How did the ideas and technology of farming spread so quickly?

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Abstract

Two major hypotheses have been suggested as potential mechanisms for the global spread of plant and animal domestication (farming) among human societies. The cultural diffusion hypothesis suggests that farming technology was shared between neighboring groups, while the demic diffusion hypothesis suggests that farming spread through the forceful eviction and replacement of non-farming competitors. Support exists for each of these hypotheses at local and regional scales, but variation in these results make it difficult to identify the dominant global mechanism that ultimately drove the spread of farming.

To disentangle the relative contribution of these mechanisms, we modeled the spatial and phylogenetic distribution of farming under four different modes of transmission: vertical transmission only, vertical transmission plus cultural diffusion, vertical transmission plus demic diffusion, and vertical transmission plus cultural and demic diffusion. The resulting phylogenetic and spatial patterns were collectively used to train a random forest machine-learning algorithm to identify the most likely mode of transmission of any given simulation output. Once trained, the algorithm was used to identify which transmission mode likely led to the current phylogenetic and spatial distribution of farming seen today.

Our preliminary results suggest that the most likely mechanism behind the spread of farming was strict cultural diffusion, with very little contribution from demic diffusion. We interpret these results as indicating that the ideas and technology of domestication spread so quickly because they were shared without incurring the resource and extinction costs associated with demic diffusion. Such unambiguous support for one hypothesis over another stands in contrast to the variable regional outcomes seen in the past and shows the power of large scale global analyses at informing long-standing research questions.