Language Sciences 36 (2013) 66–77

Contents lists available at SciVerse ScienceDirect

Language Sciences

journal homepage: www.elsevier.com/locate/langsci

Homoplasy in diachronic grammar

Freek Van de Velde *, Joop van der Horst

Department of Dutch Linguistics, University of Leuven, Blijde Inkomststraat 21, P.O. Box 3308, 3000 Leuven, Belgium

ARTICLE INFO

Article history:
Available online 1 May 2012

Keywords:
Homoplasy
Grammaticalisation
Degrammaticalisation
Reanalysis
Analogy
Evolution

ABSTRACT

The application of evolutionary thinking to language change has a long tradition, and especially in functional approaches it is currently widely accepted that certain mechanisms can be fruitfully used to describe both biological and linguistic processes. In this article, the evolutionary concept of homoplasy, the recurrence of similar traits in unrelated lineages, is applied to language change. Extending the earlier application of the concept by Lass (1997), homoplasy is here argued to operate not only on the phonological level, but on the morphosyntactic level as well, and not only between languages but also within languages, at the level of constructions. The idea is that phenotypic resemblance in constructions may hide etymological differences. In other words: what looks the same from a synchronic perspective may derive from multiple source constructions historically. On the basis of four case studies in Dutch diachronic morphosyntax, it is shown that homoplasy can offer an insightful account of some long-standing puzzles.

1. Introduction: evolutionary thinking in linguistics

The application of evolutionary thinking to language change has a long, though not uncontroversial tradition. The reason for the controversy surrounding this line of research is not so much the idea that evolutionary principles can be used to model language change, but rather regarding the precise level at which they operate. In the 19th century, the prevailing idea was that it was not the utterance, or the language user, or language as a biological trait in humans that was the relevant level to look for evolutionary mechanisms, but rather individual languages themselves, which were ‘hypostasised’: linguists such as Grimm, Humboldt, Schlegel, Schleicher and Max Müller saw language as a living organism, going through a life cycle of birth, growth and death (Bakker, 1977, pp. 120–121; Morpurgo-Davies, 1998, pp. 86–88; Janda and Joseph, 2003, pp. 6–10). In such an organic view, the analytic tools of biology evidently applied to language as well. This view was discredited in later days, by the Neogrammarians (see Harris and Campbell, 1995, pp. 18–19) and others (see Janda and Joseph, 2003, p. 7), but the idea that language change can be modelled by appealing to evolutionary processes in biology had by then become firmly rooted. Currently, the idea is well accepted (see Rosenbach (2008) for a recent overview), most so in functionalist approaches (see Nettle, 1999), not by stating that languages are biological organisms, but rather by starting from a general evolutionary framework, which is then applied to both biology and cultural systems, including linguistics (Hull, 1988; Dennett, 1995).[1] This idea was elaborated into a full-fledged theory of language change by Croft (2000), but other linguists, like Lass (1997), Givón (2002), Ritt (2004), Mufwene (2008) and Landsbergen (2009), to name just a few, have extensively drawn on evolutionary concepts as well.[2]

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* Corresponding author.
E-mail address: freek.vandevelde@arts.kuleuven.be (F. Van de Velde).

[1] The application of evolutionary thinking to (a) the emergence of language as a biological trait in humans, and (b) language classification and phylogenetic reconstruction will not be considered here.

[2] Lass and Ritt do in fact argue that languages can be treated as organisms, but their position differs from 19th-century organicism.

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http://dx.doi.org/10.1016/j.langsci.2012.03.020

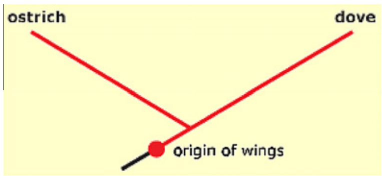

Fig. 1. Homology (see http://evolution.berkeley.edu).

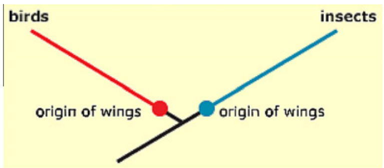

Fig. 2. Homoplasy (see http://evolution.berkeley.edu).

Some scholars doubt whether applying evolutionary thinking to linguistics is useful. As De Cuypere (2005) argues, some biological concepts are injudiciously borrowed without actually adding explanatory value to linguistic problems. Still, biological concepts can often be used as convenient metaphors. In this paper, we bring together a number of morphological changes that have been less than fully understood, and we suggest that they can be brought together under the rubric of 'homoplasy'. This concept is understood as the independent recurrence of functional traits in distinct lineages.

2. Homoplasy

2.1. Homoplasy in biology

Comparative biologists have long been intrigued by similarity in traits in different organisms. Often, such similarity is due to shared ancestry. Doves and ostriches e.g. both have wings, because they share an ancestor, more accurately their most recent common ancestor, which has wings. This is what evolutionary biologists call *homology*. In its technical sense, it is seen in opposition to *homoplasy*, a term coined by Lankester in 1870, which is defined as the emergence of similar traits in unrelated lineages (see Sanderson and Hufford, 1996; Wake, 1996). Birds and insects have wings, but they have developed them independently. The difference can be schematically represented as in Figs. 1 and 2.

Though it is not always easy to reliably detect homoplasy, it is by no means a rare phenomenon, neither at the molecular level, nor at the level of gross morphology. One of the most remarkable examples is the eye, which has evolved independently several times in the course of evolution: eyes of squids, insects and mammals are sufficiently different to argue that they have arisen independently in the different lineages.

What is the main motivation for homoplasy, or convergent evolution?[3] At the molecular level, homoplasy can be the result of random drift, but at higher levels there seem to be two main reasons why homoplasy arises. The first is that organisms respond to similar ecological pressures, and adapt in the same way. The independent emergence of the eye is a good example: using a light-sensitive tool to get sensory information about the environment is obviously advantageous to all sorts of organisms. Another obvious example is the similar morphology of dolphins and ichthyosaurs (see Figs. 3 and 4), who have adapted in similar ways to the aquatic environment. The second reason for convergent evolution is that organisms face design limitations: there are only so many ways to tinker with extant body plans (see Wake, 1991).

2.2. Homoplasy in linguistics

This paper is not the first to apply the concept of homoplasy to language change. In Lass (1997, pp. 118–123, 172–214), it is applied to sound change. This is illustrated by the change in West Germanic */oː/, which appears as /uː/ in both English and German (e.g. *cool/kuhl*). Lass (1997, pp. 120–121) argues that the innovation did not take place prior to the split between English and German, but arose independently in both lineages. Apart from a focus on sound change, Lass's account of homoplasy is also restricted by looking at independent recurrence of traits in two (or more) different languages. In this paper, the linguistic conception of homoplasy is extended from phonological change to morphosyntactic change, and from the inter-language level to the intra-language level. This last step needs some clarification. What does independent recurrence of similar traits within one language mean? What are the different lineages that the traits are observed in? The upshot of this article is that what looks superficially (phenotypically) similar in different constructions can historically derive from quite different material.

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[3] Homoplasy covers convergence, parallelism and reversal/atavism/rudiments. This subclassification will not feature in the present article, where only convergent evolutions will qualify as homoplasy (see also Hall, 2003).