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A Biolinguistic Approach to Variation

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According to Chomsky (2005), variation is the result of experience, given the genetic endowment and independent principles reducing complexity. In this perspective, variation is not endogenous to the faculty of language (FL); it requires exposition to linguistic data, as for language acquisition. If variation is exogenous to the genetic endowment, no additional machinery is needed to derive variation other than that which is part of the FL. In the Principles-and-Parameters approach (P&P) (Chomsky 1979, 1981, and related works), parameters of variation are binary choices left open in the principles of Universal Grammar (UG). In the Minimalist Program (MP) (Chomsky 1995 and related works), these choices are left unspecified, variation following from the interaction of the derivational system with factors reducing complexity (Holmberg 2009, Boeckx, in this volume). Thus, while the FL provides features (valued and unvalued) and operations checking unvalued features, the range of variation allowed by the underspecification of the FL is constrained by extralinguistic factors. Why would parameters take the form of valued/unvalued features? Why would feature-valuing operations derive language diversity? And why is variation constrained by principles external to the FL? On the one hand, the reductionist methodology of the MP leads to such theorizing, as no additional machinery is needed to derive linguistic diversity other than the one that is given by the genetic endowment; on the other hand, as language is part of human biology, there might be properties shared by language and biology that could bring further light to these questions.

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In this chapter, I focus on the linearization of affixes, clitics, and DPs, and I explore the hypothesis that asymmetry provides a link between variation in language and variation in biology.¹ First, I relate linguistic parameters to “biological parameters.” Second, I relate the directionality of language change to the directionality of phylogenetic variation in body plans. Finally, I raise the question of why asymmetry would be central in language variation.

13.1 Parameters

13.1.1 *Linguistic parameters*

In P&P, UG specifies a set of principles common to all languages and a set of parameters of variation. The parameters are fixed binary choices related to a principle of UG.² For example, the Head-directionality parameter leaves the choice to fix the position of the head of a syntactic constituent to the initial or the final position, (1), (2).

- (1) *X-bar Theory* $X_{\max} \rightarrow \text{Spec-Xbar}$
 $Xbar \rightarrow X\text{-Compl}$
- (2) *Head-directionality parameter*

Head position is initial or final.

The setting of parameter (2) covers the broad syntactic difference between head-initial languages such as English and Italian and head-final languages such as Japanese (Chomsky 1981; Radford 1997; Baker 2003, among other works). Language acquisition, too, like language variation and change, is thought to be the result of parameter setting. Given UG, language grows in contact with experience, and the language children develop will be a function of the setting of the parameters of UG, based upon the linguistic evidence they are exposed to. Since human language is an object of the natural world, it will change through time, and there will be variation in the language children develop with respect to the language of their caretakers and the sub-populations to which they are exposed. Moreover, a grammatical theory, in

¹ Broadly speaking, asymmetric relations are analogous to the “if→then” logical relation where A implies B, but B does not imply A. Domain-specific definitions are needed, however, to distinguish for example asymmetry in syntax (asymmetric c-command (Kayne 1994; Moro 2000), proper inclusion relation (Di Sciullo 2005; Di Sciullo and Isac 2008a, b)) from asymmetry in biology (fluctuating asymmetry, directional asymmetry; Palmer 1994, 1996), and in set theory (symmetry, asymmetry, antisymmetry, reflexivity).

² See also Rizzi (1982); Borer (1984); Berwick and Weinberg (1986); Niyogi and Berwick (1996, 2009); Baker (1996); Guardiano and Longobardi (2005, 2009); Longobardi and Guardiano (in this volume); Manzini and Savoia (in this volume).

conjunction with an acquisition model, is expected to be able to distinguish more likely patterns of language change from less likely ones (Lightfoot 1991, 1998, 1999; Clark and Roberts 1993; Pintzuk, Tsoulas, and Warner 2000; Roberts and Roussou 2003; among other works).

The Principles-and-Parameters model provides a way to derive observable macro differences between languages. For example, parametric syntax opened the possibility of deriving Greenberg's universals from more abstract principles, and more generally to derive cross-linguistic differences in word order from abstract properties of the grammar (see Kayne 1994, 2005; Cinque 2005). P&P covers micro-variation as well. For example, in Guardiano (2003) the syntactic behavior of demonstratives in different languages and dialects follows from the settings of a small set of syntactic parameters. Demonstratives (Dem) are universally generated in a "low area" of the nominal domain DP (D Gen₁ Adjs Dem Gen₂ NP), and the cross-linguistic differences in the position of Dem are the consequence of the setting of the following parameters:

- (3) Parameter 1: *Strong deixis* (Dem moves to Spec of DP to check *deixis*)
- Parameter 2: *Strong locality* (Dem moves to Spec of DP to check *deixis* and *locality*)
- Parameter 3: *DP over Dem* (Dem moves to the Spec of DP, DP moves to its left periphery)
- Parameter 4: *D(person)-licensing Dem* (Dem and the article never co-occur in Spec of DP)

Parametric syntax also has consequences for phylogeny. Guardiano and Longobardi (2005, 2009) and Longobardi and Guardiano (in this volume) argue that parametric syntax serves phylogenetic purposes better than lexical methods (Gray and Atkinson 2003; Pagel, Atkinson, and Meade 2007). By using abstract syntactic markers such as parameters in phylogeny, languages and dialects can be shown to be more closely related than what it might appear from the classifications based on lexical items. In the parametric-syntax approach to phylogenetic language classification, the syntactic data can be seen as being similar to genetic markers. Moreover, the parametric comparison method displays the advantages of population genetics by comparing values (alleles) of parameters (syntactic polymorphisms) in different grammars, assuming that the parameters are drawn from a finite universal list of discrete biological options.

A step forward brought about by the MP is the reduction of GB principles to more basic properties of the computational system. For example, (1) is derived by Merge, so it is dispensed with. Furthermore, the FL does not specify the values of the parameters in current minimalist theorizing. Thus, (2) is also

dispensed with. Merge derives binary branching structures; the position of the head of a constituent with respect to its complement is left unspecified, and follows from principles external to FL reducing derivational complexity. The FL says nothing about the order of a head and its complement. Since the properties of perception and articulation make it impossible to pronounce and perceive a head and its complement at the same time, they must be linearly ordered. There are exactly two options: precede and follow.

In the feature-driven approach to parametric variation (Chomsky 2000), micro-variations, such as the ones described in (3), rely on the set of features available in the languages; feature valuation contributes to derive language diversity. Viewed as binary choices (a choice between a valued or an unvalued formal feature for a category), parameters do not add to the complexity of the language design. They use what the FL makes available, namely features, valued and unvalued, and feature-valuing operations. Thus, in this framework, setting a parameter's value has consequences for the triggering or the non-triggering of an operation of the FL. Why should language diversity be implemented in these terms?

Let me start by underlying that feature-valuing is brought about by Merge and that this operation is asymmetric.³ According to Di Sciullo and Isac (2008a), Merge is asymmetric in the sense that it applies to a pair of elements in the Numeration whose sets of features are in a proper inclusion relation.⁴ This asymmetry holds for External Merge and for Internal Merge (move), as specified in (4). The example in (5) provides the feature specifications for lexical and functional categories; the partial derivation tree in (6b) is derived by Merge on the basis of the Numeration in (6a).

(4) a. *Asymmetry of External Merge*

External Merge is an operation that applies to a pair of elements in the Numeration whose categorial features are in a proper inclusion relation.

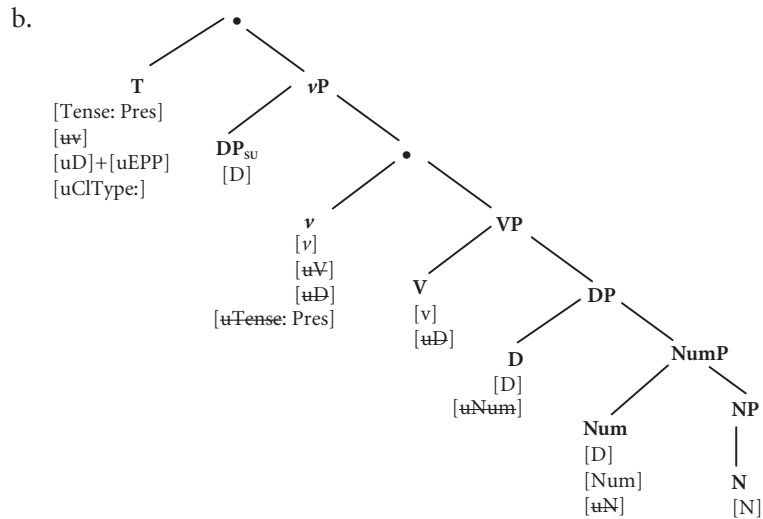
b. *Asymmetry of Internal Merge*

Internal Merge is an operation that applies to a pair of elements in the workspace whose (total set of) features are in a proper inclusion relation. (Di Sciullo and Isac 2008a: 270 (17))

³ See Chomsky (1995), Zwart (2006), and Di Sciullo and Isac (2008a) on the asymmetry of Merge. In Chomsky (2005), Merge is defined as follows: Target two syntactic objects α and β , form a new object $T\{\alpha, \beta\}$, the label LB of $T(LB(T)) = LB(\alpha)$ or $LB(\beta)$.

⁴ The proper-inclusion requirement derives the order of application of Merge. It also provides an account for the differences between possible and impossible sub-extractions. See Di Sciullo and Isac (2008a, b).

- (5) a. Nouns: [N]; Indefinite D: [Num], [uN]; Definite D: [D] [uNum]; wh-D: [D] [uNum] [wh]; Unergative V: [V]; Transitive V: [V] [uD]; Unaccusative V: [V], [uD]; *v*: [*v*] [uV] [uD], [uTense]; Unaccusative *v*: [*v*], [uV] [uTense];
- b. Tense: [Tense], [uv], [uD] [EPP] [uClauseType:]; C₁: [D], [ClauseType], [uTense]; C: [D], [ClauseType], [uTense], [wh]
- (6) a. {C, T, {D, Num, N, *v*, V, D, Num, N}}



Why should variation be brought about by feature-valuing? Beyond the fact that feature-valuing is part of Merge—that is, the recursive operation that combines linguistic elements and derives the discrete infinity of human language—the asymmetry of Merge and thus feature-valuing, might find its roots in biology.

13.1.2 *Biological parameters*

As there have been advances in our understanding of language variation since P&P, there have also been advances in evolutionary developmental biology that made it possible to further understand variation in biology. Brought together, these findings are interesting for the biolinguistic enterprise, which asks why-questions (why these principles, not others), and pursues the

biolinguistic issues that arise only when these questions are posed and at least partially answered.⁵

The biolinguistic approach to language variation opens a new domain of inquiry where why-questions can be addressed by taking into consideration the properties of biological variation. Approaching language variation from the biolinguistic perspective may lead to an understanding of this phenomenon that goes beyond explanatory adequacy. Interestingly, works in evolutionary developmental biology, including Gehring and Ikeo (1999), Montell (2008), Gehring (2005), and Palmer (1994, 1996, 2004a, 2004b, 2009), point to the central role of asymmetry in biological variation and change.

That asymmetry is part of biological variation is not surprising, since more than a decade's detailed research has led to general consensus that asymmetry is responsible for how cells move and divide. For example, Montell (2008) notes that asymmetry explains morphogenetic dynamics. She writes: "It is probably generally the case that signalling pathways . . . function to localize mechanical forces asymmetrically within cells. By definition, an asymmetry in force will cause dynamics." (Montell, 2008: 1505).

From a biolinguistic perspective, one important question is whether parameters have biological correlates. If they do, the understanding of the "biological parameters" may have consequences for the understanding of the linguistic parameters. Interestingly, the dynamics of certain gene products responsible for biological diversity may lead to a deeper understanding of language diversity. Namely, we know from evolutionary developmental biology that core aspects of biological variation could be attributed to the properties of master genes such as in the Homeobox (HOX) system. HOX genes can be selectively switched on and off in evolution, giving rise to differences and similarities amongst and within species (humans and mice), see also Berwick and Chomsky (in this volume), Berwick (in this volume), and Fitch (in this volume). For example, Gehring discovered much of the HOX system related to the *Pac-6* eye formation genes, giving rise to the variation of mammalian and non-mammalian eye types (Gehring and Ikeo 1999; Gehring 2005)—see Figure 13.1. Dyer et al. (2003, 2009) showed that a single change in the mammalian retinal cell distinguishes primates with diurnal vision from mammals with nocturnal vision.

According to Gehring and Ikeo (1999), in the evolution of the eye's morphogenetic pathway, the regulatory HOX genes act at the top of a deductive

⁵ See Lenneberg (1967); Jenkins (2000, 2004); Hauser, Chomsky, and Fitch (2002); Boeckx and Piattelli-Palmarini (2005); Di Sciullo (2007); Di Sciullo et al. (forthcoming); Piattelli-Palmarini and Uriagarek (2004, 2008); among other works on biolinguistics.

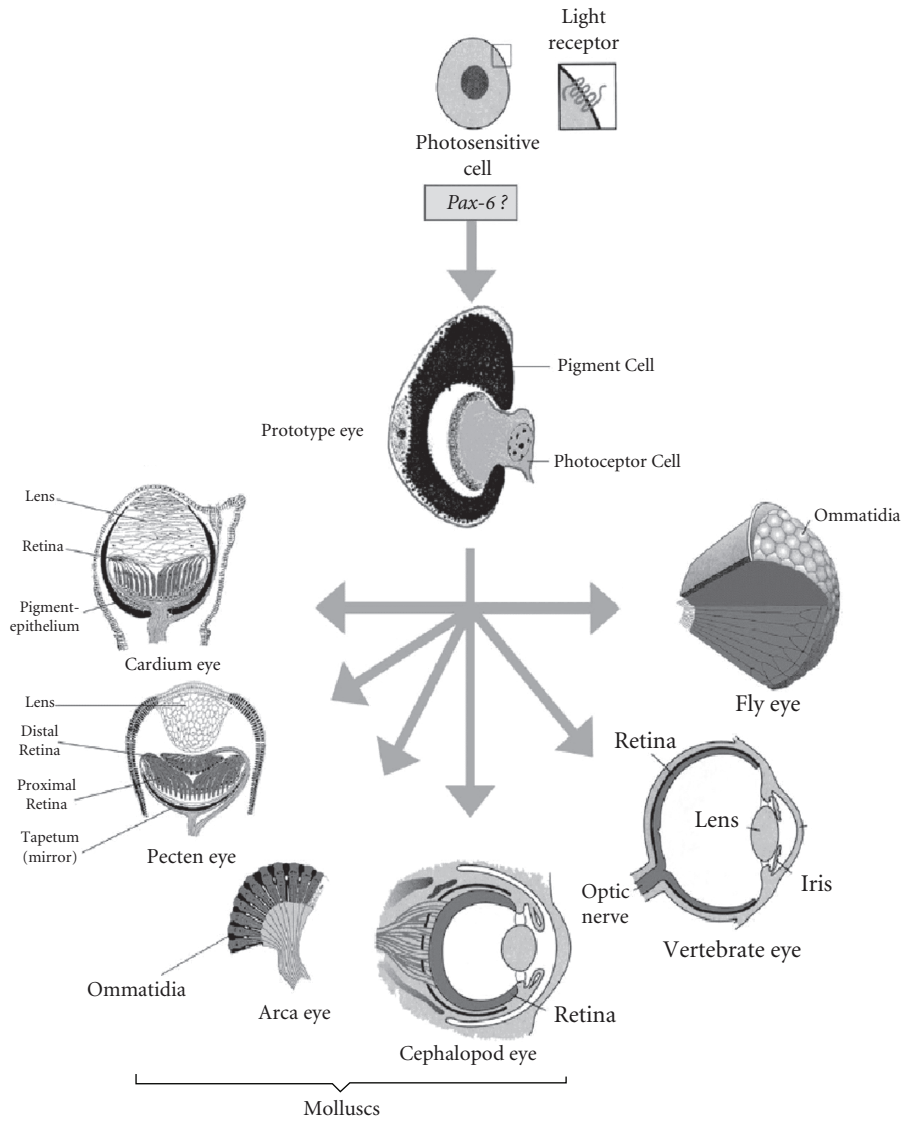


FIGURE 13.1 Hypothetical evolution of photosensitive cells containing Rhodopsin as a light receptor and monophyletic evolution of the various eye types. The eye prototype consisting of a photoreceptor cell and a pigment cell is assembled under the control of Pax6 (after Gehring and Ikeo 1999)

covers the variation observed in morphological structures, differentiating for example so-called strong suffixing languages, such as Turkish, from strong prefixing languages, such as Yekhee. The examples in (7) and (8) illustrate the variation.⁶ Needless to say, broad classifications based on distributional properties are problematic from a biolinguistic perspective, since they offer no principles from which the facts would be derived, and thus no basis to address questions that could lead to a further understanding of why certain principles are not other are at play in variation.

- | | | |
|-----|-------------------|-------------------|
| (7) | a. Yekhee | c. Turkish |
| | <i>émà-wò</i> | <i>yavaşç-a</i> |
| | able drink | slow -ly |
| | ‘drinkable’ | ‘slowly’ |
| | b. à- gùè | d. uyku-da |
| | at sleep | sleep at |
| | ‘asleep’ | ‘a sleep’ |
| (8) | a. Yekhee | c. Turkish |
| | akpa, ikpa | kitap, kitap-lar |
| | ‘cup’, ‘cups’ | ‘book’, ‘books’ |
| | b. ukpo, ikpo | d. öküz, öküz-ler |
| | ‘cloth’, ‘cloths’ | ‘ox’, ‘oxen’ |

Furthermore, besides the fact that such classifications of languages do not provide any explanation for the cross-linguistic variation in the linearization of affixes, they are also descriptively inadequate. For example, they fail to cover the cases where certain affixes follow the root in strong prefixing languages such as Yekhee, as in (9a, b) with aspectual affixes linearized to the right of the root, and cases where certain affixes precede the root in strong suffixing languages such as Turkish, as in (9c–f), where the *wh-* and *th-* affixes precede the root.⁷

- | | | |
|-----|--------------------------|-------------|
| (9) | a. Yekhee | c. Turkish |
| | dè nà pùè | ne-rede |
| | fall repeatedly complete | ‘where’ |
| | ‘finished falling’ | d. ne-vakit |

⁶ Yekhee is a North Central Edoid SVO language from the Niger-Congo family (Bendor-Samuel and Hartell 1989; Elugbe 1989). Turkish is an SOV language of the Turkic family (Sebüktekin 1971; Kornfilt 2004). In this language, vowel harmony is root rightwards (Baković 2000).

⁷ See also Di Sciullo and Fong (2005) on the bipartite structure of *wh-* and *th-* words in English and Romance languages, as well as Di Sciullo and Banksira (2009) on the bipartite structure of *wh-* words in Ethiopian Semitic languages.

- | | |
|---|---|
| b. gbà nò nè
tie repeatedly up
‘finished tying’ | ‘when’
e. bu-rada
‘here’
f. şu-rada
‘there’ |
|---|---|

Moreover, these facts would not follow straightforwardly if the Head-directionality parameter, in (2) above, taken as a descriptive statement, would be extended under the word-level. While Yekhee is an SVO language, like English, the position of the categorial head in English word structure is generally final, while it is generally initial position in Yekhee. The setting of the Head-directionality parameter would then have to be domain dependent, which would weaken the principled account for the variation.

In contrast, the feature-driven approach to variation targets abstract properties of linguistic elements, namely the valued/unvalued features of functional categories. In this approach, language diversity follows from the feature-valuing operations of the grammar, and is restricted by external factors reducing complexity. Assuming that the structure of words is binary-branching and is derived by a general operation such as Merge, which recursively combines affixes and roots, this leaves only two possibilities: an affix either precedes or follows a root. Factors reducing complexity are also at play in morphological variation.

13.1.4 *Factors reducing derivational complexity*

Di Sciullo (2004, 2005) proposes that cross-linguistic variation in the linearization of affixes with respect to roots is feature driven and proceeds by phases in the morpho-phonological component (PF). The difference between Yekhee and Turkish is reduced to the presence or absence of an unvalued feature at the edge (Specifier) of a morphological phase. This is motivated in Yekhee, where each affix is associated with a tone. A valued tone feature is located at the edge of a morphological phase, and the affix heading the phase is not ordered to the right of the root, as in (10). In Turkish, there is an unvalued feature at the edge of a morphological phase, as in (11), and feature valuing leads to the ordering of the affix to the right of the root.⁸

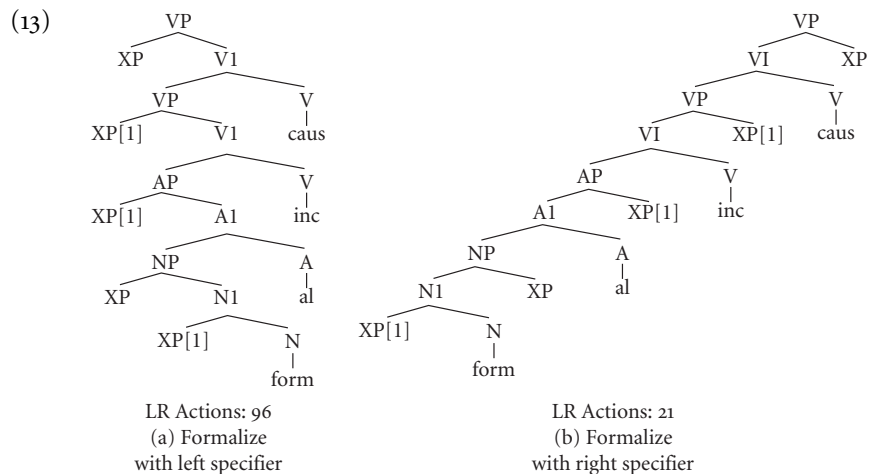
(10) [[F] [af [root]]]

(11) [[uF] [af [root]]]

⁸ Different implementations are available for affix–root linearization. One option is to derive the PF orderings by applying Internal Merge in the derivation to PF. Another option is to flip the constituents. See Di Sciullo (1999, 2005) for discussion, as well as Williams (2003) and Wurmbrand (2003) on the post-syntactic Flip operation.

Thus, according to this approach, the variation in the linearization of affixes takes place in the PF component, and it relies on the properties of the computational system, feature-valuing and derivation-by-phase. The phase is part of the factors reducing derivational complexity (Uriagereka 1999; Chomsky 2001, 2005, 2008; Legate 2003; Boeckx and Grohmann 2004; Gallego 2006; Grohmann 2009). It does so by reducing the search space for the application of the operations of FL.

Complexity-reducing mechanisms related to the presence or absence of PF features at the edge of morphological phases are needed independently for linearization. The computational results reported in Di Sciullo and Fong (2005) using the LR Shift-reduce parsing framework indicate that derivational complexity increases in parsing complex words, such as *formalize*, (12), where multiple PF-empty edge (Specifier) positions are located to the left of the head, instead of to the right.



The parse trees in (13) shows that there is a considerable difference both in terms of the number of LR actions performed and the stack depth required to process an example like *formalize*, analyzed as *form-al-i(z)-e*. The simple explanation is that the LR machine has to be able to predict an arbitrary number of empty argument positions before it can shift or “read” the first item, namely *form*, in (13a). Contrast this with the situation in (13b), where Specifiers are generated on the right side only. Here, the LR machine needs only to generate a single empty argument position before a shift can take place. Hence only 21 actions and a stack depth of two are required in this case, compared to 96 and a stack depth of five in (14a). The following table compares left and right Specifiers for a variety of examples:

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(14)

Word	LR actions		
	Items	Left Specifier	Right Specifier
form	1	8	6
read-able	2	19	11
simple(e)-i(f)-y	3	47	16
form-al-i(z)-e	4	96	21
form-al-i(z)-(e) able	5	172	26

These results suggest that factors reducing derivational complexity do play a role in the derivation of morphological expressions. Moreover, the computational constraints carry over to morphological structures and limit the variation. While strong suffixing languages such as Turkish allow for several suffixes to linearize to the right of the root, the number of prefixes that linearize to the left is more limited in strong prefixing languages such as Yekhee.

13.1.5 Summary

According to the feature-driven approach to language variation, language diversity is the consequence of the choice of a valued or unvalued functional feature, asymmetric feature-valuing, and factors reducing derivational complexity. In this perspective, the setting of a parameter requires exposure to linguistic data, but the derivation of linguistic diversity relies on the properties made available by the faculty of language and independent principles reducing derivational complexity.

Thus, from a biolinguistic perspective, our understanding of the dynamics of HOX genes, and in particular the asymmetric logic of the biological triggers, may lead to a better understanding of linguistic parameters and the role of asymmetric Merge and feature-valuing in the derivation of linguistic diversity. Linguistic variation can be linked to what we know of variation in biology, and it is likely that a further understanding of the role of asymmetry in the dynamics of HOX genes will deepen our understanding of language variation.

In the next section we relate the directionality of language evolution to the phylogenetic variation in the evolution of animal body plans. The discussion of the role of asymmetry in language evolution and change brings additional support to the hypothesis that asymmetry may very well be a link between variation in language and variation in biology.

In the symmetric stage, there is no left or right difference in the organism (e.g. amoeba). The following—anti-symmetric—stage presents random prominence of the right or the left side of the organism (e.g. fiddler crab). In the last—asymmetric—stage prominence is observed only to the right or left of the organism. The three stages in the evolution and change going from symmetry to asymmetry, through an intermediate anti-symmetric stage, are illustrated in Figure 13.3. This evolutionary sequence covers the phylogenetic variational patterns observed in the dextral/sinistral forms of certain animals and plants, such as the fiddler crab, whose development moves from a symmetric amoeboid stage to an asymmetric one, via an intermediate anti-symmetric stage, where either the organism's left or right side predominates. Because of its simplicity, the binary-switch nature of the left–right asymmetry permits meaningful comparisons among many different organisms.

Phylogenetic analyses of asymmetry variation (fluctuating asymmetry, directional asymmetry), inheritance, and molecular mechanisms reveal unexpected insights into how development evolves. These analyses have clear, yet novel extensions to human language. It is possible to view the natural evolution of bipartite organisms patterns like that of human language, given that

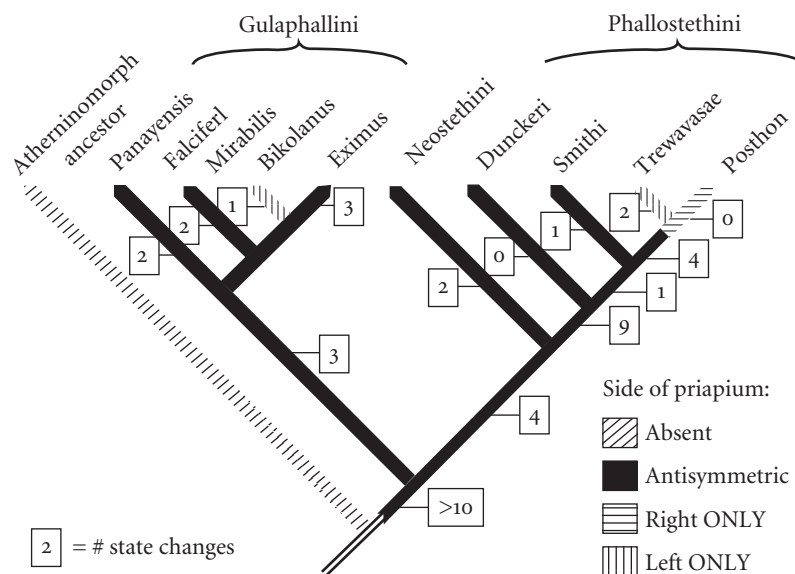
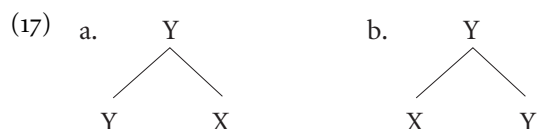


FIGURE 13.3 Phylogenetic variation in the side of the asymmetrical priapium in male phallostethid fishes (after Palmer 1996), illustrating the evolutionary changes in asymmetry stage expected for a post-larval developing trait

language expressions form hierarchical binary branching trees, with right–left asymmetries at each sub–tree.



If this is correct, language evolution can be analyzed in an innovative way via anti-symmetry breaking, identifying phylogenetic patterns of variance in terms of the evolution and changes in the linearization of constituents. However, assuming an emergent view of language (Berwick and Chomsky in this volume; Berwick in this volume) and the hypothesis that asymmetry emerged with language (Di Sciullo 2005), there would be no symmetric stage, like the amoeba stage, in language evolution and variation. Language evolution and change would be reduced to the following two stages:

(18) Anti-symmetry > asymmetry

In fact, language evolution includes stages where two options for the linearization of constituents are available, followed by stages where only one option is available. This directionality is close to the one described above for the evolution of bilateral asymmetric species. The evolutionary dynamics leading to directional asymmetry in phylogenetic patterns of variance may bring further understanding of language evolution and change. In this perspective, I hypothesize that anti-symmetry breaking (fluctuating > directional asymmetry/anti-symmetry > asymmetry) is part of the dynamics of language change. I will point to specific aspects of language acquisition and language change that support this hypothesis.

13.2.1 *Acquisition*

Assuming that the elements of linguistic variation are those that determine the growth of language in the individual (Chomsky 2005, 2007), anti-symmetry breaking is part of language acquisition, as can be observed, for example, in the acquisition of compounds.

New compounds can be coined in any language. Children produce new compound forms quite early, around age 2 or 3 (see Clark and Barron 1988; Nicoladis 2007, among other works), sometimes with meanings that they are unlikely to have heard before, and always without any formal instruction. Interestingly, around 3, English children consistently produce compounds of the type V-N instead of N-V, then they go through an intermediate stage where

both V-N (e.g. *pull-er-wagon*) and N-V (e.g. *wagon-pull-er*) are possible, before they reach a stage where only one of the two options survives (*wagon-pull-er*). This change can be understood as being the consequence of anti-symmetry breaking, since an anti-symmetric stage, where the noun in some case follows and in other cases precedes the verb, precedes an asymmetric stage, where the noun precedes the verb:

(19) V N or N V > N V

While the order of the constituents in compounds is derived by morphological merger and feature-valuing (Di Sciullo 2005, 2009; Roeper 1996), data from language development provide evidence that anti-symmetry breaking is part of the dynamics of language acquisition. Thus, an explanation for these facts can be provided within the biolinguistic program, which asks why-questions and seeks possible answers in the properties of the evolution and the development of biological organisms, which are, like human language, objects of the natural world.

13.2.2 Change in the linearization of the genitive DPs

According to the anti-symmetry breaking hypothesis, language evolution includes stages where a given constituent may be linearized to the right or to the left of a head (anti-symmetric stage), whereas in a latter stage of that language this option is no longer available (asymmetric stage). The historical change in the linearization of syntactic constituents brings support to this hypothesis. This can be illustrated by the change in the position of DPs within the nominal domain in the history of Greek (Stávrou and Terzi 2005; Horrocks 1997; Tsimpli 1995). If an anti-symmetric stage precedes an asymmetric one, we expect to find DPs to be linearized to the left or to the right of a nominal head in earlier stages of Greek, whereas only one option would survive in later stages. This is indeed the case for genitive DPs (GentHEME) in Modern Greek (Lascaratou 1998; Alexiadou 1999). Alexiadou (2002) discusses the change in the word-order patterns of Greek nominalizations that took place from the Classical Greek (CG) period to the Modern Greek (MG) period. In MG nominals, agents can only be introduced in the form of a prepositional phrase following the head noun, while they could appear pre-nominally bearing the genitive case in CG. Crucially for our purpose, the theme genitive—that is the object genitive—could precede or follow the head nominal in CG, (20), whereas it immediately follows the head in MG, (21), as described in Alexiadou 2002: 91).

- (20) a. Det-(Gen_{agent})-N_{process}-G_{entheme} (CG)
 b. Det-Gen_{theme}-N_{process}
- (21) Det-N_{process}-Gen_{theme} (PP_{agent}) (MG)

Alexiadou attributes the unavailability of prenominal genitive DPs in MG to the properties of the nominal functional projection within process nominals and to other related changes in the nominal system of Greek. This change in the linearization of DPs shows that in the evolution of Greek an anti-symmetric stage where the genitive object DPs may precede or follow a nominal head, preceded an asymmetric stage, where only post-nominal genitive objects are possible. The difference in the linearization of genitive object DPs in the history of Greek can be analyzed as following from a change in the value of functional features, with the consequent effects of the asymmetric feature-valuing mechanism. The question arises why anti-symmetry breaking is observed and its possible relatedness to anti-symmetry breaking in the natural world. In particular, the phylogenetic patterns of variance discussed by Palmer—may bring new light to our understanding of diachronic changes.

Furthermore, anti-symmetry breaking may also be part of the factors reducing derivational complexity, which would eliminate through historical evolution and change choice points for linearization—in this specific case, the choice of linearizing a DP to the right or to the left of a nominal head. The complexity brought about by two possible linearizations of a genitive DP in CG, anti-symmetric linearization, is reduced in MG to asymmetric linearization only. Anti-symmetry breaking can be viewed as part of the factors reducing the complexity brought about by a choice point in the derivation. In this perspective, anti-symmetry breaking would not drive the derivation, as in Moro (2000), but would be part of what Chomsky (2005) calls “the third factor” in the language design, computational factors external to the FL, which contribute to make language tractable for the external systems.

13.2.3 *Change in the linearization of possessive clitics*

The change in the linearization of possessive clitics in MG and Greek dialects is another example of the anti-symmetry > asymmetry historical pattern of variance and of the role of the anti-symmetry breaking mechanism in language change.

In MG, the weak forms of the genitive case of personal pronouns serve as possessive pronouns (Mackridge 1985). Possessive clitics manifest person and

number distinctions (sing.: mu_1 , Su_2 , $tu_{3\text{MASC,NEUT}}$, $tis_{3\text{FEM}}$; plural: mas_1 , sas_2 , tus_3), have gender morphology only at the third person, and show no agreement in phi-features with the possessed object. Modern Greek also uses complex possessive expressions with an emphatic possessive adjective *diko* ‘own’ (Alexiadou 2005). The possessive adjective agrees in phi features with the possessed object. Modern Greek has no other possessive adjective than *diko*, contrary to CG, which does have possessive adjectives preceding and following nominal heads. In MG, the basic position of possessive clitics is post-nominal, as in (22a), from Alexiadou and Stávrou (2000). However, possessive clitics may occupy the pre-nominal position in the presence of an adjective, (23), and must occupy this position in the presence of *diko*, (24).

- (22) Modern Greek
- | | |
|---|---|
| a. to vivlio-tu
the book-his
‘his book’ | b. to vivlio tu fititi
the book GEN STUDENT. GEN
‘the student’s book’ |
|---|---|
- (23) Modern Greek
- | | |
|--|--|
| a. to oreo vivlio-mu
the nice book-my
‘my nice book’ | b. to oreo-mu vivlio
the nice-my book
‘my nice book’ |
|--|--|
- (24) Modern Greek
- | | |
|--|---|
| a. to diko-mu vivlio
the own-my book
‘my own book’ | b. *to diko vivlio-mu
the own book my
‘my own book’ |
|--|---|

Interestingly, in Grico (GR), a Modern Greek dialect spoken in southern Italy,¹⁰ while the weak forms of the genitive case of personal pronouns also serve as possessive pronouns, as in MG, possessive clitics are only post-nominal, with or without the presence of the emphatic adjective *diko*; see (25) and (26).¹¹

- (25) Grico
- | | |
|---|---|
| a. o spiti-mu
the house my
‘my house’ | c. o spiti-tu
the house his
‘his house’ |
| b. *o mu-spiti | d. *o tu-spiti |

¹⁰ Two small Grico-speaking communities survive today in the Italian regions of Calabria (east of the province of Reggio Calabria) and Puglia (peninsula of Salento and Aspromonte).

¹¹ I thank Dimitra Melissaropoulou for the GR data and Natalia Pavlou for the CyG data.

- (26) Grico
- | | |
|--|---|
| a. o spiti diko-mmu
the house mine-my
‘my own house’ | c. o spiti diko-ttu
the house his-his
‘his own house’ |
| b. *o diko-mmu spiti | d. *o diko-ttu spiti |

The variation in the linearization of possessive clitics in MG and in GR can be analyzed as the presence or the absence of [uF] in the feature specification of functional heads within the DP, which minimally includes the projections in (27). Possessive clitics would be generated in FPPoss; feature-driven Internal Merge would apply in the derivation of the different orders. Alternatively, if the ordering of clitics is post-syntactic, and more generally if syntax (narrow syntax) is immune to variation, differences in the linearization of possessive clitics can be seen as being triggered by unvalued morpho-phonological features in the PF derivation.

- (27) [DP [AP [FPPoss [NP]]]]

I will not discuss these alternatives here, but rather focus on the fact that the difference in the linearization of possessive clitics in MG and in GR can be further understood in a bilingualistic perspective, as another case of anti-symmetry breaking, and anti-symmetry > asymmetry pattern of variance. Dialects include remnants of ancient languages, and they nevertheless provide novel developments of the languages. Thus, a dialect may preserve the anti-symmetric stage of the more ancient language from which it evolved, and it may also evolve to an asymmetric stage. However, once the asymmetric stage is reached, the anti-symmetry breaking hypothesis predicts that a language may no longer evolve into the preceding anti-symmetric stage.

Thus, in GR, the possessive pronoun follows the head noun and may not precede it, whether the emphatic adjective *diko* is part of the derivation or not. A similar situation is observed in Cypriot Greek (CyG), a MG dialect spoken in Cyprus. In CyG, bare possessive clitics are post-nominal only (see 28a, b), contrary to MG (23). However, when possession is expressed with emphatic *diko*, the possessive clitic is pre-nominal only, (29), as is the case in MG (24).

- (28) Cypriot Greek
- | | |
|--|--|
| a. to spiti-mu
the house-my
‘my house’
*to mu-spiti | b. to spiti-tu
the house-his
‘his house’
*to tu-spiri |
|--|--|

- (29) Cypriot Greek
- | | |
|----------------------|----------------------|
| a. to diko-mu spiti | c. to diko-tu spiti |
| the own-my house | the own-his house |
| ‘my own house’ | ‘his own house’ |
| b. *to spiti diko-mu | d. *to spiti diko-tu |

Anti-symmetric linearization is thus observed in MG with bare possessive clitics, which may be linearized to the right or to the left of a nominal head. However, only directional asymmetric linearization is observed in MG dialects, GR and CyG, where bare possessive clitics may only linearize to the right of a nominal head.

Further evidence for anti-symmetry breaking and the anti-symmetry > asymmetry pattern of variance in language change comes from the difference in the linearization of possessive clitics in Italian and dialects spoken in Abruzzo. While possessive adjectives may be linearized to the right or to the left of a noun in Italian, (see 30),¹² only directional asymmetric linearization is observed in certain western and eastern dialects of Italian, where the possessive clitic may follow the noun, but may not precede it. This is the case for Marcilian varieties (MA) spoken in western Abruzzo (31), (32) (data from Pescasseroli (Saltarelli 2008)),¹³ as well as for Fallese (FA) and Ariellese (AR), two varieties of Eastern Abruzzese, (29), (30).

- (30) Italian
- | | |
|-------------------|-------------------|
| a. la sorella mia | b. la mia sorella |
| the sister my | the my sister |
| ‘my sister’ | ‘my sister’ |
- (31) Marcilian
- | | |
|-------------------|----------------------|
| a. sorda-me | c. la sore maya |
| sister-my | the sister mine |
| ‘my sister’ | ‘the sister of mine’ |
| b. *(la) me sorda | d. *(la) maya sore |
- (32) Ariellese
- | | |
|----------------|----------------|
| a. la casa-mè | c. la casa-mé |
| the house-my | the house-my |
| ‘my house’ | ‘my house’ |
| b. *la mè casa | d. *la mé casa |

¹² This is also the case in the Virgilian tradition, e.g. *quoniam sic videtur filii parente suos agnoscere ... ille petit ut suos parentes ostendisset*. (Ziolkowski and Putnam 2008: 686).

¹³ Possessive clitics are morphologically restricted to personal pronouns; they are prosodically enclitics (Rohlf 1966; Maiden and Parry 1997).

The difference in the linearization of possessive clitics differentiating MG and IT from their dialectal variants, GR and CyG in the case of MG, FA, and AR in the case of IT, can be derived by asymmetric feature-valuing and is yet another example of anti-symmetry breaking where an anti-symmetric stage precedes an asymmetric stage.

13.2.4 *Summary*

Language change is directional—why is this the case? The fluctuating-directional asymmetry characterizing the variation in the evolution of the shape of bipartite asymmetric animals and plants brings new light to the directionality of language evolution and change. The trajectory of the change in the linearization of linguistic constituents from an anti-symmetric stage, where linearization may take place either to the right or to the left of a head, to an asymmetric stage, where only one option survives, is predicted not to be invertible.

Evidence from language acquisition as well as from language change in the linearization of linguistic constituents brings support to the anti-symmetry-breaking hypothesis. These findings bring language variation and change closer to variation and evolution in biology. Moreover, anti-symmetry breaking can be thought of as being part of the factors reducing the complexity brought about by the presence of choice points in the derivations.

13.3 **Conclusion and a Further Question**

In this Chapter I explored some relations between variation in language and variation in biology. Because language is grounded in biology and variation is central in biology, the understanding of biological variation is likely to shed light on linguistic diversity. First, I discussed the notion of parameter in linguistic theory and in biology, and suggested that they share asymmetric dynamical properties. Secondly, I considered the change in the linearization of linguistic constituents from the perspective of patterns of phylogenetic variation identified in evolutionary developmental biology. I suggested that the directionality of language change in the linearization of constituents observable in language change through time, as well as in the course of language acquisition, could be further understood as an effect of anti-symmetry breaking, which in turn could very well be part of the factors reducing complexity.

Why should asymmetry be central? It might be the case that asymmetry ensures stability to the FL, when symmetry is brought about by experience. This does not discard the possibility that symmetry could be available in

communication systems in place before the emergence of language. In biology, an asymmetric system might arise from a symmetric precursor, and if this asymmetric system is more robust, it will be genetically fixed in the genome. The stability brought about by asymmetric relations can be seen as a core element in the emergence and evolution of the FL. The biolinguistic approach to language variation opens the possibility to go beyond explanatory adequacy, and to ask why parametric variation is derived in the FL via asymmetric relations, why anti-symmetry breaking is part of language change, and to relate via asymmetry variation in language to variation in biology. Further understanding of diversity in language and in biology will contribute to the understanding of language as a biological object and of language variation as an instance of variation in biology.