

Selfish DNA is maladaptive: evidence from the plant Red List

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Notwithstanding an average evolutionary increase of genome size in the higher plants due to activity of transposable elements, threatened plant species (those that are now on the brink of extinction) are shown here to have on average larger genomes than their more secure relatives, which indicates that redundant DNA in the plant genome might increase the likelihood of extinction. The effect is (at least partially) independent of the duration of the plant's life cycle. Polyploidy is found not to be associated with the increased risk of extinction. These data agree with the hypothesis of 'selfish' DNA and indicate an antagonism between different selection levels, thereby supporting the concept of hierarchical selection.

The role of noncoding DNA, which constitutes the greater part of eukaryotic genomes, remains enigmatic. Although the larger genome is known to relate to a number of phenotypic traits (reviewed in Refs [1,2]), some of which can be interpreted as adaptive [3–6], it is still unclear whether genome enlargement is selected for on the organismal level or is just a result of activity of transposable elements merely tolerated by the organismal-level selection [7–10]. However, in contrast to other neutral traits, the accumulation of noncoding DNA in the genome is still promoted by selection, albeit, according to the concept of 'selfish' DNA [7,8], it is a selection of genomic parasites behaving as selfish Darwinian units. Therefore, the usual (indirect) tests for traits' neutrality based on population size, breeding system, generation time, etc. are inconclusive. For example, it is known that selection against deleterious genetic changes (including the accumulation of noncoding DNA were it deleterious for the organism) is promoted by recombination and is generally more effective in sexual breeding systems as compared with asexual systems [11–15]. At the same time, transposable elements and supernumerary B chromosomes, which are believed to be selfish, also propagate more successfully in sexual populations than in asexual ones [16–20]. Thus, it is difficult to sort out different units of selection by indirect approaches. It is not surprising that it was even argued that the hypothesis of selfish DNA is 'actually a narrative scheme', which 'serves to protect neo-Darwinian assumptions from criticism' and which is 'untestable and therefore not a hypothesis' [21]. To resolve the controversy, direct evidence of the (mal)adaptive

nature of redundant DNA for the organism is needed. In this article I show that threatened plants (i.e. ones whose populations are now on the decline) have on average larger genomes than their relatives, which indicates that the excess of noncoding DNA in the plant genome is selected against (at least at the species level), and thus supports the hypothesis of selfish DNA.

Data and analysis

The data on plant genome sizes were taken from the Plant DNA C-values Database (<http://www.rbgekew.org.uk/cval/homepage.html>). After exclusion of polyploids and poorly determined species, there remained 3036 species (records with 'sp.', 'af.', 'cf.' and '?' in the species field were excluded; data for infraspecies forms were averaged). They were checked against the United Nations Environment Programme World Conservation and Monitoring Centre (UNEP-WCMC) Species Database (<http://quin.unep-wcmc.org/isdb/taxonomy/>) in two ways: first, against the subset of plants of global conservation concern, and second, against the total dataset, which includes both plants of global and local concern. From the total 3036 species, 305 species were found to be of global concern, and 1329 species were of local concern (i.e. they are threatened only in particular countries). A spectacular 'dose-dependent' relationship between genome size and conservation status was found (Figure 1a). Phylogenetic conservatism is a usual complication of every comparative analysis [22], therefore genome size values were also tested as within-families contrasts (i.e. as ratios to a family's mean). The relationship still held (Figure 1b). A similar relation between genome size and conservation status held also for within-families contrasts for eudicots and monocots, taken separately (not shown), and at the level of within-genera contrasts for the whole dataset, at least for species of no conservation concern and species of global concern (Figure 1c).

A lower significance level in the case of within-genera contrasts can be explained, first, by a lower number of species belonging to genera with heterogeneity in conservation status (i.e. including both threatened and nonthreatened species), and second (probably, more importantly), by a lower within-genera variation in genome size, which seems to be close to infraspecies variation and measurement error. The Plant DNA C-values Database contains data obtained by many different authors using different methods, which greatly hinders the comparison of species with similar genome sizes (for discussion of the problems of genome size measurements

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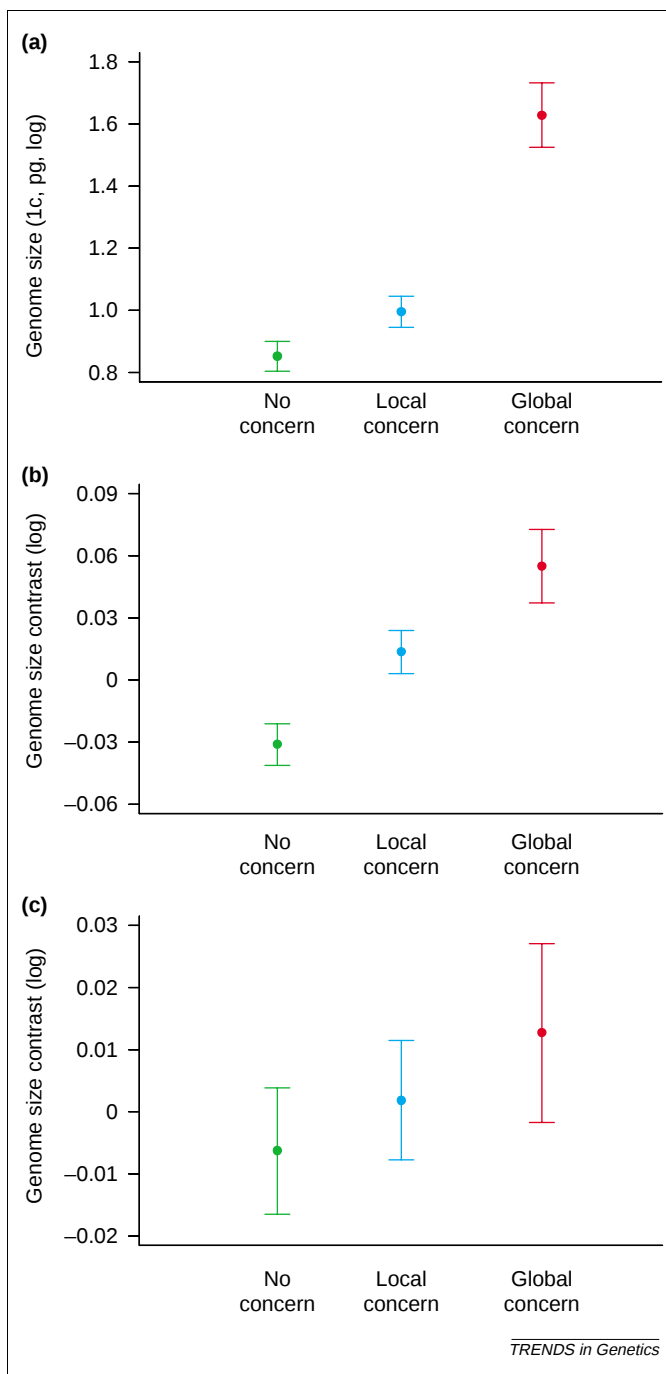


Figure 1. Differences in genome size among plants of different conservation status [means with 95% least significant difference (LSD) intervals]. (a) Raw species points ($n = 1402$, 1329 and 305 for 'No', 'Local' and 'Global', respectively; Kruskal–Wallis, $P < 10^{-10}$). (b) Within-families contrasts (i.e. ratios of genome size of a given species to average genome size of the family to which it belongs). Only species belonging to the families with within-family heterogeneity in conservation status (i.e. which included both threatened and nonthreatened species) were taken ($n = 996$, 1086 and 295 for 'No', 'Local' and 'Global', respectively; Kruskal–Wallis, $P < 10^{-4}$). (c) Within-genera genome size contrasts. Only species belonging to genera with within-genus heterogeneity in conservation status were taken ($n = 446$, 502 and 225 for 'No', 'Local' and 'Global', respectively; although the LSD intervals are overlapped, in nonparametric Mann–Whitney and Kruskal–Wallis tests $P < 0.05$ for 'No' versus 'Global'; for possible problems with the within-genera contrasts, see main text).

with different methods see, e.g., Ref. [23]). I have taken data that the curators of the database designated as the 'prime' (preferable) estimates for each species. The variance components analysis showed that variance of

(log-transformed) genome size values among taxonomic levels was partitioned in the following way: within-genera 8.1%, within-families 29.1%, and above-families 62.8%. If all the estimates (of different authors) were taken, the variance was partitioned as follows: within-species (mainly among authors) 5.3%, within-genera 6.5%, within-families 28.4%, and above-families 59.8%. Thus, we can see that within-genera variance is similar to within-species variance. The situation is probably better with the preferable estimates but we do not know to what extent. Therefore, the within-genera genome-size contrasts could be unreliable.

Polyploidy is not maladaptive

There is an obvious problem of polyploidy. In the analyses described above, all species that were not indicated in the Plant DNA C-values Database as being polyploids were taken. If species with an undefined ploidy status were excluded, the effects still held (Kruskal–Wallis, $P < 10^{-4}$). However, in many cases, even species indicated as diploids probably previously went through one or more rounds of polyploidization (with subsequent diploidization), and this preceding polyploidization might influence the results. Therefore, the effect of ploidy was tested directly (for this purpose, all species with indicated ploidy levels were taken). With the raw species points, the ploidy level negatively correlated with global conservation concern (Figure 2a). However, there were no significant effects either with the within-family or within-genera contrasts (Figure 2b). (In all these cases, the effect of genome size was removed in multifactor ANOVA; however, if it was not removed, the picture was qualitatively the same.) Thus, because no maladaptive effect of polyploidy was found, we can conclude that it is not a preceding polyploidization but the amount of noncoding DNA that determines the effect shown in Figure 1. The chromosome number (which is also provided for many species in the Plant DNA C-values Database), taken for species designated as diploids, was found to negatively correlate with conservation status (Figure 3a). The effect might be due to negative correlation between chromosome number and genome size described earlier [24]. This correlation was confirmed here using the phylogeny-controlled method. The within-families contrasts of chromosome number negatively correlated with the within-families contrasts of genome size (for diploid species; Spearman $r = -0.30$, $P < 10^{-8}$, $n = 2257$). However, after the effect of genome size was removed, the picture did not change qualitatively in regard to species of local concern (Figure 3b). When the effect of chromosome number was removed, the association between genome size and conservation status remained valid (the picture for within-families genome-size contrasts was similar to Figure 1b; ANOVA, $P < 10^{-4}$).

Speciosity is lower in lineages with larger genomes

To establish whether the increased likelihood of extinction of plants with larger genomes is a recent trend, the number of species in each genus was determined using the International Plant Names Index (<http://www.ipni.org/ipni>). A negative correlation between mean genome size and number of species in a genus was found (Spearman

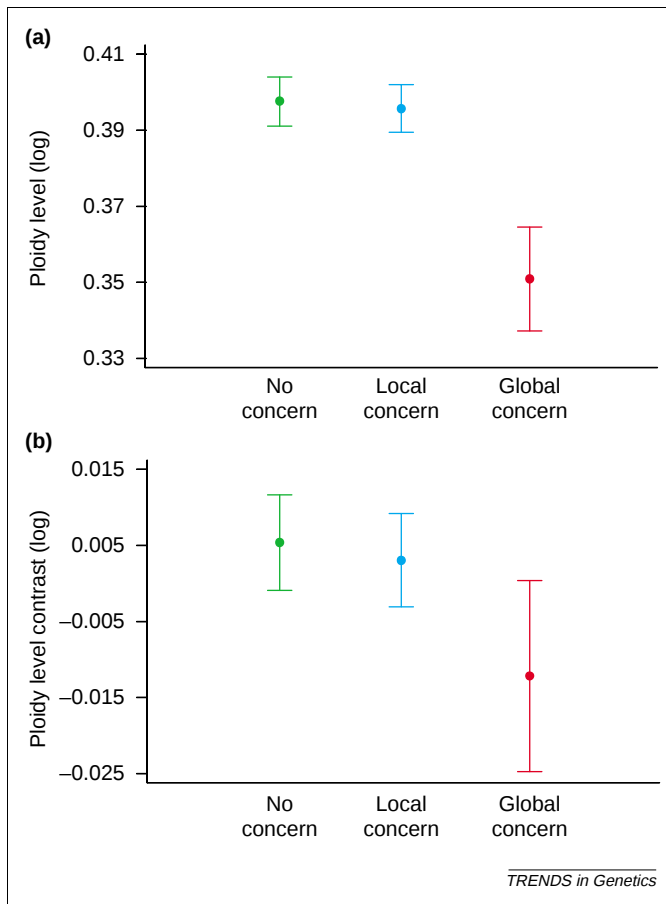


Figure 2. Differences in ploidy level among plants of different conservation status, with the effect of genome size being removed in multifactor ANOVA [means with 95% least significant difference (LSD) intervals]. Only species with indicated ploidy level were taken. (a) Raw species points ($n = 1314$, 1377 and 291 for 'No', 'Local' and 'Global', respectively; ANOVA, $P < 10^{-4}$). (b) Within-families contrasts. Only species belonging to families with within-family heterogeneity in conservation status were taken ($n = 1144$, 1195 and 286 for 'No', 'Local' and 'Global', respectively; ANOVA, $P > 0.2$).

$r = -0.11$, $P < 0.001$, $n = 756$; for angiosperms only: $r = -0.11$, $P < 0.001$, $n = 716$), which indicates that the association of a larger genome with extinction (or depressed origination) is not unique to the recent time. This result is surprising because an earlier family-level phylogenetic analysis suggested that genome size of angiosperm (flowering) plants was increasing during evolution [25]. The analysis of paleontological data using the Fossil Record 2 database (<http://palaeo.gly.bris.ac.uk/frwhole/FR2.html>) confirmed this conclusion: there is a negative correlation between mean genome size of angiosperm families and the upper limit of their first appearance in geological time ($r = -0.39$, $P < 0.001$, $n = 74$), that is, more recent families have larger genomes on average. Thus, it can be concluded that a pressure of transposable elements, which expands genomes of plants in the course of evolution, is associated with a reduced speciosity. (However, a note of caution: new families might simply not have had enough time to produce as many species as the older families, but, on the other hand, they have had less time for extinction as well.) Although analyses of the above-species level cannot distinguish between extinction and depressed origin of species, the Red List clearly demonstrates that the excess of noncoding

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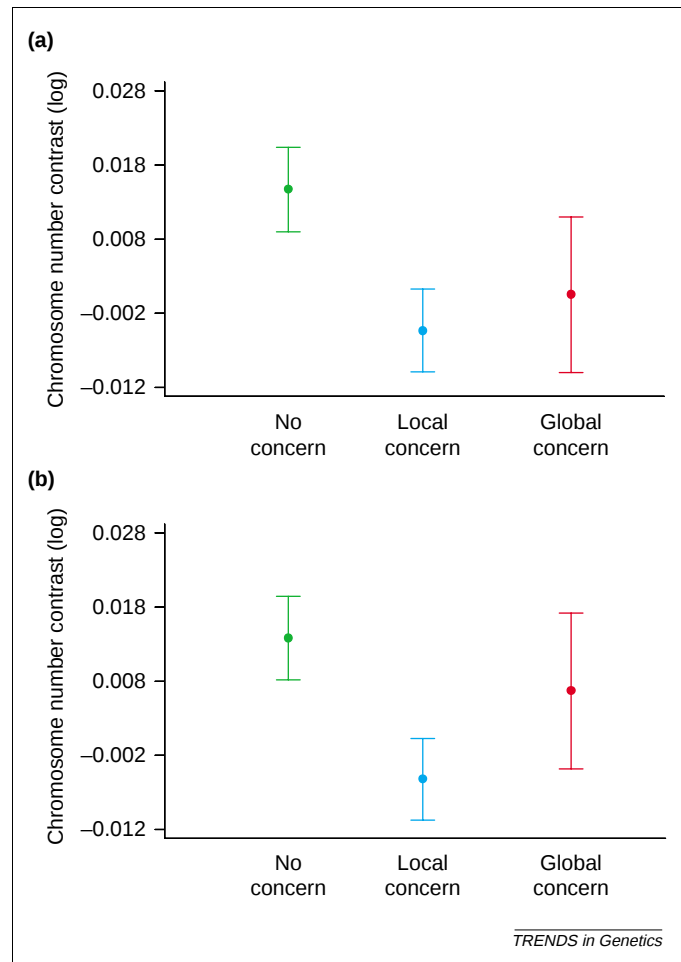


Figure 3. Differences in chromosome number among plants of different conservation status [means with 95% least significant difference (LSD) intervals]. Only species indicated as diploids and belonging to the families with within-family heterogeneity in conservation status were taken. (a) Within-families contrasts ($n = 830$, 860 and 241 for 'No', 'Local' and 'Global', respectively; Kruskal-Wallis, $P < 10^{-6}$; although the LSD intervals for 'No' versus 'Global' are overlapped, in nonparametric Mann-Whitney and Kruskal-Wallis tests $P < 10^{-3}$ for this difference). (b) Within-families contrasts, with the effect of genome size being removed (ANOVA, $P < 0.01$).

DNA in the plant genome correlates with the likelihood of extinction. It seems to be a first documented case of antagonism between different selection levels, which thereby supports the recently developed concept of hierarchical selection [26].

Other mechanisms of genome size reduction

There are at least two other mechanisms that can reduce genome size: a negative balance of small insertions and deletions [27–31] and illegitimate recombination [32], which might partly counteract the activity of transposable elements inflating the size of the genome. However, these are mutation mechanisms (or, more precisely, selectivity or neutrality of these mutations cannot so far be definitely established), whereas what is shown here is a selection vector. It should be noted that genome compaction was observed in some plant lineages [25,33,34], but the underlying mechanisms are unclear. In addition it seems that all these mechanisms cannot completely offset the activity of selfish DNA (because, for instance, noncoding DNA constitutes 99% of the human genome [35], and the

genomes of some plants, fishes and amphibians are a dozen times larger).

Phenotypic mediators of genome size

Obviously, the redundant DNA interacts with the environment (and thus is subject to selection at the organismal or species level) not directly but through intermediary phenotypic traits (e.g. retardation of development). Larger genomes are known to be associated with longer cell and life cycles [1,36]. It was shown that correlation between genome size and duration of embryonic cell cycles in related species can reach its utmost value ($r = 1.0$), which indicates not just statistical but functional dependence [37]. It was argued that retardation of development caused by genome enlargement cannot be adaptive *per se* but only if associated with some compensating adaptation, for example, a reduction of metabolic rate (due to a lower cell surface to volume ratio and also, according to the concept of 'buffering' DNA, due to an energy-independent attenuation of environmental fluctuations that reach the nucleus), which allows a species to occupy a niche with a lower energy supply [5,38,39]. The retardation of development that is necessary for phenological reasons, for instance, could probably be achieved by genetic regulatory means without accumulation of redundant DNA. Metaphorically, one can go slower without attaching a cannonball to the leg (and, after all, there are no such things as competitions to find who races the slowest). In other words, selection vectors are supposed to be asymmetrical for genome compaction and for genome enlargement: in the former selection is for speed (of development or locomotion), whereas in the latter it is for reduction in metabolic rate due to passive (energy-independent) cellular homeostasis.

The role of phenotypic mediators in the deleterious effect of selfish DNA should be emphasized because even after reading the above paragraph, one critic claimed that all phenotypic correlates should be corrected for before one can conclude on the negative effect of redundant DNA. However, according to this logic we should remove the phenotypic effect of, for instance, the gene responsible for hemophilia when comparing its wild-type and mutant alleles, and thus conclude that there is no harmful effect of the hemophilia allele. It is, however, interesting to what extent the maladaptive effect of noncoding DNA is connected with the retardation of development. It has been argued that slow-developing plants (with larger genomes) might be at increased risk of extinction [40]. But, ecologists still dispute what life-history traits are associated with extinction risk [41]. It was shown (for birds) that ecological mechanisms underlying extinction can differ depending on whether the threat is caused by habitat loss or is due to human persecution and introduced predators. Species with short generation times are more vulnerable to the former, whereas species with slower development are more vulnerable to the latter [41,42]. It is estimated that ~90% of threatened plants are affected by habitat loss, whereas introduction of alien invasive species and exploitation (mainly collecting) affect only 15% and 8% of threatened plants, respectively [43]. Thus, it is not *a priori* clear that slow-developing plants should be more vulner-

able. For angiosperms, the Plant DNA C-values Database also contains data on life cycle (annual, biennial, perennial), therefore it is possible to test this question. The association of a larger genome with increased risk of extinction does not hold for annual angiosperms taken separately (probably because of a too small variation of genome size among them). However, the effect with the within-families contrasts held for perennials taken separately (both with inclusion and exclusion of biennials; Kruskal–Wallis, $P < 10^{-3}$). It remained to check whether the difference between annuals and perennials could affect the results. After the effect of the difference between annuals and perennials was removed in multifactor ANOVA (biennials were excluded from the analysis), the association of the larger genomes with the risk of extinction still held ($P < 10^{-3}$). It is interesting that although plants of no concern and of global concern seem not to differ (significantly) in their average life-cycle duration, plants of local concern show on average shorter life cycles (Figure 4). After removing the effect of genome size, the picture remained qualitatively the same (not shown). As another approach, the within-genera contrast in conservation status (i.e. ratio of conservation status for a given species, which was set to 0 in case of no concern or 1 in case of global or local concern, to average conservation status of a given genus) was checked for plants with different life-cycle durations. It was found that for plants of global concern the within-genera contrast in conservation status was apparently but not significantly higher for perennials than for annuals (Kruskal–Wallis, $P < 0.12$), whereas for plants of local concern the within-genera contrast was significantly lower for perennials than for annuals (Kruskal–Wallis, $P < 10^{-4}$), which was qualitatively equivalent to the picture shown in Figure 4. Thus, it can be concluded that the maladaptive nature of larger genomes is (at least, partially) independent of duration of plant life cycle.

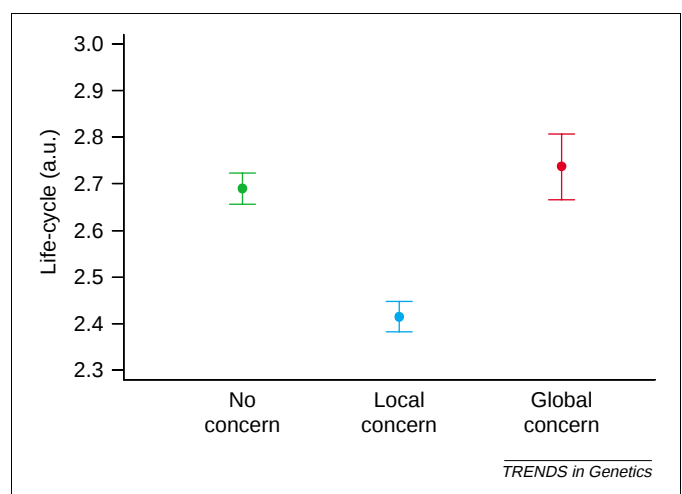


Figure 4. Life cycle of angiosperms with different conservation status [means with 95% least significant difference (LSD) intervals]. Life cycle was set to one for annuals, two for biennials and three for perennials. ($n = 1096$, 1169 and 245 for 'No', 'Local' and 'Global', respectively; Kruskal–Wallis, $P < 10^{-10}$; for difference between 'No' and 'Global' Kruskal–Wallis, $P > 0.2$.) Abbreviation: a.u., arbitrary units.

'Bureaucratic' DNA

The accumulation of noncoding DNA in the genome, even if this first happened accidentally, might become a trap: besides the fact that transposable elements form 'landing pads' for other such elements [44,45], the longer life cycles and the lower population sizes (because of the larger body sizes), caused by genome enlargement, might attenuate purifying selection against larger genomes, thereby simulating a neutralist effect of 'permissive' selection. Then, probably only a shift into a niche with, for instance, a lower energy supply can protect such forms from competition with lineages with smaller genomes (in this case, the activity of selfish DNA can be considered at the organismal level as a preadaptation to such a niche or even symbiosis [5]). It has often been argued that noncoding DNA is necessary for gene regulation, forming an 'epigenetic machine' of the genome [46], but it is unclear what part of it is really necessary (especially in the larger genomes). Possibly, the term 'bureaucratic' DNA can embrace both the selfish and the regulatory aspects of noncoding DNA. Viewing the genome as a large bureaucratic machine, where it is hard to disentangle the regulatory function from the selfish activity and where a family of selfish DNA elements can propagate by participating in the same, already excessive, regulatory functions, probably is closer to the truth than the extremes – a perfect organization where each element is totally devoted to the higher cause, or a permanent battleground between ultimately selfish elements. Although a certain amount of bureaucracy is necessary for the organism, it could grow, according to Parkinson's law, to fill the work available. Organizations (and organisms) that have a larger bureaucratic machinery might not be organizationally more advanced, but one cannot say that any element in them is without a function. The larger machinery probably copes better with environmental fluctuations, but works slower.

Evolution and extinctions

It is possible that negative traits associated with a larger genome become especially vulnerable in the periods of augmented extinction (as, for instance, during the recent augmentation of extinction, which began ~30 000 years ago [47]). But there have been at least five mass extinctions over evolutionary time (the 'Big Five'), much greater in scale than the recent augmented extinction period, with habitat loss caused by a change of climate and other cataclysms, plus myriad smaller ones [48]. The overall frequency distribution of extinction intensities is a skewed unimodal continuum [49]. Therefore, an augmented extinction period is not an unusual state in evolution. It is recognized now that besides their negative role, the extinctions can reshape the evolutionary landscape in more creative ways, via the differential survival of lineages and the evolutionary opportunities afforded by the demise of dominant groups [48]. Possibly, they are also the periods when genomes lose excessive weight (or, more exactly, when genomes that contain too much selfish DNA go off the scene).

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