A new model is proposed for the earliest colonization of Europe in the Early and Middle Pleistocene that takes account of recent discoveries at Dmanisi, Georgia, and Atapuerca, Spain, as well as other localities such as Happisburgh and Pakefield in England. This model differs structurally from previous ones in two important respects. First, it re-evaluates the European (and where appropriate, African and West Asian) fossil hominin evidence within its wider continental-level archaeological, climatic and faunal contexts instead of focusing largely or exclusively on one line of evidence, whether fossil hominin or archaeological. Secondly, the model is presented as a series of explicit hypotheses, each of which could be challenged from present evidence, or confirmed or falsified by future discoveries, instead of the usual type of narrative structure (on the lines of “first this happened, then that”) that underpins most overviews of human evolution in Europe and/or the Middle Pleistocene. These hypotheses lead to a model for the initial colonization of Europe and western Eurasia in which the evolutionary history of Eurasian and African populations is seen as relatively independent in the Early Pleistocene, and almost entirely independent in the Middle Pleistocene. This model explains the colonization of Europe through non-linear population dynamics, envisaging pulses of migrations from a central area of dispersals continuously inhabited by a ‘source population’. The proposed central area of dispersals is located in Western Eurasia (the Central Area of Dispersals of Eurasia, or CADE), and was not always connected to East Africa. The ‘source population’ would have experienced its own evolution in the CADE, changing its genotype by mutation and natural selection. These changes are reflected in the different pulses of demes towards Europe and East Asia. Hominin dispersals in Eurasia probably followed an expansion/contraction model (with frequent population wipe-outs and local extinctions in glacial periods), rather than a lineal and directional emigrational wave. Populations in the central (CADE) and peripheral areas of Eurasia were often isolated, and geographical and climatic barriers favoured processes of genetic drift and random allelic variation in their ‘descendants’. During dispersals, populations would have undergone genetic processes such as genetic drift, founder effect, local adaptations and eventually, allopatric speciation. Populations with a recent common origin that occupied the same territory may have interbred. The core of the model is contained in a set of nine hypotheses that are presented and discussed with the available evidence, as well as with ways that these hypotheses could be potentially falsified. These are: Hypothesis 1: hominins (including early Homo) left Africa ≥1.8 Ma; Hypothesis 2: Homo erectus originated in Southwest Asia, which was a central area for the dispersal in Eurasia (CADE) of hominins, including H. erectus; Hypothesis 3: Hominin dispersals (and extinctions) in Eurasia during the Early Pleistocene were primarily driven by climate change that was both long-term (i.e. over a glacial-interglacial cycle) and short-term (i.e. millennial-length fluctuations within a glacial and occasional an interglacial); Hypothesis 4: Dispersals from the CADE into southern Europe were possible by the early part of the Early Pleistocene (i.e. ≤1.75 Ma); Hypothesis 5: At least one hominin dispersal event from the CADE into Europe led to a speciation event by 1.2 Ma; Hypothesis 6: Sub-Saharan Africa was isolated from Eurasia after 800 ka because of the desert barrier between the Sahara and Arabia; Hypothesis 7: Homo heidelbergensis is primarily a West Eurasian taxon that is absent from Africa and East Asia; Hypothesis 8: The Acheulean in Europe (and possibly India) was introduced from Southwest Asia, not sub-Saharan Africa; and Hypothesis 9: after H. heidelbergensis dispersed into Europe, it replaced or may have interbred with some remnant populations of Homo antecessor.

The hypotheses presented underpin a model of human evolution in western Eurasia that has three main features. The first is that the primary population source of hominins in Europe in the Early and Middle Pleistocene is likely to have been from Southwest Asia – the central area of dispersals in Eurasia (CADE) – rather than Africa. The second is that within Europe, the primary driver of population expansion and contraction would have been climatic shifts in rainfall and temperature at Milankovitch-length glacial-interglacial cycles, and probably during shorter periods of climatic instability. Thirdly, the severance of faunal connections between Eurasia and Africa in the Middle Pleistocene meant that sub-Saharan Africa was irrelevant to developments in Eurasia between 0.8 Ma and the arrival of Homo sapiens in Southwest Asia ca. 125 ka. Africa should not therefore be regarded as the source of either H. heidelbergensis or the European Acheulean during the Middle Pleistocene.