

# Research pushes back history of crop development 10,000 years

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Researchers led by Dr Robin Allaby of the University of Warwick's plant research arm Warwick HRI have found evidence that genetics supports the idea that the emergence of agriculture in prehistory took much longer than originally thought.

Until recently researchers say the story of the origin of agriculture was one of a relatively sudden appearance of plant cultivation in the Near East around 10,000 years ago spreading quickly into Europe and dovetailing conveniently with ideas about how quickly language and population genes spread from the Near East to Europe. Initially, genetics appeared to support this idea but now cracks are beginning to appear in the evidence underpinning that model

Now a team led by Dr Robin Allaby from the University of Warwick have developed a new mathematical model that shows how plant agriculture actually began much earlier than first thought, well before the Younger Dryas (the last "big freeze" with glacial conditions in the higher latitudes of the Northern Hemisphere). It also shows that useful gene types could have actually taken thousands of years to become stable.

Up till now researchers believed in a rapid establishment of efficient agriculture which came about as artificial selection was easily able to dominate natural plant selection, and, crucially, as a consequence they thought most crops came from a single location and single domestication event.

However recent archaeological evidence has already begun to undermine this model pushing back the date of the first appearance of plant agriculture. The best example of this being the archaeological site Ohalo II in Syria where more than 90,000 plant fragments from 23,000 years ago show that wild cereals were being gathered over 10,000 years earlier than previously thought, and before the last glacial maximum (18,000-15,000 years ago).

The field of Archaeobotany is also producing further evidence to undermine the quick development model. The tough rachis mutant is caused by a single recessive allele (one gene on a pair or group of genes) , and this mutant is easily identifiable in the archaeological specimens as a jagged scar on the chaff of the plant noting an abscission (shedding of a body part) as opposed to the smooth abscission scar associated with the wild type brittle rachis.

Simply counting the proportion of chaff types in a sample gives a direct measure of frequency of the two different gene types in this plant. That study has shown that the tough rachis mutant appeared some 9,250 years ago and had not reached fixation over 3,000 years later even after the spread of agriculture into Europe was well underway. Studies like these have shown that the rise of the domestication syndrome was a slow process and that plant traits appeared in slow sequence, not together over a short period of time.

Genome wide surveys of crops such as einkorn and barley that in the past that have suggested a single origin from a narrow geographical range, supporting the rapid establishment view, have long been in conflict with other gene studies. The most notable conflict is in the case of barley for which there is a large body of evidence that suggests more than one common ancestor was used in its development.

These challenges to the fast model of agricultural development need a

new model to explain how and why the development was so slow and demonstrate why artificial selection of just one plant type does not have the expected quick result. This computer model has now been provided by Dr Robin Allaby and his team at the University of Warwick, the Institute of Archaeology, University College London, and Manchester Interdisciplinary Biocentre has outlined the new mathematical model in a paper published in *Proceedings of the National Academy of Sciences USA* 2008 and in a summary article in the *Biologist* (2008 55:94-99).

Their paper entitled *The genetic expectations of a protracted model for the origins of domesticated crops* used computer simulations that showed that over time a cultivated population will become monophyletic (settle into one stable species) at a rate proportional to its population size as compared various gene variations in the wild populations. They found this rate of change matched closely the 3000 years it took the tough rachis mutant to become established.

Ironically, this process is actually accelerated if there is more than one wild source population (in other words if attempts at domestication happen more than once) because any resulting hybrid between those domesticated populations then has a heightened differentiation compared with either one of the wild populations of the two parent plants.

This mathematical model also more supportive of a longer complex origin of plants through cross breeding of a number of attempts at domestication rather than a single plant type being selectively bred and from a single useful mutation that is selectively grown quickly out paces the benefits natural selection

Dr Robin Allaby says:

"This picture of protracted development of crops has major implications

for the understanding of the biology of the domestication process and these strike chords with other areas of evolutionary biology."

"This lengthy development should favour the close linkage of domestication syndrome trait genes which may become much more important because linked genes will not be broken up by gene flow – and this makes trait selection and retention easier. Interestingly, as more crop genomes become mapped, the close linkage of two or more domestication syndrome genes has been reported on several occasions."

"This process has similarities to the evolution of 'supergenes' in which many genes cluster around a single locus to contribute to one overall purpose."

"We now need to move this research area to a new level. Domestication was a complex process and can now be viewed more legitimately as the paragon of evolutionary process that Darwin originally recognized. There are many interacting factors involved that we know about operating on a wide range of levels from the gene to the farmer and climate – the challenge is to integrate them into a single story."

Source: University of Warwick

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