



# A Virtue Made of Necessity: Is the Increasing Hierarchical Complexity of Sexual Clades an Inevitable Outcome of Their Declining (Macro) evolutionary Potential?

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## Abstract

The increasing maximal hierarchical complexity of organisms is one of the best-supported macroevolutionary trends. The nature and causes of this trend, as well as several accompanying macroevolutionary phenomena are, however, still unclear. In this theoretical article, we propose that the cause of this trend could be the increasing pressure of species selection, which results from the gradual decrease of (macro)evolutionary potential (i.e. the probability of producing major evolutionary innovations). As follows from the Theory of Frozen Evolution, this process is an inevitable consequence of the sorting of genes, traits, and their integrated groups (modules) based on their contextually dependent stability. In turn, this causes effectively unchangeable elements of genetic architecture to accumulate during the existence of evolutionary lineages. Although (macro)evolutionary potential can be partially restored by several processes, a profound restoration of (macro)evolutionary potential is probably possible only by means of a transition to a higher level of hierarchical complexity. However, the accumulation of contextually more stable elements continues even on this higher level. This leads to the integration of the modular character of composite organisms and a repeated pressure to increase the level of hierarchical complexity. Our model explains all components of McShea's "Evolutionary Syndrome," i.e. the trend of increasing the hierarchical complexity of organisms, the growth of variability among elements on the immediately lower level, and their gradual machinification. This pattern should be characteristic of sexual eukaryotes and especially their complex representatives. Our model also sheds new light on several related macroevolutionary phenomena, such as the gradual acceleration of the trend or the striking difference between pre-Neoproterozoic and Phanerozoic evolution.

**Keywords** Evolvability · (Macro)evolutionary potential · Evolutionary trends · Hierarchical complexity · Frozen evolution theory · Frozen plasticity theory · Stability-based sorting

## Introduction: The Trend of Increasing Hierarchical Complexity

An evolutionary trend is usually understood as a "persistent, directional change in a character state, or set of character states, resulting in a significant change through time" (McNamara 1990, 2006). More broadly, they constitute

"identifiable patterns in which the overall evolution of a trait occurs in a given direction within a group for a prolonged period of time" (Gregory 2008). The most interesting global evolutionary trend—at least from the macroevolutionary point of view—is probably the increasing organismal complexity in the history of life on Earth. Dozens of theoretical concepts aim to explain this pattern, either as a driven or a passive trend (these concepts are extensively summarised, e.g. in Novák 1982; McShea 1991, 1994, 2001a, b; Pettersson 1996; Michod 2000; Jablonka and Lamb 2006; Buss 2014; or; Corning and Szathmari 2015). Despite all this effort, there is no agreement on the nature, or even existence of this trend. The major source of confusion is the difficult conceptualisation of this trend that results from an unclear definition of the term complexity. Indeed, complexity could be understood in several different ways (see, e.g. McShea

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1991, 1996; Carroll 2001; Mitchell 2009). For example, it can mean morphological complexity on the level of organisms or their parts (see, e.g. Bonner 1988, 1998; McShea 1993, 1996; Valentine et al. 1994; Carroll 2001). In another way, it can be defined as the complexity of genetic information (i.e. the number and complexity of genes or proteins, eventually interactions of these entities or some of their classes, such as developmental genes) (Adami et al. 2000; Carroll 2001; Rasskin-Gutman and Esteve-Altava 2008), but also, for example, the complexity of behaviour (McShea 1991).

The trend of increasing morphological complexity has been tested most often. At least in some evolutionary lineages, its maximum was proven to have been growing for a considerable time (see, e.g. McShea 1996, 2001a, b; Marcot and McShea 2007). Therefore, there is probably a relatively frequent trend in the growth of the maximal level of this factor. However, it is not clear whether this trend is driven or passive. Moreover, it is not present in all groups, and certain evolutionary lineages may even exhibit a directly opposite trend (McShea 1996, 2001a, b; Marcot and McShea 2007). Testing the general nature of this trend is even more difficult (McShea 1996). In spite of that, it was well supported that a certain type of morphological complexity—hierarchical complexity—increases even globally (McShea 1996, 2001a, b, 2015; McShea and Changizi 2003; Marcot and McShea 2007). This trend can be described as the increase in the hierarchical level of organisms by the means of their modular builds, i.e. nesting of lower-level entities within higher-level individuals (McShea 1996, 2001a, b; McShea and Changizi 2003; Marcot and McShea 2007). The whole process is also called the growth of vertical complexity (Sterelny 1999).

Hierarchical increasing of organismal complexity was widely commented upon by a number of authors, as was summarised, e.g. by Novák (1982), McShea (1991, 1994, 2001a, b), Pettersson (1996), Michod (2000), Jablonka and Lamb (2006), Marcot and McShea (2007), Buss (2014), or Corning and Szathmary (2015). One characteristic evolutionary motive that is common in all transitions to a higher level of organismal complexity is the combination of lower-level entities into a higher-level individual followed by differentiation and specialisation of formerly independent parts and their integration. This is usually followed by a transition to an even higher hierarchical level of organisation after some time (McShea 2001a). Moreover, the trend of increasing hierarchical complexity is seemingly associated with several other macroevolutionary phenomena. The frequency of transitions to a higher level probably accelerates in time and with the increasing hierarchical level of complexity (McShea 2001a, b, 2015; McShea and Changizi 2003). This acceleration is remarkable, and it is not probable that it would be an artifact. Another major question

is why hierarchical complexity started to increase more markedly as late as in the Neoproterozoic (about 1.2 billion years ago) and especially at the beginning of Phanerozoic (about 540 million years ago), even though life on Earth has existed for about 4 billion years (Carroll 2001; McShea and Changizi 2003; McShea 2015). It also remains an open question as to why the trend is more pronounced in sexual, and especially complex multicellular, organisms (Flegr 2015; Toman and Flegr 2017b, 2018). On top of that, as a consequence of the transition to a higher level, we see an increase in the number of parts and differentiation among them on the immediately lower hierarchical level. However, this pattern is inseparably associated with strong a decrease in complexity, streamlining and simplification on this and lower levels (machinification) (Schank and Wimsatt 1986; McShea 2002, 2015; McShea and Anderson 2005). These two phenomena are associated with increasing hierarchical complexity so tightly that McShea (2015) termed the whole trinity “Evolutionary Syndrome,” a prominent macroevolutionary pattern that asks for a common explanation. At the same time, this explanation need not be trivial (see McShea 2005).

In this theoretical paper, we propose that that the trend of increasing hierarchical complexity may be caused by a growing pressure of effectively irreversible decreasing of (macro)evolutionary potential (i.e. the probability of producing major evolutionary innovations) that is probably characteristic of sexual organisms (Toman and Flegr 2018). This is a direct consequence of the accumulation of effectively unchangeable genes, traits and their integrated groups (modules) in the evolution of sexual lineages that is postulated by Frozen Evolution Theory (FET) (Flegr 2008, 2010, 2013, 2015), or, more generally, how follows from the principle of stability-based sorting (SBS) (Toman and Flegr 2017b). In other words, we propose that the trend of increasing hierarchical complexity in the history of life, as well as other points of McShea’s (2015) “Evolutionary Syndrome” and associated macroevolutionary phenomena, might be by-products of species selection on the restoration of (macro)evolutionary potential.

## Results and Discussion: Macroevolutionary Freezing and Restoring of the (Macro)evolutionary Potential

### Macroevolutionary Freezing

Stability-based sorting (SBS) is a universally recognised but rarely studied process that affects all entities on all levels of historic (evolving *s.l.*) systems (Toman and Flegr 2017b). Whether these are systems consisting of material or immaterial, living or non-living entities, as long as they undergo historical development, they accumulate contextually more

stable (persistent) entities and their groups. These entities, over time, predominate in the system. On the other hand, entities that are less stable sooner or later change or perish and disappear from the system. Abstract on the first sight, this is a rather trivial (although fundamentally important) phenomenon. Stable space objects such as planets, stars and galaxies in the history of our Universe, heat more resistant snowflakes in a melting snowdrift, or even more stable memes and their complexes, such as stories, religions, and useful technological processes in human cultural history, all accumulate by SBS (whereas their less stable counterparts disappear). SBS in its strict and usual conception therefore represents sorting based on static stability (the slowest disappearance of entities that constitute the system). It is true that Toman and Flegr (2017b) documented that even natural selection (sorting based on dynamic stability), or the largest difference among the speeds of originating and disappearance of new entities, is in fact a special case of SBS in the systems of entities that reproduce with heredity. However, SBS, in its strict sense, still operates (in parallel with selection) on all levels of systems whose evolution is driven mostly by natural selection.<sup>1</sup>

SBS is a decisive force in evolution and it is capable of completely changing the course of evolution driven by opportunistic natural selection (2017b). One of the examples of this phenomenon, and also one of the most spectacular manifestations of SBS in biological evolution, might be its effect on evolvability, or the (macro)evolutionary potential of evolutionary lineages. As was emphasized by Toman and Flegr (2018), SBS likely plays an important role in the evolution of evolvability. Evolvability is usually defined as “the genome’s ability to produce adaptive variants when acted upon by the genetic system” (Wagner and Altenberg 1996). In simpler words, the ability to evolve in an adaptive way. It can be, however, understood in several inter-related but distinct ways associated with the extent or mode of evolutionary change—from the ability of a population to adaptively and “plastically” respond to selection (Flegr and Ponížil 2018), to the ability of an evolutionary lineage to evolve major evolutionary innovations, i.e. (macro)evolutionary potential (see, e.g. Pigliucci 2008; Toman and Flegr 2018). On longer timescales, SBS decreases (macro)evolutionary potential in evolutionary lineages, which leads to a decreasing intraspecific and interspecific disparity during their existence. Later in this paper, we will argue that this trend may apply more strongly to sexual lineages.

<sup>1</sup> Similar or comparable claims were made also by several other theoretical biologists (see, e.g. Bouchard 2011; Pross 2012; Shcherbakov 2012; Bourrat 2014; Doolittle 2014). For details on SBS, the aforementioned concepts, and their mutual relationships, see Toman and Flegr (2017b).

We have already demonstrated elsewhere (Flegr 2008, 2010, 2013, 2015; Toman and Flegr 2017b, 2018) that the gradual reduction of (macro)evolutionary potential, intraspecific and interspecific disparity are real trends, which have been documented in various eukaryotic clades by a long series of paleontological and paleobiological observations (see also “General Discussion”). The cause of this “macroevolutionary freezing” is probably two complementary manifestations of SBS (Toman and Flegr 2017b, 2018) described by previously postulated FET (Flegr 2008, 2010, 2013, 2015).

The first of these two processes follows from the fact that various organismal traits exhibit varying degree of evolvability, which is based on the specificity of their genotype-phenotype mapping. This genetic architecture, i.e. a sort of transducer between genotype and phenotype, and, consequently, the evolvability of traits may change during evolution. It follows from the principle of SBS that more stable traits with limited evolvability and their groups will accumulate during the existence of evolutionary lineages. The character and common features of macroevolutionary freezing traits were described elsewhere in considerable detail (Toman and Flegr 2018). In this place, we can summarise that macroevolutionary freezing traits are generally coded by a high number of strongly integrated genes. Such genes are usually also essential for multiple processes, deployed in the early stages of individual development and phylogenetically older. These are, for example, the genes that govern basic metabolic pathways in the cell, mitosis, meiosis, or early stages of the development of multicellular body (e.g. polarization of body axis, regionalization etc.) (Riedl 1977, 1978; Schank and Wimsatt 1986; Galis and Metz 2001; Wimsatt and Schank 2004; Wimsatt 2013, 2015). As a result, evolvability should be (at least theoretically) irreversibly decreasing in all evolutionary lineages (Flegr 2008, 2010, 2013, 2015; Shcherbakov 2012; Toman and Flegr 2017b, 2018).<sup>2</sup>

The idea that the ultimate outcome of biological evolution is stasis, or, more plainly, that evolution is going to end, sounds quite radical (although it was proposed, e.g. by Shcherbakov 2012). Nevertheless, it is clear that the whole process is not so simple (see, e.g. Toman and Flegr 2018). In the first place, there are some traits coded by one gene or a small number of genes (e.g. hair colour) that are highly evolvable (not very burdened in the Riedl’s 1977, 1978, sense) and considerably resistant to evolutionary freezing.

<sup>2</sup> Note that major innovations, including meta-adaptations that increase variability (e.g. sexual reproduction), may still originate, albeit with a very low probability. Moreover, smaller adaptations that may later become important exaptations (preadaptations) still originate with considerable probability (at least initially, see the section “Transition to a Higher Level of Complexity” and Toman and Flegr 2018).

More importantly, evolvability in general probably does not simply decrease, but also gets to some extent optimised during its evolution. To a considerable degree, genetic architecture evolves to most effectively reflect the structure of a phenotype and the environment with all its selective pressures (Riedl 1977, 1978; Wagner and Altenberg 1996; Kirschner and Gerhart 1998; Turney 1999; Pigliucci 2008). On the one hand, this reduces the risk of lethality or deleteriousness of mutations, or even increases the probability that a mutation will be adaptive. This reduces the number of mutations necessary to produce an adaptive phenotype. On the other hand, the same process strongly constrains the origin of major evolutionary innovations. By accumulating constraints that channel the depth and character of further possible evolutionary reactions, the evolution of evolvability optimises microevolution at the expense of macroevolution. In other words, evolvability on the lower level (in the sense of the ability to respond to selective pressures of natural environment) increases at the cost of decreasing evolvability on the higher level (in the sense of the (macro)evolutionary potential, or the ability to produce major evolutionary innovations) (Wagner and Altenberg 1996; Pigliucci 2008; Toman and Flegr 2018).

This sounds rather abstract, but it is similar to the way that we adapt in our lives. For example, after moving to a new city (evolution of evolvability and learning are, in fact, intriguingly similar phenomena, see, e.g. Watson and Szathmari 2016). At first, we are totally unaware about the layout of the city. We explore new routes every day with a high probability of experiencing something new—discovering a new shop, making a new friend, finding whole new neighbourhood, driving through a dangerous road crossing, or even getting stabbed in a back alley. In time, we learn our routines. Sometimes we do something “new”, but this is usually only iteration of something we are already used to doing (i.e. visiting a new shopping centre). This makes us more effective in daily life, more easily able to adapt to “new” but familiar things, and much less likely to experience any inconvenient “adventures”. However, it also reduces the probability of finding or experiencing something genuinely unexpected.

It seems that the most common way that organisms optimise their evolvability is by structuring further unchangeable (or only narrowly changeable) natural groups of genes with a closely related influence on phenotype into internally largely unchangeable quasi-independent modules. Such modules are characterised by strong pleiotropic links within the module and weaker linking in relation to its surroundings. Therefore, these (developmental, morphological or functional) modules can be duplicated in evolution. The duplicates can be individually regulated and deployed (to a considerable degree) independently in different settings, i.e. on different locations of the body or at different developmental phases

(Simon 1962; Lewontin 1978; Schank and Wimsatt 1986; Bonner 1988; Wagner and Altenberg 1996; McShea 2000; Schlosser 2002, 2004; Schlosser and Wagner 2004; Callebaut and Rasskin-Gutman 2005; Melo et al. 2016). This is corroborated by the fact that a large number of developmental genes, their modules, and signalling pathways are shared in nearly identical state—even among phylogenetically very distant lineages. Schlosser (2004), for example, stresses this evolutionary-developmental pattern and lists a broad array of gene regulatory (transcriptional regulation), signalling (e.g. hedgehog, TGF $\beta$ , Wnt, receptor tyrosine kinase, or Notch pathways), or positional (e.g. *Hox* or *Pax* genes) modules that are shared among large groups of metazoans. Evolution based on the combination and regulation of semi-independent modules is sometimes compared to playing with a Lego building kit. Using relatively few types of essentially unchangeable modules, it enables construction of extremely variable outcomes.

However, even organismal modularity cannot stop macroevolutionary freezing in the long term. SBS acts on all levels. Therefore, it causes macroevolutionary frozen elements (in this case higher order integrated modules consisting of the genes and modules of the lower level) to accumulate even on the higher level of the modular organism. On this level, the process of macroevolutionary freezing is expected to manifest as a gradual specialization and integration of the initially modular organismal build. An excellent macroevolutionary example of this process is the evolution of arthropod appendages. A series of identical modules (that probably originated by multiple copying of the same module) differentially specialized in various arthropod groups (see, e.g. Shubin et al. 1997). Some of them gained locomotory function, others serve for reproduction, etc. Different groups of these modules integrated (e.g. because they serve for a common function) and formed evolutionary modules of a higher level (see, e.g. Schlosser 2004). These modules of a higher order are bound internally by numerous pleiotropic interactions, they share morphogens that specify their development (e.g. *Hox* genes), etc. This renders them less evolvable internally. For example, it is not easy to change the right leg without changing the left one and compromising the locomotory function. An extreme example of this is when several initially (semi)independent appendages in the anterior part of the body became highly integrated and formed mouthparts (see, e.g. Hughes and Kaufman 2002, or; Auman and Chipman 2017 on genetics of arthropod development). Note that similar integration may proceed indefinitely. It may proceed because it is adaptive, but also for purely random reasons—for example, when a new selectively neutral interconnection among modules arise. As a general consequence of this process, modularly structured organisms are expected to decrease their (macro)evolutionary potential in the long term as well (Toman and Flegr 2018).

It can be argued that lineages maintaining relatively high (macro)evolutionary potential are initially advantageous in species selection. This makes them less prone to extinction when the conditions change and more likely to split off into significantly distinct daughter species that would be able to colonize new areas of ecophenotypic space, or even undergo adaptive radiations under such conditions. It would make them displace more “frozen” lineages and ultimately stop macroevolutionary freezing on a global level. However, species selection based on the highest remaining (macro)evolutionary potential probably cannot stop macroevolutionary freezing. The reason is that SBS proceeds in all lineages simultaneously and most changes that reduce (macro)evolutionary potential probably remain under the resolution of species selection.

As we outlined above, different genes, modules and traits are differentially evolvable. Some of them may change easily in evolution. From time to time, however, integrated units that cannot be easily changed emerge. The first problem (from the viewpoint of adaptive evolution) is that such evolutionary frozen units may be advantageous in the individual selection. This can be because they are adaptive, and because they are not easily evolvable. (It was proven that the evolvability of a trait correlates with its developmental robustness and that developmental robustness might be highly advantageous in the individual selection, see, e.g. Pavlicev and Wagner 2012). In case the frozen elements gravely reduced the evolvability of a species, they would probably be easily eliminated by species selection. This might be the case of some uniform taxa with low phenotypic disparity and species diversity, such as modern lungfish (Dipnoi) (Lloyd et al. 2012). However, most of the macroevolutionary frozen units probably reduce only one aspect of evolvability—the (macro)evolutionary potential of evolutionary lineages. They likely do it very moderately (for example, binding together the development of eyes and pigment patches on *Heliconius* butterfly wings by co-option of the eye selector gene *optix*, see Monteiro 2012). Any individual advantage stemming from their presence would therefore trump any long-term disadvantage stemming from the reduction of (macro)evolutionary potential (because individual selection is stronger than species selection, see Williams 1966). The second (and more important) problem, is that most of the macroevolutionary frozen units probably appear selectively neutral in the short term under most circumstances (birds, for example, seem morphologically rather constrained but reached immense diversity, see, e.g., Dececchi and Larsson 2013). Therefore, they accumulate in the history of evolutionary lineages purely based on their stability. Whereas other possible configurations change constantly, macroevolutionary frozen units persist. In other words, minor decreases of (macro)evolutionary potential probably remain (especially in sexual eukaryotic organisms, as will be shown later) under

the resolution of species selection, and gradually accumulate (Toman and Flegr 2018).

The decreasing of the (macro)evolutionary potential may, in fact, be a process similar to the accumulation of slightly deleterious mutations by the principle of Muller’s ratchet in realistically sized populations of asexual species (Toman and Flegr 2018). Muller’s ratchet cannot be easily stopped in finite populations because most of the mildly deleterious mutations remain under the resolution of individual selection and new mutations appear in all individuals (Muller 1964). Analogically, our “macroevolutionary ratchet” cannot be stopped because most of the macroevolutionary frozen elements remain under the resolution of species selection and various macroevolutionary frozen elements originate in all lineages simultaneously.<sup>3</sup> It has been proven that the accumulation of deleterious mutations may lead to a considerable decrease of fitness, or even a complete non-viability of the affected population (Chao 1990). It is, therefore, conceivable that the accumulation of macroevolutionary frozen elements may lead to a comparably severe decrease in (macro)evolutionary potential.

To sum up the previous section, the process of macroevolutionary freezing seems to be effectively irreversible under normal conditions (later in the paper, we will note several specific ways that evolutionary lineages can avoid decreasing their (macro)evolutionary potential or even restore it) and continue even on the higher level of whole genetic modules.

The second SBS-driven process that may cause an irreversible decrease of (macro)evolutionary potential brings us from the field of macroevolution and evolutionary developmental biology to the realm of microevolution and population genetics. This process is based on the SBS-driven accumulation of alleles and their groups, which are kept in stable frequency in the gene pool of a species by some form of the frequency-dependent selection. When the negative dependence of fitness of a particular allele on the frequency of another allele (of the same or another gene) is steep enough, the allele cannot be fixed or eliminated by positive selection. Alleles with these properties probably originate by mutagenesis in relatively low frequency. However, they continuously accumulate in the populations via the process of SBS. Due to the complex genetic architecture of modern organisms (namely due to pleiotropy, i.e. the effect of one gene on many traits, and epistasis, i.e. the effects of many genes on the same trait), even a small number of alleles with a frequency dependent effect on fitness may stabilise

<sup>3</sup> The problem of Muller’s ratchet has been heavily studied, pointing especially to the importance of the form and strength of epistasis among slightly deleterious mutations. Mutual interactions among freezing genes, modules and traits, as well as their consequences for evolvability in general therefore may also be of great importance for the study of the “macroevolutionary ratchet”.

the composition of a whole gene pool, and by this make the population resistant to natural selection of usual strength (Flegr 1998, 2010).

We are limited by the maximal length and scope of this paper, but we can illustrate the nature of these alleles with several brief examples. A recessive *HBB* allele for sickle cell disease is relatively benign in heterozygous condition. On the other hand, it significantly impairs human health in homozygous condition. However, both homozygotes and heterozygotes have a significantly elevated resistance to malaria. Providing protection from one of the most dangerous parasitoses, the frequency of the allele for sickle cell disease elevates in areas with abundant *Plasmodium falciparum*. However, when the frequency of this allele rises too much, a disproportionate fraction of nonviable homozygotes is born. Therefore, it is kept in the polymorphic condition with the frequency of both alleles closely following the risk of the exposure to the parasite. The heterozygous advantage is only one special type of frequency-dependent selection. Other examples are, for example: the presence of colour polymorphisms in prey under predation pressure, the frequency-dependent fitness of various MHC variants under the pressure of parasites and pathogens (see, e.g. Ridley 1994), or the frequency-dependent sexual success of three male morphs of the lizard *Uta stansburiana* (Sinervo and Lively 1996).

As is predicted by the Frozen Plasticity Theory (FPT) (Flegr 1998, 2008, 2010, 2013; Toman and Flegr 2017b, 2018), the evolutionary theory describing the microevolution of sexual species and specific aspects of their adaptive evolution, the effectively irreversible accumulation of polymorphic alleles should be predominantly related to the diploidy of sexual species. In asexual species, the diploidy is not stable, as one of the gene copies in a locus is always inactivated by mutations. On the other hand, many genes can be sustained in the polymorphic state in diploid organisms due to their context-dependent fitness value, heterozygote advantage, and other forms of frequency-dependent selection. According to punctuationalist evolutionary theories formulated by Wright, Mayr, Carson, Templeton, Eldredge, and Flegr (see Flegr 2013), some of these polymorphic alleles may get fixed or eliminated during specific periods of a species' evolution. Under FPT, this is expected to be possible after a major non-selective reduction in population counts followed by a long period of survival in small population dominated by genetic drift and ended by a rapid inflation of the population. (Complicated at first sight, this is in fact a typical situation accompanying successful colonization of a new island and subsequent speciation). In such a situation, a population can start to transiently respond to selection until new alleles with frequency-dependent effects on fitness accumulate in its gene pool. From the viewpoint of (macro)evolutionary potential, it is important that some of

the polymorphic alleles would require such a radical reduction in population counts and/or such long survival at such a low number of individuals that they cannot be fixed or eliminated under any realistic conditions. Therefore, they would only accumulate in the gene pool of the evolutionary lineage and reduce its ability to respond to directional selection.

It should be also noted that Toman and Flegr (2018) have proposed that it is possible that such alleles may act as persistent "crystallization cores" around which modules of functionally interconnected genes can form. Moreover, polymorphism in a large and still growing number of genes that increase the diversity of genetic background may increase the pressure on robusticity of development (Von Dassow and Meir 2004; Wimsatt 2013) and thus further accelerate the accumulation of any (macro)evolutionary frozen elements (Toman and Flegr 2017b, 2018).

Both aforementioned processes proposed to reduce (macro)evolutionary potential were documented in particular studies (summarised, e.g. in Flegr 1998, 2008, 2010, 2013, 2015; Toman and Flegr 2017b, 2018). Whereas irreversibly polymorphic alleles (second process) accumulate almost exclusively in sexual species (see Flegr 2015), more stable elements of genetic architecture (first process) could theoretically accumulate even in the evolution of asexual species. This raises the question as to whether we should expect (macro)evolutionary potential to decrease in all evolutionary lineages, or whether is this trend restricted to sexual clades. Equally important queries can be made as to its possible consequences such as increasing hierarchical complexity. In our opinion, the restriction of the trend to sexual clades is more probable. The reason is that asexual (overwhelmingly prokaryotic) species usually have large populations that are characterised by strong individual selection. Moreover, individual selection is *de facto* analogous to species selection in asexual organisms because each of their members establish his own asexual evolutionary lineage. Consequently, species selection is strong enough in these groups to effectively select lineages with the highest remaining (macro)evolutionary potential and to stop (or at least considerably slow down) macroevolutionary freezing.

If we return to the example with Muller's ratchet, asexual organisms might be in the same position as prokaryotes in the Muller's concept. Prokaryotic populations are large enough for individual selection to detect and eliminate even very slightly deleterious mutations and effectively stop Muller's ratchet. Species selection in (most) asexual organisms might be strong enough to detect and eliminate frozen elements that reduce their (macro)evolutionary potential only very slightly and effectively stop "macroevolutionary ratchet" (Toman and Flegr 2018). Macroevolutionary freezing and the accompanying phenomena thus should be characteristic of eukaryotic sexual organisms and, as we suggested above, it is possible that they are more prominent in

those of their representatives that are endowed with complex multilevel genetic architecture, i.e. especially complex multicellular animals.

### Transition to a Higher Level of Complexity

SBS thus causes further effectively unchangeable components of genetic architecture to accumulate effectively irreversibly (especially) in sexual eukaryotes. Are there any ways out of this “dead end”? One possibility is to organise genetic architecture differently. It has been repeatedly suggested that organisms may be organised on a different (macroevolutionary possibly more perspective) basis than the macroevolutionary freezing modular arrangement. However, empirical studies show that modular organisation completely dominates among complex organisms with elaborate adaptations. This is probably due to the fact that it brings substantial short to medium term natural advantages over other ways of forming and operating organisms (see Carroll 2001; Toman and Flegr 2018).

It follows that, statistically speaking, the (macro)evolutionary potential should only be decreasing in the long term. Let us start with a simple, possibly unrealistic, example that takes this into extreme consequences (Toman and Flegr 2017b, 2018). Every clade (including clades of high taxonomic rank such as eukaryotes or metazoans) has minimal diversity and disparity at the beginning. The number of species and phenotypic disparity, as well as the number of different phenotypically distinct clades, later described as higher taxa by paleontologists, then grow. However, as particular (sub)lineages go extinct over time, newly originated species (the potential founders of new evolutionary lineages) in the remaining (sub)lineages differ in a low and still decreasing percentage of increasingly derived and less essential traits. Species diversity of the whole clade does not necessarily decrease. In fact, it may even grow for a considerable time, producing variations on the gradually freezing phenotypic motive. This may be the reason we observe increasing species diversity in Phanerozoic (see, e.g. Smith 2007). Disparity of the clade, however, decreases. Strange at first sight, similar trends were in fact documented in numerous clades (see “General Discussion”).

Setting aside other factors, eukaryotic clades should be gradually abandoning large areas of morphospace. In some cases, their places can be occupied by other, perhaps even completely unrelated, clades, in which the (macro)evolutionary freezing has not yet gone so far, or which have maintained sufficient developmental plasticity or evolvability in traits relevant for adaptation to the current environment. In the long run, however, the (macro)evolutionary potential of all sexual lineages approaches zero (see the previous section “Macroevolutionary Freezing”). The decreasing probability of producing major evolutionary novelties associated with

the sorting out of more persistent species should also manifest by changing the dynamics of their evolution. A large and still growing percentage of traits should become more or less unchangeable and evolution should gradually limit itself to small peripheral changes. In the end, Earth should be inhabited only by several universal and broadly distributed or obscure and distinctly stable environment inhabiting sexual eukaryotic clades. However, even these clades would ultimately succumb to a sufficiently large fluctuation of environmental condition, leaving the Earth to prokaryotes and possibly several lineages of ancient asexual eukaryotic organisms (Toman and Flegr 2017a). These organisms would probably be prone to macroevolutionary freezing and maintain their (macro)evolutionary potential.

In such a situation, lineages capable of restoring their (macro)evolutionary potential would have a great advantage over macroevolutionary more frozen lineages. We commented on the processes that may stop evolutionary freezing or even restore (macro)evolutionary potential thoroughly in Toman and Flegr (2018). Since particular traits and modules differ in the depth of their freezing, some of them may probably rarely loosen their inner links and “thaw” (see, e.g. Melo et al. 2016). This may be facilitated by a small population size, a relaxation of selection, a redundancy, and other factors that were summarised, e.g. in Toman and Flegr (2018). Such an event could happen, for example, at the beginning of angiosperm (Magnoliophyta) evolution. It is likely that the enormous success of this plant group was enabled by their ability to quickly and operatively change the size of their genome. Although the original purpose of this ability is unknown, a subsequent “miniaturization” of genomes, nuclei and cells of some angiosperm lineages lead to a more elaborate leaf morphology and an improved effectiveness of photosynthesis. This has resulted in their expansion to almost all conceivable habitats beginning in the Cretaceous period (Simonin and Roddy 2018). One possible alternative may be a heterochronic change in development (e.g. neoteny) that has the potential to release some modules from their functional links for other purposes. These events were documented in the evolution of several taxa (e.g. the famous *Axolotl* but also many other, see Raff and Wray 1989). Moreover, as was pinpointed by one of our reviewers, many cases of simplified interstitial meiofauna indicate that it might be a relatively frequent mode of evolution (Westheide 1987). More radical cases of such events (i.e. developmental changes that would lead to “thawing” of even very deeply macroevolutionary frozen modules or traits) are usually associated with fundamental simplification of individual development (i.e. *sacculinization*). Radical simplifications of development might play an important role in the evolution of Rhizocephala (Glennier and Hebsgaard 2006), Myxozoa (Canning et al. 2004), or biting- or sexually-transmitted mammalian cancers (Murchison 2008).

Although we know of several occasions in which the above-mentioned processes took part in evolution, it seems that none of them can completely stop macroevolutionary freezing in the long term. Evidence supporting this conclusion is mainly empirical. Although current major successful taxa are probably descendants of lineages that managed to produce a major evolutionary innovation or simplify their development, disparity in many of them, as well as higher eukaryotic taxa such as metazoans, was shown to be generally decreasing (see “[General Discussion](#)”). The reason is that the probability of evolutionary “thawing” is inversely proportional to the degree of macroevolutionary freezing of the module. (This is imperative; if it does not apply, macroevolutionary frozen entities would not be stable, persistent, and would not accumulate via SBS in the first place). Weakly frozen traits and modules may “thaw” relatively easily. Deeply frozen ones, however, remain basically unchangeable and accumulate. Considering *sacculinizations*, these events are probably very rare. We do not know any large, diverse and successful eukaryotic lineage that would have originated this way. These macroevolutionary events thus probably have only a limited role in evolution. If we return to the comparison with Muller’s ratchet one more time, the processes mentioned above can be analogized with rare reverse mutations in Muller’s case. Mutations that restore the original function of a defective allele are possible. The same counts for changes that restore the (macro)evolutionary potential of the evolutionary lineage. However, both of these events are probably so rare that they do not play major role in evolution.

In our opinion, the only way to completely and at least temporarily restore (macro)evolutionary potential is through a transition to a hierarchically higher level, which makes the entity of the original level a limitedly changeable module within a new (macro)evolutionary potent whole.<sup>4</sup> The organism of the higher level is thus naturally modular (Carroll 2001). Macroevolutionary frozen units, i.e. quasi-independent modules, then can be to a large degree independently regulated, multiplied, combined, or deployed in different places, in different times, or different contexts by a higher-level individual (Simon 1962; Lewontin 1978; Schank and Wimsatt 1986; Bonner 1988; Wagner and Altenberg 1996; McShea 2000; Schlosser 2002, 2004; Schlosser and Wagner 2004; Callebaut and Rasskin-Gutman 2005; Melo et al. 2016).

Various transitions to a higher level of organisation significantly differ. Some of them are natively less burdened

by constraints, and thus evolutionary more perspective than others (Nedelcu and Michod 2004; Calcott 2008). However, under normal circumstances, a transition to a hierarchically higher level is usually a relatively risky endeavour that is under the threat of breakdown from many directions. The initial, usually not very significant, benefits may not outweigh the risks associated with a transition to a higher level (Michod 2000, 2007; Queller 2000; McShea 2001a; Michod and Nedelcu 2003; Michod and Herron 2006; Calcott 2008; Godfrey-Smith 2009; Queller and Strassmann 2009; Corning and Szathmáry 2015). The risk of selfish behaviour of individual parts at the expense of the whole is especially noteworthy. Therefore, long-term stable and successful transitions to a higher level are relatively rare (see, e.g. Novák 1982; Szathmáry and Maynard Smith 1995; McShea 1996, 2001a, b, 2015; Pettersson 1996; Knoll and Bambach 2000; Michod 2000; Calcott and Sterelny 2001; McShea and Simpson 2001; McShea and Changizi 2003; Jablonka and Lamb 2006; Okasha 2006; Marcot and McShea 2007; Maynard Smith and Szathmáry 2010, 2015; Bouchard and Huneman 2013; Buss 2014; Corning and Szathmáry 2015). However, the perpetually decreasing (macro)evolutionary potential on one level causes a constantly growing pressure favouring entities with (if only very slightly) restored (macro)evolutionary potential. In a situation when this factor decreases to a critical point at one level, even a momentarily very suboptimal but evolutionary viable solution associated with restoration of (macro)evolutionary potential—transition to a higher level of hierarchical complexity—may become competitive.

However, SBS that leads to macroevolutionary freezing acts even on the new, hierarchically higher, level of organisation. Although one of the sources of irreversible (macro)evolutionary freezing—the accumulation of irreversibly polymorphic alleles and their groups—acts only on the level of populations of sexual species (see the section “[Macroevolutionary Freezing](#)”), the second source of macroevolutionary freezing—the accumulation of stable elements of genetic architecture—applies to all levels. This should not be surprising. It is the nature of SBS to accumulate further unchangeable parts on all levels of all systems regardless of their nature. Consequences of this process can be more interesting.

In time, a modular organism of a higher level may delegate many functions of initially identical subunits only to some of them. For example, a newly originated multicellular organism (i.e. volvocine algae) initially consists of many identical cells. However, a lot of essential organismal processes can be maintained only by one or few cells. Some cells may thus specialise for these purposes (i.e. reproduction, digestion, movement etc.), whereas the same function is lost in other cells who are free to specialise differently (Nedelcu and Michod 2004). As a result, the mutual diversity

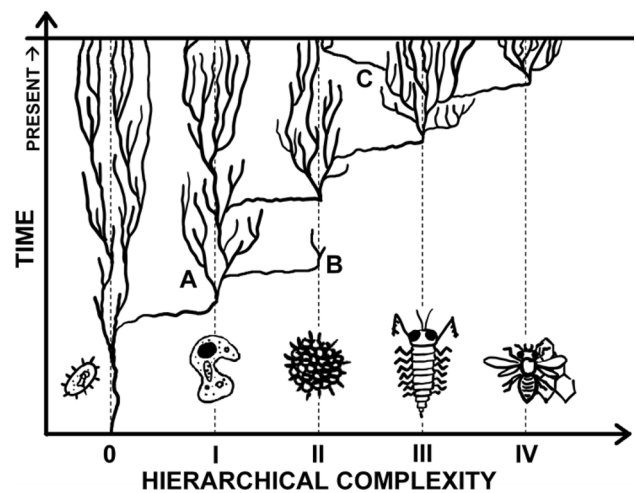
<sup>4</sup> We are aware that this might be a bold claim. It could be—and should be—debated. Especially in the light of the evolutionary processes that can theoretically restore (macro)evolutionary potential or at least slow down the macroevolutionary freezing mentioned above.



of subunits (or, from the viewpoint of the whole organism, the variability among its subunits) grows at the next lower level of a modular organism (Lewontin 1978; Bonner 1988, 1998; Wagner and Altenberg 1996; McShea 2000, 2002, 2015; Schlosser and Wagner 2004; Callebaut and Rasskin-Gutman 2005; McShea and Anderson 2005). Note that this does not count only for multicellular organisms or organisms of this hierarchical level. It applies to organisms of all subsequent levels of organismal complexity, from simple unicellular eukaryotes to colonies of eusocial insects. Even neutral mechanisms such as Zero Force Evolutionary Law (McShea and Brandon 2010) contribute to this process of increasing variability among subunits—they may also diversify as a result of pure chance.

However, as modules at the next lower level specialise, they establish new functional interconnections. Those interconnections that are further unchangeable accumulate by SBS. Modules gradually form a complex web of functional links, whereas those integrated wholes that reach higher persistence (i.e. become integrated by effectively unbreakable interconnections), will preferentially accumulate. Modules become less and less (semi)independent and the originally modular organism integrates. Just as on the lower hierarchical level before, this process is probably effectively irreversible. (Macro)evolutionary potential on this level decreases again, and when it reaches a critical level, even suboptimal organisms of the new, even higher, level of hierarchical complexity get the advantage (see Fig. 1). Moreover, it cannot be ruled out that the resulting increasingly complex multilevel genetic architecture that is characteristic of many functional interconnections on the current level (and among different levels) further accelerates macroevolutionary freezing on every subsequent level (see, e.g. the model of Thomas 2005).

We can only speculate as to whether this complication of organismal structure and function will continue indefinitely, or whether organisms may eventually reach their limits, become indifferent to selectional pressures, and stop restoring their (macro)evolutionary potential (Bonner 1988; Carroll 2001; Wimsatt 2013). As was mentioned by one of our reviewers, it seems that there could be an upper limit, because we don't see any super–super organisms, e.g. colonies of colonies, integrated enough to qualify (at least theoretically) as individuals. Moreover, such entities are hardly even imaginable. On the other hand, this scepticism may result only from our lack of creativity. It was documented that in some organisms, e.g. in the ant *Linepithema humile*, loosely arranged supercolonies are slowly emerging (Human and Gordon 1996). In a similar manner, human societies become integrated on a growing number of levels (states, federations of states etc.). These higher-level entities surely do not qualify as individuals, but it somehow urges us to be cautious. It is not set in stone that super–superorganisms or organisms of



**Fig. 1** Schematic representation of the trend of increasing maximal hierarchical complexity according to FET. Reaching a higher hierarchical level of organization is advantageous because of the temporary restoration of (macro)evolutionary potential that otherwise gradually decreases on every level. For the same reason, the overall disparity of numerous groups on the lower level could have been higher in the past compared to the present (a see also “General Discussion”). Not every evolutionary attempt to establish an organism of higher hierarchical level is equally successful; many such attempts could end up being evolutionary nonviable or marginal in the long term (b) because organisms on the original level still retained enough (macro)evolutionary potential or because the organisms of the higher level were loaded with a number of constraints that severely limited their further evolution. Reversals to a lower level of hierarchical organization (c) are possible but, based on the available evidence (see “Results and Discussion” or Toman and Flegr 2018), seem to be very rare in the history of life on Earth. The transition from hierarchical level 0 to level I (i.e. the origin of eukaryotic cells) corresponds to the egalitarian transition in individuality. The transition from level I to level II (i.e. the origin of simple multicellular organisms) corresponds to the fraternal transition in individuality. The third transition (i.e. the origin of complex multicellular organisms with modular genetic architecture and development) corresponds to the internal modularization. The last depicted transition (i.e. the origin of colonial or eusocial complex multicellular organisms) corresponds to the fraternal transition in individuality. Note that this is only a schematic representation, i.e. it does not follow the evolution of any particular lineage and does not make any claims about the proportions of the three ways to increase hierarchical complexity or the overall number of the levels of hierarchical complexity (those that are depicted, 0 to IV, surely need not be comprehensive)

even higher hierarchical levels are impossible, or that they would resemble any organism already present on Earth. Could we imagine eusocial insects with their specialized castes, complex life strategies and complicated mounds if we did not know them? In any case, transitions to a new level repeated many times, especially in the evolution of sexual eukaryotic organisms (as was described, e.g. by McShea 2001b).

## Various Types of Transitions

The first way through which an organism can achieve a higher level of hierarchical complexity was de facto described in the section “[Macroevolutionary Freezing](#)”. It is the internal modularisation of an organism that is based on the establishment of genetic, strongly interconnected modules that are to a considerable degree unchangeable, but independently regulable, repeatable, combinable, and deployable. This results in the modular character of an organism on physiological, morphological and other levels. The proximal reasons of modularisation (which is intimately connected to the evolution of evolvability), the direct mechanism of the origin of modules and, eventually, the involvement of various ways of modularisation are beyond the scope of this article (see, e.g. Lewontin 1978; Wagner and Altenberg 1996; McShea 2000, 2002; Schlosser 2002; Schlosser and Wagner 2004; Callebaut and Rasskin-Gutman 2005); it was also summarised in Toman and Flegr (2018). It is, however, important to note that both selection on multiple levels and SBS may play important roles in this process.

In most cases, internal modularisation probably happens through multiple duplications of the original modules. This occurs at lower levels of hierarchical complexity represented by genes (as was summarised, e.g. by Wagner and Altenberg 1996), and at higher levels of hierarchical complexity represented by whole (genetic, physiological, morphological, developmental etc.) modules. It broadly corresponds to the origin of modularity by the process of parcellation (loosening of interconnections in a tightly integrated whole). This process should manifest externally by the origin of organismal genetic modularity, and, in multicellular animals, also by the origin of developmental modules such as body segments or appendages that reflect the modular organisation of the genotype-phenotype map (Wagner 1989a, b). At every level, however, we should expect a subsequent integration (creating new interconnections among elements at a given level) of the modular character (see the section “[Transition to a Higher Level of Complexity](#)”) and the formation of higher-level modules of organisation (see McShea 2002, 2015; McShea and Anderson 2005). This mode of transition to a higher level of complexity may repeat several times in the evolution of the lineage, which leads to the complication of its genetic architecture. It has already been suggested by some authors that the processes of parcellation and integration may regularly alternate at neighbouring hierarchical levels (Wagner and Altenberg 1996; Kirschner and Gerhart 1998; Eble 2005). This is a nontrivial pattern that was, at least to our knowledge, never satisfactorily explained. It is, however, predicted by our theory as a natural consequence of macroevolutionary freezing and the restoration of (macro)evolutionary potential. An extreme example of the rebuilding of genetic architecture is the duplication of the whole

genome. Such events are relatively frequent in certain evolutionary lineages and could play a key role, e.g. in potentiating early evolution of vertebrates (Vertebrata) of actinopterygian fish (Actinopterygii) (Meyer and Van de Peer 2005).

Evolutionary entities may also reach a new hierarchical level of organisation and restore their (macro)evolutionary potential on the higher level by combining several originally separate entities of the lower level. The remaining two ways thus correspond with two types of transitions in individuality—fraternal and egalitarian (Queller 1997, 2000).

Fraternal transition in individuality is based on either the multiplication of identical or nearly identical entities of the lower level, e.g. closely related individuals, the progeny of one individual, or clones (Queller 2000). This transition in individuality might play a role in the formation of cells, specifically the formation of compartments consisting of the same molecules. Beyond that, it is the process through which the colonies of prokaryotic and eukaryotic unicellular organisms originate, as well as various forms of multicellular organisms, their colonies, and eusocial organisms (see, e.g. Novák 1982; McShea 1991, 1994, 2001b; Szathmáry and Maynard Smith 1995; Pettersson 1996; Knoll and Bambach 2000; Michod 2000; Calcott and Sterelny 2001; Jablonka and Lamb 2006; Okasha 2006; Calcott 2008; Maynard Smith and Szathmáry 2010, 2015; Bouchard and Huneman 2013; Corning and Szathmáry 2015). The close relation of entities that constitute the higher-level individual brings specific advantages but also specific disadvantages. The immediate advantage is a lower risk of intraindividual conflict that follows from the close relation of constituting entities (see, e.g. Michod 2000, 2007; Queller 2000; Michod and Nedelcu 2003; Michod and Herron 2006; Calcott 2008; Godfrey-Smith 2009; Queller and Strassmann 2009; Corning and Szathmáry 2015). The major problem of such higher-level entities is their weak initial advantage over lower-level individuals (see, e.g. Calcott 2008). This advantage, if any, apparently results mainly from body enlargement and the economics of scale (see, e.g. Bonner 1988, 1998; Queller 1997). Secondly, the selective specialisation (i.e. separation of germinal lineage, or general division of labour and its synergistic effects) of the elements composing the composite entity may occur (see, e.g. Bonner 1988, 1998, 2003; Szathmáry and Maynard Smith 1995; Queller 1997; Calcott 2008; Maynard Smith and Szathmáry 2010, 2015; Simpson 2012; Corning and Szathmáry 2015). Regardless of this, another major advantage that would manifest, especially in species selection, over the longer term may result from the restoration of (macro)evolutionary potential.

An egalitarian transition in individuality is based on the combination of two or more different entities of the lower level, not exclusively organisms from very remote evolutionary lineages (Queller 2000). Generally, it is the case of all symbioses and symbiogenetic events. From the

macroevolutionary point of view, the origin of endosymbiotic organelles (and probably also the nucleus) seems to be the most important of these events (see, e.g. Szathmáry and Maynard Smith 1995; Pettersson 1996; Knoll and Bambach 2000; Michod 2000; Calcott and Sterelny 2001; McShea 2001b; Sterelny 2004; Jablonka and Lamb 2006; Okasha 2006; Queller and Strassmann 2009; Maynard Smith and Szathmáry 2010, 2015; Bouchard and Huneman 2013; Corning and Szathmáry 2015). This transition could also play an important role in the early evolution, specifically during the formation of compartments consisting of different molecules, or chromosome consisting of linked genes. In contrast to the previous case, the advantages and drawbacks of egalitarian transitions in individuality stem from the unrelatedness of the constituting entities. The major initial advantage lies in the combination of different functions and properties, i.e. the division of labour and further synergistic interactions. A further advantage may stem from the restoration of (macro)evolutionary potential. The major problem is probably the control over conflicting interests of unrelated individuals that can be ensured by a fair distribution of reproduction allocations and enforced by their mutual dependence (see, e.g. Szathmáry and Maynard Smith 1995; Michod 2000, 2007; Queller 2000; Michod and Nedelcu 2003; Michod and Herron 2006; Calcott 2008; Godfrey-Smith 2009; Queller and Strassmann 2009; Maynard Smith and Szathmáry 2010, 2015; Corning and Szathmáry 2015). Therefore, it can take some time for egalitarian entities to evolutionary merge, integrate and start producing common propagules.

## General Discussion: The Context of Frozen Evolution Theory

### “Evolutionary Syndrome” and Related Phenomena

As was mentioned in Introduction, several accompanying phenomena are clearly associated with the global trend of increasing maximal hierarchical complexity. These phenomena correlate with the aforementioned trend on a macroevolutionary scale, but their mutual relationship is unclear. These are especially: (1) an increasing number and differentiation of parts at the next lower hierarchical level that follows transition to a higher level, and (2) a radical decrease of complexity on this level and all lower levels (i.e. their machinification) (Schank and Wimsatt 1986; McShea 2002, 2015; McShea and Anderson 2005). The coincidence of these three phenomena is so noticeable that McShea (2015) labelled it an “Evolutionary Syndrome”—a striking, yet unexplained, macroevolutionary pattern.

In the event that the trend of increasing hierarchical complexity is really caused by decreasing (macro)

evolutionary potential accompanied by growing pressure on its restoration by transitions to new hierarchically higher modularly organised levels, as we suggest in this paper, then the above-mentioned accompanying phenomena are natural side-effects of these processes. After reaching a new hierarchical level, macroevolutionary freezing starts anew. The modules, initially separate organisms or units that originated by internal modularisation, are regulated largely independently of each other at first. As we described in Results and Discussion, various neutral mechanisms and forms of selection make them multiply, differentiate, and deploy in various contexts, which leads to the documented increase in horizontal variability (Lewontin 1978; Bonner 1988, 1998; Wagner and Altenberg 1996; McShea 2000, 2002, 2015; Schlosser and Wagner 2004; Callebaut and Rasskin-Gutman 2005; McShea and Anderson 2005). The second accompanying phenomenon of “Evolutionary Syndrome,” streamlining or even machinification of modules, is related to the same processes. According to FET, the streamlining of modules is the consequence of their gradual specialization and integration caused by stability-based sorting on the highest level of composite entities. Variability among modules and their specialisation over time inevitably leads to differentiation, the emergence of new interconnections, the sorting of further unchangeable interconnections and elements by SBS, integration, and finally the diminishing of the originally modular character of the organism (Toman and Flegr 2018). One symptom of this is the simplification of lower levels that usually lose many of their functions and get streamlined in order to achieve an increased effectiveness (McShea 2002, 2015; McShea and Anderson 2005). Modules themselves are variable only in a very limited way. They are largely macroevolutionary frozen units of lower levels, which makes them much more prone to lose functions than to gain them. Considering the developmental viewpoint, adding new hierarchical levels increases the macroevolutionary freezing (see also the concepts of burden and generative entrenchment in the next section) of the lower levels of development. We can therefore expect complexity on the lowest levels to minimize up to a macroevolutionary completely frozen state that is characteristic of minimal evolvability and a high resistance to changes—the most machine-like state. It is noteworthy that this tendency to mechanize deep mechanisms in complex organisms was already predicted by Schank and Wimsatt (1986). Beyond that, machinification may be facilitated by other factors. Selection probably leads to a preferential preservation of interconnections that ensure a higher robusticity, which is favourable in the development and function of composite organisms (Kirschner and Gerhart 1998; Schoch 2010; Brigandt 2015). A greater interconnection of subunits may be also advantageous as a prevention against their eventual

selfish actions at the expense of the whole individual (Szathmáry and Maynard Smith 1995; Michod 2000; McShea 2001a, b; Michod and Herron 2006).

It is noteworthy that the whole pattern—the reduction in the number of initially identical modular and serially repeated parts, their gradual specialisation and integration—is known as Williston’s law (Gregory et al. 1935). FET therefore also offers an explanation for this macroevolutionary rule. To summarise, FET can explain “Evolutionary Syndrome” without major difficulties as a series of interrelated and causally following events resulting from the evolutionary dynamics of macroevolutionary freezing organisms. The common cause of all phenomena that compose the McShea’s (2015) evolutionary syndrome thus may be the process of macroevolutionary freezing. On top of that, our concept can shed new light on several related mysterious evolutionary patterns.

As we argued in “Results and Discussion”, macroevolutionary freezing and the associated trend of increasing hierarchical complexity should, according to FET, apply dominantly to sexual, i.e. eukaryotic, organisms. The effectively irreversible accumulation of further unchangeable elements is facilitated by sexual reproduction itself, the associated ability to form species that has changed the intensive struggle among asexual lineages to a much slower classical species selection, and the generally smaller size of eukaryotic populations (Flegr 2008, 2010, 2013, 2015; Toman and Flegr 2017b, 2018). Therefore, we should not be surprised that the trend of increasing hierarchical complexity has not proceeded evenly since the origin of life. After the initial increase that had accompanied the origin of cellular life approximately 4 billion years ago, there followed a long period when the maximal hierarchical level more or less stagnated. This period lasted about 2.2–2.8 billion years until the next impetus for further advancement of the trend took place—the invention of sexual reproduction by first eukaryotes (Carroll 2001; McShea and Changizi 2003; McShea 2015).

The more puzzling question is: why has the trend of increasing hierarchical complexity, as appears from available paleontological indices, gradually accelerated since that time (McShea 2001a, b, 2015; McShea and Changizi 2003)? It has been proposed, for example, that this acceleration might be caused by increasing biodiversity, or that it was potentiated by the rise of oxygen content in the atmosphere. However, the ratio of internal and external influences on this phenomenon remains unclear (McShea 2001a, b). The explanation based on FET, i.e. the hypothesis that macroevolutionary freezing proceeds faster on every subsequent level due to the evolution of evolvability, thus seems at least a realistic alternative worthy of further testing. As we mentioned in “Results and Discussion”,

polymorphism in an ever-increasing number of genes that increases the diversity of genetic background can put pressure on the robustness of development (Von Dassow and Meir 2004; Wimsatt 2013) and can further accelerate the accumulation of (macro)evolutionary frozen elements (Toman and Flegr 2017b, 2018). Also, it cannot be excluded from consideration that macroevolutionary freezing on every subsequent level is further accelerated by an ever-complicating multilevel genetic architecture that is characterised by many functional interconnections at a given level and between levels (see, e.g. the model of Thomas 2005). This should be clearly observable, especially on the evolution of organisms with the most complex individual development. It is consistent with observations that the most pronounced acceleration of the increasing of hierarchical complexity can be seen in complex multicellular organisms and that its beginning can be dated to the time shortly preceding Cambrian and Cambrian explosion, i.e. the time when multicellular animals (Metazoa) evolved and reached their modern forms (McShea 2001a, b; Davidson and Erwin 2006).

For the same reasons, we should not be surprised by the fundamentally different character and dynamics of pre-Neoproterozoic (and especially pre-Cambrian) and Phanerozoic evolution (see, e.g. Knoll and Bambach 2000; Carroll 2001; Butterfield 2007). While the time preceding the Neoproterozoic was dominated exclusively by prokaryotes characterised by their “two dimensional” evolution (i.e. in the absence of significant selective pressures usually slow and stabilizing evolution devoid of a continuous increase of hierarchical complexity), the Neoproterozoic gave birth to eukaryotes with their “three dimensional” evolution characterised by the trends of increasing diversity and hierarchical complexity. It is true that more complex cells (see, e.g. McInerney et al. 2011) or hierarchically more complex colonies (see, e.g. Claessen et al. 2014) emerged several times in the prokaryotic evolution. However, if we exclude one of their very specialised derived lineage—eukaryotes—prokaryotes do not exhibit any continuous trend of increase in any form of complexity (McShea 2001a, b, 2015; McShea and Changizi 2003; Marcot and McShea 2007). In contrast to that, the maximal level of hierarchical complexity has increased several times in eukaryotes, which has led directly (through the development of new ecological strategies, the occupation of new areas of ecophenotypic space, etc.) and indirectly (through the (co-)creation of new habitats, the influence on environmental conditions etc.) to the complete rebuilding of the whole ecological space of our planet and a fundamental change in the dynamics of evolution (Knoll and Bambach 2000; Carroll 2001; Butterfield 2007; Toman and Flegr 2017a).

## Analogical Older Concepts

The study of the trend of decreasing evolvability (including its special cases such as (macro)evolutionary potential), or the reduction of intraspecific and interspecific disparity during the existence of clades, has a long history. A number of theoretical studies (see, e.g. Riedl 1977, 1978; Wagner and Laubichler 2004; Budd 2006; Schoch 2010; Wimsatt 2013) and observations (see, e.g. Rosa 1899; Erwin et al. 1987; Gould 1989; DiMichele and Bateman 1996; McShea 1996; Foote 1997; Eble 1998, 1999; Kirschner and Gerhart 1998; Rasnitsyn 2005; Budd 2006; Erwin 2007; Webster 2007; Hughes et al. 2013; Lee et al. 2013) have supported its existence. Especially in the macroevolution of eukaryotic organisms (metazoans were most thoroughly studied in this context), the above-mentioned trend applies almost universally (it was summarised, e.g. by Toman and Flegr 2017b, 2018).

If we leave out some more eccentric explanations (e.g. that the trend is caused by meiosis, which is understood as a derived process hampering any adaptive change; Davison 1998), or that the evolution of any system leads to stasis (Shcherbakov 2012), we can divide the proposed explanations of this trend into two groups (Erwin 2007)—ecospace and developmental (or genetic) hypotheses. According to the ecospace concept, the success of newly originating and significantly differing evolutionary lineages is inversely proportional to the saturation of the ecospace in which representative groups reside. Their chances of significant success thus decrease in time. According to the developmental (genetic) explanations, the trend is based on the decreasing potential of lineages to generate major evolutionary innovations (Valentine 1995; Davidson and Erwin 2006; Erwin 2007; Webster 2007). Both of these groups of explanations were supported by evidence and it should be noted that they need not exclude each other (Erwin 2007). However, the global trend of gradually decreasing intraspecific variability during the evolution of taxa, which is known today as Rosa's rule (Rosa 1899), speaks in favour of the developmental explanations. Leaving aside older anecdotal evidence, Rosa's rule was demonstrated even quantitatively. As was proven by Webster (2007), the number of intraspecifically variable traits and the degree of their variability were much higher in older species of the taxon Trilobita in comparison to the younger ones. Moreover, certain data indicates that similar phenomena might also take place in the evolution of cockroaches (Blattodea) (Vrsansky 2000; Vrsansky et al. 2017). The above-mentioned trends therefore most likely result from the decreasing variability on the species level.

The possible long-term consequences of one-way constraining of the clades' evolution were studied, e.g. by Wimsatt (2013) or Riedl (1977, 1978; see also Wagner and Laubichler 2004; Budd 2006; and; Schoch 2010). However,

an analogous view was also offered by Arthur (1982) and similar topics were touched upon even by other, often much older, researchers that have been summarised, e.g. by Riedl (1977, 1978), Schank and Wimsatt (1986), Gould (2002), Schoch (2010), or Wimsatt (2013, 2015). According to these authors, evolutionary lineages may ultimately reach the extreme state when the origin of major evolutionary novelties becomes limitally improbable (Budd 2006). According to Riedl (1977, 1978; Wagner and Laubichler 2004; Budd 2006; Schoch 2010), processes or elements that are associated with a greater number of more important features and functions, i.e. processes or elements that are more substantial and probably also phylogenetically older, exhibit a decreasing changeability (increasing "burden") due to a high risk of rendering organism unviable when changed. This leads to a gradual "cementation" of traits and consequent "evolutionary sclerosis" of evolutionary lineages. This manifests in strong restrictions to their evolvability, constraining of possible adaptations, and changeability limited only to minor peripheral traits or one direction. The resulting evolution of clades has a cyclistic (i.e. assuming a gradual transition of taxa from adaptive and experimenting "youth" to strongly constrained "old age") and typrostrophic (i.e. assuming changeable nature of new traits and their increasing conservativeness as they are burdened by characters build upon them) character (Schoch 2010). In such a case, evolvability can be restored only through radical rebuilding of the organism's development, i.e. major heterochronic change (Budd 2006).

In a similar vein, Wimsatt (2013; Schank and Wimsatt 1986; Wimsatt and Schank 2004) writes about "generative entrenchment," which is a property of traits analogical to burden, but derived from timing in the individual development and (consequently) integration into the system. In any case, sets of genes and genetic modules that take place early in development (so that they influence a high number of various characters and processes), those that code characters and processes more fundamental for the functioning of the organism, and those that code characters and processes phylogenetically older, should, to a large extent, correspond (see Riedl 1978; Arthur 1982; Schank and Wimsatt 1986).<sup>5</sup> Strongly entrenched traits are under constant risk that their change through internal (e.g., mutation) or external (e.g., change of environment) factors would negatively influence some of the later developmental processes or elements. They also have a lower probability that their change would be adaptive. The modification or extension of individual development is therefore possible only on the least entrenched components of development. Moreover, every extension of

<sup>5</sup> This does, in fact, follow already from von Baer's laws of development, see Schoch (2010).

development increases the entrenchment of all the developmental components that it is built upon. Wimsatt (2013) went even further and considered an extreme situation in which the system reaches a state when any further increase of effectivity or size of an organism that would be selected upon would be redeemed by a disproportionately large increase of its inner complexity and the risk of catastrophe of complexity. At the same time, Wimsatt was also probably the first author to propose that the only possible way out of this dead end is to transition to a higher level of organisation. Such a radical and restrictive conception of evolutionary constraints became one of the sources of criticism on Riedl's account (Schoch 2010) and accounts of older understandings of evolution of evolvability in general (Brigandt 2015). However, in the light of FET and SBS (Toman and Flegr 2017b), which inevitably proceeds on all levels, these ideas seem greatly justified (Toman and Flegr 2018). Moreover, the conserved nature of early embryonic development (the phylotypic stage), especially due to intensive pleiotropic interactions among genes, is becoming increasingly supported (Galis and Metz 2001; Hu et al. 2017).

Concerning the increasing hierarchical complexity in the history of life, the trend itself, as well as the existence of "transitions in individuality," have been known to biologists for a long time and are the subject of intensive research in several directions (for some recent discussions, see, e.g. Novák 1982; McShea 1991, 1994, 1996, 2001a, b; Szathmáry and Maynard Smith 1995; Pettersson 1996; Knoll and Bambach 2000; Michod 2000; Calcott and Sterelny 2001; Jablonka and Lamb 2006; Okasha 2006; Marcot and McShea 2007; Maynard Smith and Szathmáry 2010, 2015; Bouchard and Huneman 2013; Buss 2014; Corning and Szathmáry 2015). The best-known concept in this area is probably "Major transitions in evolution," which emphasizes the merging of originally separate entities into higher-level units, their specialisation and the fact that these transitions were accompanied by the emergence of new ways of storing, transmitting, and interpreting information, i.e. the origin of new forms of inheritance (Szathmáry and Maynard Smith 1995; Calcott and Sterelny 2001; Maynard Smith and Szathmáry 2010, 2015; Corning and Szathmáry 2015).

Similar alternative approaches ("levels of organisation," "integrative levels," "levels of selection," various kinds of major transitions, etc.) and their resulting hierarchies differ in their emphasis on partial aspects of the growth of biological complexity (horizontal, vertical, filial, ecological, integration on various levels etc.) and terminology (see, e.g. the concepts and reviews of this problem in Novák 1982; McShea 1991, 1994, 2001a, b; Pettersson 1996; Knoll and Bambach 2000; Michod 2000; McShea and Simpson 2001; Jablonka and Lamb 2006; Buss 2014; or; Corning and Szathmáry 2015). Concerning lesser-known concepts, the theory of sociogenesis of Novák (1982) is worth mentioning. In

his theory, Novák postulated that the growth of hierarchical complexity by the repeated merging of modular wholes into higher-level units and the integration of initially autonomous modules are processes common to the whole universe. The author largely neglected the role of egalitarian transitions (especially symbiogenesis). On the other hand, he considered both fraternal transitions and internal modularisation of organisms to be possible ways to a new level. According to Novák, sociogenesis occurs on all five postulated organismal levels including the psychological-social level in humans. In modern terminology, Novák considered the trend to be driven. Increasing hierarchical complexity was considered to reflect a universal tendency for cooperation and to be selectively advantageous both in the short and in the long term. However, the concept was based on *a priori* ideological, specifically Marxist, assumptions and has no realistic support in the paradigm of modern evolutionary biology. Among other problems, the theory (as well as Marxism in general) completely ignores natural threats to a higher-level entity resulting from the selfish interests of its partial elements.

Only some of the previously proposed concepts have addressed the issue of the causes of the trend of increasing hierarchical complexity. Even so, many potential explanations of specific transitions to higher levels, or entire trends leading to repeated transitions to higher levels, have been proposed over time. These concepts were summarised, for example, by McShea (1991), Corning and Szathmáry (2015), McShea and Simpson (2001), or Marcot and McShea (2007). Nevertheless, we should note that the whole problem historically overlaps with the problem of the general increase in organismal complexity (see Introduction). Darwinian and non-Darwinian (Corning and Szathmáry 2015), or internalistic, externalistic, and undriven (McShea 1991) mechanisms can be distinguished. It is, however, clear that most proposed concepts cannot be considered disparate because of the high number of commonalities (McShea 1991).

According to Darwinian (or externalistic) explanations of this phenomenon, transitions to higher levels of organisation are generally selectively advantageous. This applies (albeit with some reservations, as transitions may also bring a number of problems, see the section "Various Types of Transitions") also to FET. However, the main cause of transitions is not a simple advantage of increasing biological fitness after reaching a new hierarchical level in our concept. The primary cause is the restoration of (macro)evolutionary potential and, consequently, the advantage in species selection. Moreover, FET exhibits at least some elements of internalist concepts that consider the source of the trend to be some non-Darwinian, most often developmental, mechanism. In our case, this mechanism is proposed to be SBS mediated macroevolutionary freezing. From the formal viewpoint, it is thus hard to decide whether FET is (in the sense of McShea 1991) rather internalist (and consider

the trend to be a side-effect of decreasing (macro)evolutionary potential) or externalist (and consider the trend to be a side-effect of species selection on restoration of the (macro)evolutionary potential). In any case, the trend of increasing hierarchical complexity appears undriven most of the time. However, when the (macro)evolutionary potential of the evolutionary lineage reaches a critical point, the chances that an entity of a hierarchically higher level would be evolutionary viable, succeed, and establish a new major evolutionary lineage dramatically rise. From the global perspective, this trend thus constitutes a special case of a driven trend in the sense of McShea (1994, 1998; Marcot and McShea 2007) that is based on SBS and “driven” at the large scale. Therefore, we expect its course (see Fig. 1) to correspond to the pattern depicted section E of Fig. 7 in McShea (1996) or Fig. 2 in McShea (1998).

In some respects, our concept approaches the hypotheses of Cope and Gregory, who stressed the role of multiplication and diversification of modular wholes in evolution, or Saunders and Ho, who postulated asymmetry between the simple addition of components and their much harder deletion due to their integration into functional units (this was summarised, e.g. in McShea 1991). The possibility that the trend of increasing hierarchical complexity is a result of species selection has been proposed in the past (see, e.g. Wagner 1996; McShea and Changizi 2003; Marcot and McShea 2007). However, according to our knowledge, the trend has never been associated with decreasing evolvability or (macro)evolutionary potential. Theories that assume a similar drive as SBS at the base level (see, e.g. Zuckerkandl 1997) are generally quite exceptional. In any case, the permanence of this trend, its characteristic course with diversification and machinification of lower-level subunits, its occurrence predominantly in primary sexual eukaryotes and especially complex multicellular organisms, its gradual acceleration and significant boost since Neoproterozoic-Cambrian, cannot be coherently explained by any other theory presented so far.

## Conclusions

Several global macroevolutionary trends, particularly the trends of decreasing (macro)evolutionary potential, disparity, and intraspecific variability in the evolution of (especially) sexual lineages, and the trend of increasing of the maximum of their hierarchical complexity may have one common explanation—stability-based sorting (SBS). Moreover, it may also coherently explain the accompanying phenomena of these processes: (1) the gradual acceleration of the growth of hierarchical complexity, (2) the boost in this acceleration since the Neoproterozoic-Cambrian, (3) the typicality of the aforementioned trends for sexual eukaryotes (and, especially, complex multicellular organisms), (4) the

modular character of higher-level organisms, (5) the increasing mutual diversity (from the viewpoint of subunits), or variability (from the viewpoint of higher-level organism) on the next lower level of organisation, and (6) the decrease in complexity at this level and at lower levels.

We have previously demonstrated that all complex adaptations probably have their origin in the joint action of SBS and its special case, sorting based on dynamic stability, i.e. natural selection (Toman and Flegr 2017b). Moreover, SBS itself can explain many mysterious evolutionary phenomena. In this article, we proposed that one of these phenomena may be the trend of increasing hierarchical complexity of organisms that is based, according to Frozen Evolution Theory (FET), on the repeated nearly irreversible accumulation of effectively unchangeable genes, their interrelated groups, traits, and whole functional or morphological modules (i.e. the process of macroevolutionary freezing). According to FET, this phenomenon is characteristic of sexual eukaryotes and it can be more pronounced in organisms with complex development. Because of the ratchet-like character of the accumulation of macroevolutionary frozen elements, selection both on an individual and a species level seem rather ineffective at stopping it or slowing it down (see also Toman and Flegr 2018). It is widely accepted that the evolution of evolvability leads to the origin of the genotype-phenotype map that enables existence, development, and evolution of complex organisms. However, the same processes may significantly limit the (macro)evolutionary potential of these organisms in the long term (Toman and Flegr 2018). The accumulation of effectively unchangeable elements by SBS decreases the (macro)evolutionary potential of evolutionary lineages at a given hierarchical level and increases pressure to restore this property, which is essential in species selection. (Macro)evolutionary potential can be restored, at least theoretically, by the means of the rare “thawing” of seemingly irreversibly frozen elements, heterochrony, or radical simplification of individual development, i.e. *sacculinization* (Toman and Flegr 2018). However, it remains an open question whether these processes can restore (macro)evolutionary potential completely, at least significantly, or only partially (i.e. only in some, potentially less frozen traits or modules). We are convinced (and we presented some arguments to support this idea in “Results and Discussion”) that the (macro)evolutionary potential can be significantly restored only through a transition to a higher hierarchical level by means of internal modularisation, fraternal, or egalitarian transition.<sup>6</sup> Continuously originating lineages

<sup>6</sup> Nevertheless, note that transitions to higher levels of complexity might be important ways to overcome the decreasing of (macro)evolutionary potential even if other means to restore this property were open.

of modular organisms increase their advantage as (macro) evolutionary potential of the whole lineage decreases. At one point, they reach evolutionary viability. Initially, they have a great advantage. They can produce major evolutionary innovations and occupy (or even co-create) new niches or whole so-far unoccupied environments. Neutral processes and processes that increase the fitness of composite organisms on the new level (i.e. the differentiation of modules, their specialisation, integration of the whole organism, or even the origin of further unchangeable elements of body organisation), however, irreversibly lead to SBS induced macroevolutionary freezing at the new level. Therefore, the whole process repeats itself.

FET can explain McShea's (2015) "Evolutionary Syndrome" and associated aforementioned macroevolutionary patterns that have defied simple explanation so far. Consequently, it can shed new light on other problems met by researchers in fields of evolutionary and theoretical biology. One of the largest problems of traditional hypotheses that predict the trend of increasing complexity in evolution is the fact that this trend has never been replicated in computer models or laboratory experiments aimed at simulating the conditions of open-ended evolution (see, e.g. Oehlschläger and Eigen 1997; Bedau et al. 2000; Channon and Damper 2000; McMullin 2000; Watson 2006; Bedau 2009). Neither computer simulations of open-ended evolution (see Langton 1984; Ray 1993, 1997; Thearling and Ray 1994, 1996; Yaeger 1994; Bedau et al. 1997; Ray and Hart 1998; Sayama 1999; Adami et al. 2000; Channon 2001; Suzuki et al. 2003; de Vladar et al. 2017), nor observations of the evolution of simple pre-cellular or prokaryotic systems in the laboratory (see Spiegelman et al. 1965; Mills et al. 1967; Oehlschläger and Eigen 1997; Lenski 2004; Blount et al. 2008) led, under natural conditions (i.e. without introducing a strong artificial selection to the advantage of more complex entities), to open-ended evolution with continuously emerging novelties or even increasing hierarchical complexity. On the contrary, after the facultative short phase of the origination of new phenotypes, streamlining, simplification, and reduction of replicating entities, which did not change much after that, took place (Adami et al. 2000). Reasons for these failures may vary. It is possible that a sufficiently complex environment with practically unlimited variability, unlimited genetic system, dispersion of entities, and possibly other factors are necessary aside from basic prerequisites for the action of natural selection (the inheritance of properties and the overproduction of variable offspring) (de Vladar et al. 2017). However, even if these conditions are met, it may be necessary to simulate the evolution of evolvability and effectively irreversible freezing of (macro)evolutionary potential on the given level to reproduce the trend of increasing (hierarchical) complexity.

Given that the 'complexification' of life on Earth has directly and indirectly affected (and still affects) all lower levels of the organismal organisation, the trend of increasing hierarchical complexity may represent one of the most important macroevolutionary phenomena. From a conceptual point of view, FET enables microevolution to be connected with macroevolution, classical modern synthesis with "extended synthesis", and an ecologically-population genetic approach to study evolution with a developmentally-paleontological one (Budd 2006). Although other hypotheses and theories have been proposed to explain all the trends and patterns mentioned above, only FET can explain these phenomena as an integral set of interconnected macroevolutionary processes.

Regardless of how conceivable the theory might sound, testing it will be essential. It is obvious that FET is a wide theoretical concept whose direct testing will not be an easy task. In our view, there are basically two ways to easily falsify this theory. It is clear it would not hold in the case that the trends of decreasing evolvability or (macro)evolutionary potential, intraspecific disparity (i.e. Rosa's rule), or interspecific disparity do not apply to most clades. These patterns are still disputed, especially in the field of paleobiology, and it would be fruitful to verify their existence (and possibly explore details of their form) in more fossil taxa. Taking the opposite approach, particular developmental processes that lead to a solidification of development are being studied in the field of evolutionary developmental biology (see, e.g. Galis and Metz 2001; Hu et al. 2017). Finding that development is comparably evolvable for the whole time of clades' existence, or that evolution of evolvability follows no clear trends in its evolution would greatly challenge our theory as well.

These are, however, quite negative and non-specific tests. Concerning more specific ways to test our concept, it may be best to verify whether the process of SBS (in this case the accumulation of further unevolvable components of organisms) may lead to transitions to new hierarchical levels in the first place. This could be done, for example, in a virtual simulation of open-ended evolution. There were several comparable attempts (see above). Alternatively, it is possible to model the evolution of evolvability in particular (see, e.g. Crombach and Hogeweg 2008). However, it might not be easy to construct a model that enables SBS. Even those models which are capable of simulating the evolution of evolvability might not be able to incorporate decreasing evolvability or an indefinitely increasing hierarchical level of simulated entities. Note that FET is not only about pleiotropic interactions, origin of modules, and evolvability on the given level, but rather ever increasing and complicating genetic architecture. Concerning numerical models, it may be also useful to calculate the range of conditions under which the "macroevolutionary ratchet" that accumulates



further unchangeable components of organismal structure, function, and development may operate. Related equations might be similar or even identical to those used in calculations concerning the operation of Muller's ratchet. It is also clear that factors important for the progression of Muller's ratchet (i.e. epistasis among harmful mutations) may be of great importance also in the macroevolutionary case (Muller 1964). All of this, however, remains open to further research. It would be also extremely interesting to compare the dynamics of evolution in sexual and asexual lineages. According to FET, trends mentioned above should be characteristic exclusively for sexual clades or be more prominent in the evolution of sexual organisms. It is, however, unclear whether we could detect macroevolutionary changes in a laboratory experiment without extreme simplification of tested hypotheses (e.g. replacing sexual organisms by recombining viruses as in some earlier studies on the evolution of sexuality). Quantitative study of macroevolutionary patterns may present another way to test our concept. In the case that FET holds, we should expect some evolutionary lineages to be much more changeable and express a disproportionately larger disparity than other lineages in every time slice. This should follow a transition to a higher hierarchical level or any other restoration of (macro)evolutionary potential. The same lineages should, however, gradually lose this potential, whereas other lineages may randomly gain it. This tendency would probably lead to specific macroevolutionary patterns that could be detectable, for example, in paleobiological or phylogenetical data and possibly distinguished from other possible causes (see, e.g. Morlon et al. 2010; Hughes et al. 2013). Last but not least, non-trivial insights into these problems can also be achieved by the study of analogical processes in other evolving systems, e.g. cultural evolution (Toman and Flegr 2017a, 2018).

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## Compliance with Ethical Standards

**Conflict of interest** The authors declare that they have no conflict of interest.

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