealed striking cases of convergent adaptation in cheese-making fungi. Indeed, the two fungi used as starters for soft cheese production, *P. camemberti* and *G. candidum*, evolved towards greater fluffiness and whiteness of filamentous colonies compared to their closely related lineages, at the expense of radial growth speed [36,41]. *Penicillium nalgiovense* and *P. salamii* strains isolated from dry-cured meat also evolved greater whiteness [38]. The two cheese populations of *P. roqueforti* also changed color compared to non-cheese populations, both having independently evolved to produce bluer cheeses than non-cheese populations [37,42].

The different cheese filamentous fungi have evolved greater competitive ability against competitors, e.g. fungal food spoilers. When grown as filamentous lawns on Petri dishes, they prevented the growth of fungal challengers. This was the case in the non-Roquefort *P. roqueforti* population, *P. biforme*, *P. camemberti* and *G. candidum* [36,41,43].

The non-Roquefort *P. roqueforti* population evolved faster lipolysis and proteolysis than Roquefort and non-cheese populations [37], which can be beneficial for the production of cheeses with short ripening times, such as Gorgonzola (30 days of ripening) or industrial blue cheeses. In contrast, the Roquefort population displayed slow lipolysis and proteolysis, which is desirable for Roquefort cheeses whose PDO (protected designation of origin) requires a long ripening period (at least 90 days). The dry-cured meat populations of *P. nalgiovense* and *P. salamii*, as well as the cheese populations of *G. candidum* also showed slower proteolysis and lipolysis than their wild-type conspecifics, which can be beneficial to avoid obtaining degraded products [38,41].

Volatile organic compounds are extremely important for food aroma and odor; specific, attractive and more diverse volatiles are produced by cheese populations in *P. roqueforti* and *G. candidum* [41,42]. A particular volatile characteristic of blue cheeses, the 2-heptanone, produced by cheese *P. roqueforti* populations, is also produced by one of the three populations of *G. candidum* [41]. In *S. cerevisiae*, cheese strains produce more glycerol and butyric acid, which is the most potent odorant in Camembert and cheddar cheeses [44].

The non-Roquefort *P. roqueforti* population evolved a higher salt tolerance than non-cheese populations [37]. In contrast, salt tolerance was no higher in the Roquefort *P. roqueforti* population, *P. camemberti*, *G. candidum* or dry-cured meat strains of *P. nalgiovense* and *P. salamii* [36–38,41]. Salt tolerance is generally high in *Penicillium* fungi and higher salt tolerance may be either not beneficial or too constrained to evolve.

The cheese *S. cerevisiae* population also displayed a specific phenotype related to the use of galactose, a sugar present in cheese, produced by members of the cheese microbiota, such as *Kluyveromyces lactis* or *Lactobacillus lactis*, by lactose hydrolysis. The *S. cerevisiae* cheese

population exhibited the highest mean maximal growth rate on galactose compared to all other genetic groups [25].

## Convergence of adaptation genomic mechanisms

Recent studies have thus revealed striking cases of convergent adaptation, and some of these adaptation events involved identical mechanisms, i.e. horizontal gene transfers. Even more striking, the very same genomic regions have been horizontally transferred in multiple cheese *Penicillium* species, including *P. camemberti*, *P. biforme* and *P. roqueforti* [43,45]. These cheese-specific genomic regions displayed 100% nucleotide sequence identity across hundreds of kilobases despite the substantial phylogenetic distance between the species, while these regions were absent in more closely related species, suggesting very recent acquisition by horizontal gene transfer, probably during the massive industrialisation of cheese production. These horizontally transferred regions contained protein-coding genes involved in milk metabolism and competition, and were restricted to cheese populations in *P. roqueforti* [43,45].

Multiple horizontal gene transfers were also particularly abundant between *P. nalgiovense* and *P. salamii*, compared to species from other environments of the same phylogenetic distance [38]. Some horizontal gene transfers which occurred between the two dry-cured meat fungi were also shared with *P. biforme*, another mold also found in dry-cured meat products [38].

Positive selection on amino-acid changes has also been detected in dry-cured meat fungi [38], in cheese *P. roqueforti* [37] and cheese *G. candidum* [41] populations, for example on genes involved in volatile compound production in *P. roqueforti* [37] and in proteolysis in *G. candidum* [41]. In the cheese *S. cerevisiae* population, selective sweeps also involved metabolism genes, in particular for galactose transport, with alleles that seem to provide cheese strains with the ability to assimilate galactose faster than other *S. cerevisiae* strains [25]. Selective sweeps could not be studied in the dry-cured meat and cheese *Penicillium* fungi, due to largely clonal population structures.

## Convergence in bottlenecks and degeneration

All these fungal populations domesticated for cheese-making or dry-cured meat production displayed very little diversity, lower than non-cheese populations of the same species or closely related species, indicating bottlenecks. Some domesticated populations even constituted of only a single clonal lineage, as *P. camemberti* and the non-Roquefort *P. roqueforti* population [36,37], and the *P. nalgiovense* population in dry-cured meat [38]. The *G. candidum* cheese populations kept higher diversity than *Penicillium* cheese fungi but still displayed bottleneck footprints [41], the less genetically diverse cheese population of *G. candidum* being as genetically diverse as *P. biforme*. In the Roquefort *P. roqueforti* population, the Roquefort PDO



has protected genetic diversity, as PDO requires the use of local strains; the clonal lineage used worldwide could therefore not replace those strains. In contrast, Camembert and Brie PDO enforces the use of a single clonal lineage of *P. camemberti*, selected for its white color and fluffy aspect, and therefore prevents the use of more genetic diversity. The genetic diversity of the dairy population in *S. cerevisiae* is lower than in beer or mixed-origin populations, but greater than in the wine population, and of the same order of magnitude as the whole cheese clade of *G. candidum*, including its three genetically differentiated populations.

Several domesticated fungi for food production have lost their ability to produce toxins due to deletion events in the genes of the corresponding pathways, such as mycophenolic acid in *P. roqueforti* [46,47] or cyclopiazonic acid in *P. camemberti* var *caseifulvum* [36]. In *G. candidum*, the cheese populations have lost two beta lactamase-like genes involved in xenobiotic clearance, likely due to relaxed selection [41]. In *S. cerevisiae*, the cheese population displays a high amount of missing genomic fragments and disrupted genes due to presence of stop codons or frameshifts and was unable to efficiently achieve wine fermentation [25]. Cheese populations have lost sexual fertility due to asexual replication since domestication. This was the case in *P. roqueforti*, the two cheese populations convergently displaying infertility, but at different steps in the life cycle, while non-cheese populations were fertile [48]. In *P. camemberti*, no sexual reproduction could be induced at all (unpublished).

## Conclusion

Recent studies provide evidence for convergence evolution towards similar beneficial traits for food fermentation in fungi. This shows that selection for adaptation to similar ecological niches can repeatedly lead to similar phenotypes. Despite convergent evolution, the different cheese fungi each evolved different varieties with contrasting phenotypes.

Other filamentous fungi are used for cheese-making but have not been studied so far, e.g. *Bisifusarium domesticum* (previously named *Fusarium domesticum*), *Scopulariopsis asperula*, *S. flava* or *Sporendonema casei*. *Bisifusarium domesticum* is present on the surface of smear ripened cheeses such as Reblochon or Saint Nectaire and prevents stickiness, while *Scopulariopsis* species occur on the surface of ripened cheeses such as Tommes. *Sporendonema casei* is the dazzling red mold found as spots on Tomme cheeses. It would be interesting to assess whether these fungi have adapted to the cheese environment and, if so, with the same regions, genes or phenotypic traits as other cheese fungi, and if these convergences are the result of the same genomic mechanisms.

Evidence from other domesticated fungi, used in other products than cheeses or dry-cured meat, also suggests the acquisition of beneficial traits, in *S. cerevisiae* for making wine, beer, bread, in *Brettanomyces bruxellensis* for producing beer and kombucha and in *Aspergillus oryzae* for producing Asian soy fermented products such as sake or miso [13,25,27–32,49–52]. These populations have also acquired specific phenotypes, and also by similar mechanisms

such as horizontal gene transfers [53,54] or hybridization such as the hybrid species *S. pastorianus* used for the production of lager beer [55]. For example, horizontal gene transfers have likely facilitated adaptation in the filamentous fungus *A. oryzae*, by the acquisition of the sesquiterpene gene cluster, whose product belongs to a class of food-flavoring aromatic compounds [52]. Selective sweeps have also been detected in *A. oryzae*, containing genes involved in primary metabolism and secondary metabolism clusters; these included notably one gene for the biosynthesis of the tremorgenic mycotoxin aflatrem, as well as protein and peptide degradation and carbohydrate metabolism. *Aspergillus oryzae* has lost the ability to produce the carcinogen aflatoxin of its sister species *A. flavus*, a plant pathogen [52], harmful for human health. Fungal pathogens on crops have also evolved under indirect human pressure, leading to specific phenotypes on crops, e.g. being more aggressive or more virulent, and with also often bottlenecks and horizontal gene transfers [56,57] ; this process has been called pestification [57].

Most domesticated fungi have suffered from drastic bottlenecks, with sometimes a single clonal lineage per variety. This jeopardizes future strain improvement and leads to degeneration. It is recognized that old and rare breeds of domesticated animals may have valuable traits which complement those of the most popular breeds, while landraces of crop species are genetic resources for plant breeding. Equally, we need to take care to conserve the genetic diversity of domesticated microorganisms, for the sake of the future of nutritious, delicious food and drink [58].

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## Reference

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37. Dumas E, Feurtey A, Vega RCR de la, Prieur SL, Snirc A, Coton M, Thierry A, Coton E, Piver ML, Roueyre D, et al.: Independent domestication events in the blue-cheese fungus *Penicillium roqueforti*. Mol Ecol 2020, 29:2639–2660.

In this paper, Dumas et al. elucidate the domestication history of the blue cheese mold *P. roqueforti*. This fungus used for blue cheese production worldwide has been domesticated twice independently for cheese ripening: the population of Roquefort originated from an old domestication event while the second cheese population originated more recently from the

selection of a single clonal lineage. These two cheese populations display contrasting phenotypes in terms of growth, color, volatiles, lipolysis and proteolysis activities.

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36. Ropars J, Didiot E, Rodríguez de la Vega RC, Bennetot B, Coton M, Poirier E, Coton E, Snirc A, Le Prieur S, Giraud T: Domestication of the emblematic white cheese-making fungus *Penicillium camemberti* and its diversification into two varieties. *Curr Biol* 2020, 30:4441–4453.

This study elucidates the evolutionary history of the white mold *P. camemberti* used for soft cheese production. This clonal white and fluffy mold is the result of multiple domestication steps by divergence from its gray-green cheese-specific relative *P. biforme*. Two varieties occur in *P. camemberti*, with contrasting phenotypes in terms of color, growth, mycotoxin production and competitive abilities.

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41. Bennetot B, Vernadet J-P, Perkins V, Hautefeuille S, Rodriguez de la Vega RC, O'Donnell S, Snirc A, Grondin C, Lessard M-H, Péron A-C, et al.: Domestication of different varieties in the cheese-making fungus *Geotrichum candidum*. *bioRxiv* 2022, doi:10.1101/2022.05.17.492043.

This is the first population genomics analysis of the cheese-making fungus *Geotrichum candidum* found in many different kinds of cheeses, in raw milk and in other environments. The domestication of *G. candidum* has occurred in several steps, as in *P. camemberti*, and led to diversification into three varieties with contrasted phenotypes in terms of fluffiness, proteolysis activity, volatiles and competitive abilities.

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38. Lo Y-C, Bruxaux J, Vega RCR de la, Snirc A, Coton M, Piver ML, Prieur SL, Roueyre D, Dupont J, Houbraeken J, et al.: Footprints of domestication in dry-cured meat *Penicillium* fungi: convergent specific phenotypes and horizontal gene transfers. *bioRxiv* 2022, doi:10.1101/2022.03.25.485132.

This study reveals convergent adaptation to dry-cured meat production in *Penicillium salami* and *P. nalgioense* in terms of slower lipolysis and proteolysis. These two fungi, despite being very distantly related, shared multiple horizontal gene transfers.

1. Diamond J: Evolution, consequences and future of plant and animal domestication. *Nature* 2002, 418:700–707.
2. Frantz LAF, Schraiber JG, Madsen O, Megens H-J, Cagan A, Bosse M, Paudel Y, Crooijmans RPMA, Larson G, Groenen MAM: Evidence of long-term gene flow and selection during domestication from analyses of Eurasian wild and domestic pig genomes. *Nat Genet* 2015, 47:1141–1148.

3. Warmuth V, Eriksson A, Bower MA, Cañon J, Cothran G, Distl O, Glowatzki-Mullis M-L, Hunt H, Luís C, do Mar Oom M, et al.: European Domestic Horses Originated in Two Holocene Refugia. *PLoS ONE* 2011, 6:e18194.
4. Hufford MB, Xu X, van Heerwaarden J, Pyhäjärvi T, Chia J-M, Cartwright RA, Elshire RJ, Glaubitz JC, Guill KE, Kaeppler SM, et al.: Comparative population genomics of maize domestication and improvement. *Nat Genet* 2012, 44:808–811.
5. Orlando L: The Evolutionary and Historical Foundation of the Modern Horse: Lessons from Ancient Genomics. *Annu Rev Genet* 2020, 54:563–581.
6. Mabry ME, Turner-Hissong SD, Gallagher EY, McAlvay AC, An H, Edger PP, Moore JD, Pink DAC, Teakle GR, Stevens CJ, et al.: The Evolutionary History of Wild, Domesticated, and Feral *Brassica oleracea* (Brassicaceae). *Mol Biol Evol* 2021, 38:4419–4434.
7. Peng JH, Sun D, Nevo E: Domestication evolution, genetics and genomics in wheat. *Mol Breed* 2011, 28:281.
8. Darwin C: The origin of species. 1859.
9. Tang H, Sezen U, Paterson AH: Domestication and plant genomes. *Curr Opin Plant Biol* 2010, 13:160–166.
10. Gladieux P, Ropars J, Badouin H, Branca A, Aguilera G, de Vienne DM, Rodríguez de la Vega RC, Branco S, Giraud T: Fungal evolutionary genomics provides insight into the mechanisms of adaptive divergence in eukaryotes. *Mol Ecol* 2014, 23:753–773.
11. Purugganan MD: Evolutionary Insights into the Nature of Plant Domestication. *Curr Biol* 2019, 29:R705–R714.
12. Steensels J, Gallone B, Verstreppe KJ: Interspecific hybridization as a driver of fungal evolution and adaptation. *Nat Rev Microbiol* 2021, doi:10.1038/s41579-021-00537-4.
13. Steensels J, Gallone B, Voordeckers K, Verstreppe KJ: Domestication of Industrial Microbes. *Curr Biol* 2019, 29:R381–R393.
14. Alberto FJ, Boyer F, Orozco-terWengel P, Streeter I, Servin B, Villemereuil P, Benjelloun B, Librado P, Biscarini F, Colli L, et al.: Convergent genomic signatures of domestication in sheep and goats. *Nat Commun* 2018, 9:813.
15. Martínez-Ainsworth NE, Tenaillon MI: Superheroes and masterminds of plant domestication. *C R Biol* 2016, 339:268–273.
16. Gross BL, Olsen KM: Genetic perspectives on crop domestication. *Trends Plant Sci* 2010, 15:529–537.
17. Lin Z, Li X, Shannon LM, Yeh C-T, Wang ML, Bai G, Peng Z, Li J, Trick HN, Clemente TE, et al.: Parallel domestication of the *Shattering1* genes in cereals. *Nat Genet* 2012, 44:720–724.
18. Jia G, Huang X, Zhi H, Zhao Y, Zhao Q, Li W, Chai Y, Yang L, Liu K, Lu H, et al.: A haplotype map of genomic variations and genome-wide association studies of agronomic traits in foxtail millet (*Setaria italica*). *Nat Genet* 2013, 45:957–961.
19. Wang M, Yu Y, Haberer G, Marri PR, Fan C, Goicoechea JL, Zuccolo A, Song X, Kudrna D, Ammiraju JSS, et al.: The genome sequence of African rice (*Oryza glaberrima*) and evidence for independent domestication. *Nat Genet* 2014, 46:982–988.
20. Marsden CD, Ortega-Del Vecchyo D, O'Brien DP, Taylor JF, Ramirez O, Vilà C, Marques-Bonet T, Schnabel RD, Wayne RK, Lohmueller KE: Bottlenecks and selective sweeps during domestication have increased deleterious genetic variation in dogs. *Proc Natl Acad Sci* 2015,
21. Fages A, Hanghøj K, Khan N, Gaunitz C, Seguin-Orlando A, Leonardi M, Constantz CM, Gamba C, Al-Rasheid KAS, Albizuri S, et al.: Tracking Five Millennia of Horse Management with Extensive Ancient

Genome Time Series. *Cell* 2019, 177:1419–1435.e31.

22. Zhu Q, Zheng X, Luo J, Gaut BS, Ge S: Multilocus analysis of nucleotide variation of *Oryza sativa* and its wild relatives: severe bottleneck during domestication of rice. *Mol Biol Evol* 2007, 24:875–888.
23. Whitehead SR, Poveda K: Resource allocation trade-offs and the loss of chemical defences during apple domestication. *Ann Bot* 2019, 123:1029–1041.
24. Makino T, Rubin C-J, Carneiro M, Axelsson E, Andersson L, Webster MT: Elevated Proportions of Deleterious Genetic Variation in Domestic Animals and Plants. *Genome Biol Evol* 2018, 10:276–290.
25. Legras J-L, Galeote V, Bigey F, Camarasa C, Marsit S, Nidelet T, Sanchez I, Couloux A, Guy J, Franco-Duarte R, et al.: Adaptation of *S. cerevisiae* to fermented food environments reveals remarkable genome plasticity and the footprints of domestication. *Mol Biol Evol* 2018, 35:1712–1727.
26. Duan S-F, Han P-J, Wang Q-M, Liu W-Q, Shi J-Y, Li K, Zhang X-L, Bai F-Y: The origin and adaptive evolution of domesticated populations of yeast from Far East Asia. *Nat Commun* 2018, 9.
27. Fay JC, Benavides JA: Evidence for domesticated and wild populations of *Saccharomyces cerevisiae*. *PLoS Genet* 2005, 1:e5.
28. Gallone B, Steensels J, Prah T, Soriaga L, Saels V, Herrera-Malaver B, Merlevede A, Roncoroni M, Voordeckers K, Miraglia L, et al.: Domestication and divergence of *Saccharomyces cerevisiae* beer yeasts. *Cell* 2016, 166:1397–1410.e16.
29. Libkind D, Hittinger CT, Valério E, Gonçalves C, Dover J, Johnston M, Gonçalves P, Sampaio JP: Microbe domestication and the identification of the wild genetic stock of lager-brewing yeast. *Proc Natl Acad Sci* 2011, 108:14539–14544.
30. Liti G, Carter DM, Moses AM, Warringer J, Parts L, James SA, Davey RP, Roberts IN, Burt A, Koufopanou V, et al.: Population genomics of domestic and wild yeasts. *Nature* 2009, 458:337–341.
31. Peter J, Chiara MD, Friedrich A, Yue J-X, Pflieger D, Bergström A, Sigwalt A, Barre B, Freel K, Llored A, et al.: Genome evolution across 1,011 *Saccharomyces cerevisiae* isolates. *Nature* 2018, 556:339–344.
32. Gallone B, Mertens S, Gordon JL, Maere S, Verstrepen KJ, Steensels J: Origins, evolution, domestication and diversity of *Saccharomyces* beer yeasts. *Curr Opin Biotechnol* 2018, 49:148–155.
33. Saada OA, Tsouris A, Large C, Friedrich A, Dunham MJ, Schacherer J: Phased polyploid genomes provide deeper insight into the multiple origins of domesticated *Saccharomyces cerevisiae* beer yeasts. *Curr Biol* 2022, 32:1350–1361.
34. Almeida P, Barbosa R, Zalar P, Imanishi Y, Shimizu K, Turchetti B, Legras J-L, Serra M, Dequin S, Couloux A, et al.: A population genomics insight into the Mediterranean origins of wine yeast domestication. *Mol Ecol* 2015, 24:5412–5427.
35. Ropars J, Caron T, Lo Y, Benetot B, Giraud T: The domestication of *Penicillium* cheese fungi. *C R Biol* 2020, 343:155–176.
36. Ropars J, Didiot E, Rodríguez de la Vega RC, Benetot B, Coton M, Poirier E, Coton E, Snirc A, Le Prieur S, Giraud T: Domestication of the emblematic white cheese-making fungus *Penicillium camemberti* and its diversification into two varieties. *Curr Biol* 2020, 30:4441–4453.
37. Dumas E, Feurtey A, Vega RCR de la, Prieur SL, Snirc A, Coton M, Thierry A, Coton E, Piver ML, Roueyre D, et al.: Independent domestication events in the blue-cheese fungus *Penicillium roqueforti*. *Mol Ecol* 2020, 29:2639–2660.
38. Lo Y-C, Bruxaux J, Vega RCR de la, Snirc A, Coton M, Piver ML, Prieur SL, Roueyre D, Dupont J, Houbraken J, et al.: Footprints of domestication in dry-cured meat *Penicillium* fungi: convergent specific phenotypes and horizontal gene transfers. *bioRxiv* 2022, doi:10.1101/2022.03.25.485132.
39. Steenwyk JL, Shen X-X, Lind AL, Goldman GH, Rokas A: A robust phylogenomic time tree for

- biotechnologically and medically important fungi in the genera *Aspergillus* and *Penicillium*. mBio 2019, 10.
40. Springer MS, Meredith RW, Gatesy J, Emerling CA, Park J, Rabosky DL, Stadler T, Steiner C, Ryder OA, Janečka JE, et al.: Macroevo­lutionary Dynamics and Historical Biogeography of Primate Diversification Inferred from a Species Supermatrix. PLOS ONE 2012, 7:e49521.
  41. Bennetot B, Vernadet J-P, Perkins V, Haute­feuille S, Rodriguez de la Vega RC, O'Donnell S, Snirc A, Grondin C, Lessard M-H, Péron A-C, et al.: Domestica­tion of different varieties in the cheese-making fungus *Geotrichum candidum*. bioRxiv 2022, doi:10.1101/2022.05.17.492043.
  42. Caron T, Piver ML, Péron A-C, Lieben P, Lavigne R, Brunel S, Roueyre D, Place M, Bonnarme P, Giraud T, et al.: Strong effect of *Penicillium roqueforti* populations on volatile and metabolic compounds responsible for aromas, flavor and texture in blue cheeses. Int J Food Microbiol 2021, 354:109174.
  43. Ropars J, Rodríguez de la Vega RC, López-Villavicencio M, Gouzy J, Sallet E, Dumas É, Lacoste S, Debuchy R, Dupont J, Branca A, et al.: Adaptive horizontal gene transfers between multiple cheese-associated Fungi. Curr Biol 2015, 25:2562–2569.
  44. Yvon M, Rijnen L: Cheese flavour formation by amino acid catabolism. Int Dairy J 2001, 11:185–201.
  45. Cheeseman K, Ropars J, Renault P, Dupont J, Gouzy J, Branca A, Abraham A-L, Ceppi M, Conseiller E, Debuchy R, et al.: Multiple recent horizontal transfers of a large genomic region in cheese making fungi. Nat Commun 2014, 5:2876.
  46. Gillot G, Jany J-L, Poirier E, Maillard M-B, Debaets S, Thierry A, Coton E, Coton M: Functional diversity within the *Penicillium roqueforti* species. Int J Food Microbiol 2017, 241:141–150.
  47. Coton E, Coton M, Hymery N, Mounier J, Jany J-L: *Penicillium roqueforti*: an overview of its genetics, physiology, metabolism and biotechnological applications. Fungal Biol Rev 2020,
  48. Ropars J, Lo Y, Dumas E, Snirc A, Begerow D, Rollnik T, Lacoste S, Dupont J, Giraud T, López-Villavicencio M: Fertility depression among cheese-making *Penicillium roqueforti* strains suggests degeneration during domestica­tion. Evolution 2016, 70:2099–2109.
  49. Harrouard J, Eberlein C, Ballestra P, Dols-Lafargue M, Masneuf-Pomarede I, Miot-Sertier C, Schacherer J, Albertin W: *Brettanomyces bruxellensis*: Overview of the genetic and phenotypic diversity of an anthropized yeast. Mol Ecol 2022, doi:10.1111/mec.16439.
  50. Galagan JE, Calvo SE, Cuomo C, Ma L-J, Wortman JR, Batzoglou S, Lee S-I, Baştürkmen M, Spevak CC, Clutterbuck J, et al.: Sequencing of *Aspergillus nidulans* and comparative analysis with *A. fumigatus* and *A. oryzae*. Nature 2005, 438:1105–1115.
  51. Machida M, Asai K, Sano M, Tanaka T, Kumagai T, Terai G, Kusumoto K-I, Arima T, Akita O, Kashiwagi Y, et al.: Genome sequencing and analysis of *Aspergillus oryzae*. Nature 2005, 438:1157–1161.
  52. Gibbons JG, Salichos L, Slot JC, Rinker DC, McGary KL, King JG, Klich MA, Tabb DL, McDonald WH, Rokas A: The evolutionary imprint of domestica­tion on genome variation and function of the filamentous fungus *Aspergillus oryzae*. Curr Biol 2012, 22:1403–1409.
  53. Marsit S, Mena A, Bigey F, Sauvage F-X, Couloux A, Guy J, Legras J-L, Barrio E, Dequin S, Galeote V: Evolutionary advantage conferred by an eukaryote-to-eukaryote gene transfer event in wine yeasts. Mol Biol Evol 2015, 32:1695–1707.
  54. Novo M, Bigey F, Beyne E, Galeote V, Gavory F, Mallet S, Cambon B, Legras J-L, Wincker P, Casaregola S, et al.: Eukaryote-to-eukaryote gene transfer events revealed by the genome sequence of the wine yeast *Saccharomyces cerevisiae* EC1118. Proc Natl Acad Sci 2009, 106:16333–16338.
  55. Naumova ES, Naumov GI, Masneuf-Pomarède I, Aigle M, Dubourdieu D: Molecular genetic

- study of introgression between *Saccharomyces bayanus* and *S. cerevisiae*. *Yeast* 2005, 22:1099–1115.
56. Friesen TL, Stukenbrock EH, Liu Z, Meinhardt S, Ling H, Faris JD, Rasmussen JB, Solomon PS, McDonald BA, Oliver RP: Emergence of a new disease as a result of interspecific virulence gene transfer. *Nat Genet* 2006, 38:953–956.
57. Feurtey A, Guitton E, De Gracia Coquerel M, Duvaux L, Shiller J, Bellanger M-N, Expert P, Sannier M, Caffier V, Giraud T, et al.: Threat to Asian wild apple trees posed by gene flow from domesticated apple trees and their “pestified” pathogens. *Mol Ecol* 2020, 29:4925–4941.
58. Vavilov NI, Vavilov MI, Vavilov NI, Dorofeev VF: *Origin and Geography of Cultivated Plants*. Cambridge University Press; 1992.