CHAPTER 16

Feature pools show that creoles are distinct languages due to their special origin

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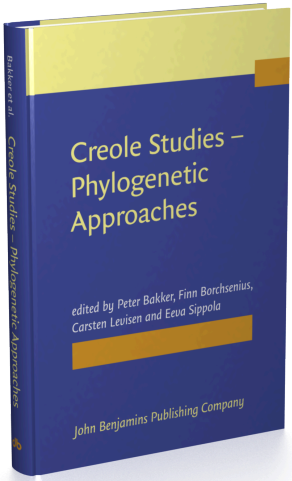

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This book presents the main results of the Cognitive Creolistics project, sponsored by the Velux Foundation (2012–2015), to whom we express our gratitude. In the project we wanted to obtain a better idea of the typological and historical connections between creole languages, as well as a better idea of the cognitive foundations behind the typical properties behind creole morphosyntax.

How can we identify a creole language? We found that a limited set of four or five features would characterize all creoles, but no non-creoles (Chapter 4) – at least not among the approx. 100 languages for which we had data available. If these four or five multi-value features do indeed characterize all and only creoles, this can be used a test. One could potentially use this set of features to flag up languages as creoles that were not previously identified as such. Assuming that a special process of creolization is responsible for their collective emergence, then the presence of a negative particle, a verb 'to have', an indefinite article derived from the numeral 'one', and a lack of tense/aspect inflection characterize creoles.

In this book, we can also see new challenges and new horizons. The three levels of research are reflected in the three parts of the book: The first part (Chapters 5 to 7) compares samples of creoles world-wide with each other and with samples of non-creoles world-wide. In many cases, the non-creoles include the languages that are known to have been spoken by the population groups who contributed to the formation of the creoles. The second part (Chapers 8 to 12) explores historical relations between creoles with the same lexifiers and the possible historical relations between them. The third part (Chapters 13 to 15) relates to the micro-level: semantic connections between creoles (sometimes form-based) and the languages from which the creole lexicons derive. In all cases, phylogenetic programs have been used to shed light on the issues at hand.

The chapters are highly empirical and based on feature pools of varying sizes. One theoretical musing about feature pools was that creoles, and all other results of language contact, are the result of more or less arbitrary combinations of structural features of the languages in contact. The results presented in this book do not lend

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support to those suggestions, as the creoles are more similar to one another than to substrates or superstrates, or their combinations. Creoles always have properties not found in any of the contributing languages.

This book is probably among the most balanced in its use of many different creoles. It has chapters focusing on French-derived creoles (6), Arabic-derived creoles (7), Dutch-derived creoles (8), Spanish-Portuguese derived creoles (9,10) and English based-creoles (11, 12, 13). Non-European based creoles are also included, as part of the larger samples in the world-wide survey (5).

Software for phylogenetic developments was created to map biological evolution. Language evolution and the evolution of life can both be seen as the result of continuous modification by descent. There are important differences in the rate of change, the nature of change and the quantity of horizontal transmission. Biologists have used these techniques not only for DNA sequences and on the molecular level, but also on very different, superficial levels such as looking at the presence of wings, feathers, fins and similar. All forms of life on earth seem to go back to one origin, but it is far from certain that all languages go back to one origin. Based on the strict principles of the comparative method, Harald Hammarström identifies over 400 language families and isolates (Glottolog 2.7 lists 430 in February 2017). This number may eventually be reduced, but it is still a staggering number: it is unlikely that language was invented from scratch more than 400 times.

Working with creole languages and phylogenetic networks, we use software developed for biological purposes. We utilize it sometimes to discover historical relationships between creoles, or creoles and non-creoles – which is along the lines of the original purpose of the software. We also use it to track morphosyntactic or semantic similarities that are often not due to shared inheritance. This was not the original aim of these programs, but they have proved to be a really useful tool, for instance in working with a large amount of data, and in the visualization of similarities and differences between the languages involved in creole genesis, and other non-creole languages.

Is there a creole typological profile? I think the results point in different directions. For phonology (even though not investigated in this book), there is nothing special about creoles – except perhaps that they are average. For morphology and syntax, we can be confident in our conclusions that creoles indeed have a special place in the typological space of the languages of the world. This was a conclusion reached earlier by Szmrecsanyi & Kortmann (2009) on the basis of varieties of English (including vernacular varieties), by Bakker et al. (2011/2013) on the basis of linking different sets of existing world-wide databases of creoles and non-creoles, and of gathering comparable information on additional languages, by Bakker (2014b) who added non-European creoles to the set, and by Muysken (2015) on the basis of a project on the roles of African languages on Caribbean creoles, where creoles also cluster apart from the lexifiers and substrates.

Nevertheless, these conclusions have been criticized. Critical voices pointed to errors in assigning specific features, attacked the feasibility of the program, claimed that the selection of features is biased towards European or creole properties, expressed serious doubts about the quantity of features (too few, too many), conjectured that this work had an Indo-European bias, or a European bias in the lexifiers, or objected that it had only one set of biclans (all European lexifiers and Niger-Congo substrates). See Bakker (2014a, b) for discussion of criticisms.

The studies in this book generally lead to the same conclusions as the earlier ones, and most of the objections (to the extent that it was possible) have been addressed in this book. Attacking the program goes against decades of successful work in biology, and one decade of successful work in linguistics by now. We have also included non-European creoles, to the extent that they exist. The authors have used different sets of features in this book – almost all of them based on lists compiled by others (e.g. APiCS; stability studies based on WALS; lists of number distinctions in Nilo-Saharan and Arabic varieties; independently defined semantic primes, translations of a set of sentences, in Chapters 7–9, 11–15), and not specially designed to prove a specific idea. Sometimes features were also used that were triggered by availability of data collected for their study (8–10, 12–15).

Influence from substrate languages could be detected in a number of features in the case of Iberian creoles. The same is true for a number of semantic patterns (13–15), but hardly any African influence could be observed when looking at the most stable features (Chapter 7).

Chapter 7 (and future work by Daval-Markussen, in press) also shows that the inclusion of creoles with different biclans, still finds creoles distinct from non-creoles, so the distinctness is not the result of the specific biclans in earlier studies.

In the book, the authors reach a number of seemingly contradictory conclusions. On the one hand, creoles appear to be incredibly diverse in their structural properties (e.g. not only verb-medial, but also verb-initial and verb-final). On the other hand, all the tests including samples of creoles, non-creoles and a large set of features, lead to results where creoles and non-creoles form separate clusters. Only very rarely are non-creoles found among creoles, or the other way around, with only a few percent of overlap. When focusing on stable features, however, we find that Western European and Semitic languages are a central part of the creole cluster (Chapter 7). This can be interpreted in different ways. First, creoles continue many lexifier structures. This interpretation, however, collides with the observation that other lexifiers such as Japanese and Tupinamba are not part of the creole cluster, even though the Yilan and Nheengatu creoles clearly are (Figure 7.8). Second, it could be that the European and Middle Eastern languages have undergone language contact effects similar to what is found in creolization. Creolization has been invoked as having an effect at least on English, French and colloquial

Arabic. A third interpretation may be that it is just by chance – a possibility, but unsatisfactory.

In my view, empirical studies based on large pools of features have firmly established that creoles inhabit a special place in the typological space of the languages of the world. No opponents have proposed alternative selections of features to contest this. No one has offered any other form of proof of the opposite, nor have they even attempted to do so.

Another important result is the reduction of features that set the creoles apart from non-creoles. Distinct sets of creoles and non-creoles have resulted from studies using 46 features (Cysouw 2009 based on preliminary data), or 76 (Szmrecsanyi & Kortmann. 2009), 97 (Bakker et al 2013, based on Holm & Patrick 2007), 43 (Bakker et al 2013, based on Parkvall 2008), 83 (Muysken 2015) features, all based on different datasets and/or different features. But also selections of 30 features (Chapter 7 and Chapter 9, which deal with totally different sets), 48 features (Chapter 12), 72 features (Chapter 12), perhaps also 130 (Chapter 11), and 65 (Chapter 13) or even merely four or five features (Daval-Markussen 2013, and Chapter 6 in this volume) can distinguish creoles from non-creoles in the available samples. McWhorter (1998) proposed as few as three features as being found in all and only creoles. This includes one phonological feature, and all of these relate to absence rather than presence. The only successful challenge is Harald Hammarström, who proved that it is possible to select 12 features with 12 creoles and 12 non-creoles, in which creoles do not form a separate group. Any other selection of existing data sets, based on existing lists of features, sets creoles apart, as shown with different sets in e.g. Bakker et al. (2013).

It should be pointed out that lexical semantics (Chapters 13, 14 and 15) yields results that most often link the creoles to the lexifiers, but in some cases I think the authors have only measured the forms of the words with specific meanings (Chapter 13 and especially Chapter 14), rather than the range of meanings of specific primes.

Are creoles a distinctive subgroup? I see myself as a careful and conservative scientist who takes empirical observations as a point of departure. As a scientist, I am more interested in the observable facts and theories explaining them, and not in politics or ideologies. If all tests point to creole distinctiveness, we have to accept it as an empirical fact. This is not a revolutionary statement. In fact, this is what all creolists were in agreement about until the 1990s, until a small group of non-empirical ideologists were able to change public opinion among creolists to an idea that creoles cannot be structurally distinguishable from non-creoles, without backing this hypothesis up at any point with facts about creole and non-creole grammars.

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