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SYMMETRY AND EVOLUTION: A GENOMIC ANTAGONISM APPROACH

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"Parts which are homologous tend to vary in the same manner; and this is what might have been expected, for such parts are identical in form and structure during an early period of embryonic development, and are exposed in the egg or womb to similar conditions. The symmetry, in most kinds of animals, of the corresponding or homologous organs on the right and left sides of the body, is the simplest case in point; but this symmetry sometimes fails…"[1]

Darwin was one of the first biologists interested in the developmental failure of perfect symmetry, what is now known as fluctuating asymmetry. Fluctuating asymmetry is the random left-right size differences in bilateral traits designed by selection to be perfectly symmetrical. Thus at the population level genuine fluctuating asymmetry (as opposed to directional or antisymmetry, neither of which are the focus of this chapter) should be normally distributed with an asymmetry mean of zero. Arguably Van Valen helped to facilitate the modern scientific study of fluctuating symmetry, despite a long history of its use.[2] Fluctuating asymmetry (FA) is an indicator of underlying developmental instability which displays the inability of an organism to survive adverse environments or conditions during ontogeny. [3 4 5 6 7] FA is often used as an indicator that structural features are developing under environmental and genetic stress, essentially FA may be an important example of a disruption in homeostasis.[8] Developmental instability can be measured in two ways: (a) as major developmental errors that occur as birth defects i.e. phenodeviants and (b) as subtle deviations from bilateral symmetry i.e. fluctuating asymmetry. The latter of which is the focus of this chapter. Further, this chapter introduces a new genetic co-adaptation theory for developmental stability called *genomic antagonism reduction*. Simply stated when intragenomic and intergenomic conflicts are minimised, individuals will be better at buffering ontogenetic stressors. Some previous findings are consistent with this proposition, and they will be reviewed.

An array of studies in conservation biology have shown that asymmetries in bilateral morphological traits indicate underlying developmental instability. [9] It is assumed, due to considerable

evidence, that low fluctuating asymmetry indicates good genotypic or phenotypic quality (i.e., good development). [10] [11] FA covaries negatively with health and physical performance in a diverse array of species including humans, and appears to be a marker underlying the reproductive viability and health of a given phenotype. [12] [13] [14] [15] [16] [17]

Fluctuating asymmetry provides a 'window' with which to view how an organism has adapted to the environment and hence its ability to resist the harmful development perturbations. [18] [19] Møller has reported that symmetrical individuals generally have better survival and mating success than their asymmetrical counterparts. [20] Perfect symmetry is the optimum for traits designed by selection to be perfectly symmetrical, the larger the fluctuating asymmetry the lower the developmental stability. [21] [22] [23] It is important to note that fluctuating asymmetries emerge with increasing exposure to a wide range of stressors such as pollutants, extreme temperatures and genetic perturbations. [24] For example, captive ornamental goldfish, *Carassius auratus,* and carp, *Cyprinus carpio* showed significantly higher FA than wild samples in response to environmental stress such as overcrowding and lower water quality. [25] Further Hódar found that leaf asymmetry in Holm oak, *Quercus ilex,* decreased in rainy sites compared to dry sites. [26] FA in house flies, *Musca domestica,* appears to be influenced by rearing conditions, showing higher FA at lower temperatures and finally Møller et al. found that disruptive light regimes when rearing domesticated chickens *Gallus gallus* caused increased FA. [27] [28]

Degree of symmetry can be shaped by artificial selection, such as selection for endurance wheel-running in mice and has been linked to natural selection and sexual selection outcomes. [29] [30] [31] In terms of sexual selection, studies across diverse species reveal that low asymmetry males tend to obtain more mates. In lekking black grouse, *Tetrao tetrix,* symmetry of their tarsi (joint between the leg and foot) predicted copulation success. [32] FA in yellow dung flies, *Scathophaga stercoraria,* also accounted for decreased mating success. [33] Swaddle reports that FA is a negative predictor of hunting and mating success in the yellow dung fly, *Scathophaga stercoraria.* [34] Males in one class of British yellow dung fly,

Sepsis cynipsea, that were more symmetrical in fore tibia length had more mates. [35] Paired male field crickets, *Gryllus campestris L,* were older, larger and more symmetrical. [36] Low wing length FA in house flies, *Musca domestica,* are found to have a higher mating success.[37]

Across diverse species, a large literature points to meaningful connections between FA, genotypic and phenotypic quality. It has been reported that FA is negatively correlated with attractiveness in humans. [38] The 'good genes' model of sexual selection assumes that due to the benefits associated with the selection of a healthy mate i.e. enhanced offspring viability, mate preferences favour healthy individuals. [39] Along with this, studies have found a relationship between attractiveness and facial symmetry. [40 41 42] Likewise, lower FA is related to an array of human sexual behaviours, such as increasing number of sex partners, younger age of first sexual contact, and sexual contact outside a stable relationship. [43] Furthermore, FA is negatively associated with the attractiveness of the human vocalisations, a sexually dimorphic feature in humans.[44]

Examinations of physiological and physical health correlates of FA have shown an array of theoretically consistent associations. [45] For example sex-typical body size is associated with low FA. [46] Male testosterone levels (an important correlate of muscle development) and athleticism are both positively associated with attractiveness possible due to underlying developmental stability. [47] Indeed one would expect that greater body mass in men (within the normal range of healthy variation) would be negatively correlated with FA. [48]

FA is also associated with diverse outcomes associated with central nervous system development in humans. For example Malina & Buschang tested a group of normal and retarded males and found that FA was significantly greater among mentally retarded individuals compared to normal subjects.[49] This could suggests a possible connection between developmental instability and central nervous system functioning. Thoma et al found a negative correlation between FA and neural speed as measured by magnetoencephalographic (MEG) dipole latencies during a sensory-motor integration task (i.e., index

finger response to a visual stimulus). [50] Increased FA was a predictor of slower neural-processing across all stages of the visual-motor task in a sample of men. There are other diverse psychological correlates with asymmetry. For example, patients with schizophrenia have increased brain asymmetries. [51] Finally Martin et al. found a positive relationship between FA and depression in men. [52]

Increasingly there are negative associations between FA and locomotory efficiency (a commonly used proxy for physical health). Areas relating to mechanical efficiency across species have shown that low FA is associated with increased performance. [53] For example wing asymmetry in wild-caught adult European starlings, *Sturnus vulgaris,* revealed that wing asymmetry is negatively related to flight performance whereby investigations indicate that asymmetry of both wings and tails decreases mobility and swiftness. [54] Martin & Lopez found in male lizards *Psammodromus algirus* that femur length FA resulted in decreased escape speed and ability. [55] In human studies, low FA was associated with higher running ability rankings.[56] More recently, Longman, Stock & Wells found that FA was a negative predictor of rowing performance.[57] These associations could be due to anatomical impairments or possibility neuromuscular coordination. For example of anatomical impairments, lower back pain sufferers have greater asymmetry in pelvis, ulnar length and bistyloid breadth. [58] The positive association between dance ability and symmetry in a healthy sample suggests that motor movements and neuromuscular coordination may also reflect degree of underlying developmental instability. [59]

WEAKNESSES AND FUTURE RESEARCH

Despite the FA literature revealing significant associations with biologically important outcomes across diverse species, including humans, the field is not without controversy. Most human FA studies have a similar rationale (i.e., researchers expect that since high FA reflects an inability to reach an adaptive end-point, then it must correlate with all things bad). However, there are notable exceptions to this pattern worth considering. Brown and Moore predicted that since high FA individuals may be

vulnerable to extrapair copulations, then they may benefit from increased mate guarding behaviours via a facultative use of romantic jealousy. [60] Indeed this is what Brown and Moore found, and it highlights the importance that if an organism is developing under genomic or environmental stress, they may employ alternative tactics to cope with the costs of high FA (i.e., 'doing the best in a bad situation'). [61]

Another misconception is the erroneous idea that since low FA is an indicator of 'good genes', this asymmetry level must be fixed at birth. Note that 'good genes' has largely been used as short-hand for good development (where genes only play a part among other factors). Regardless of this terminological issue (i.e., accuracy of the good genes metaphor), it is important to note that FA is not fixed at birth, it changes over the course of development and there is mounting evidence that there is a yet to be discovered developmental homeostatic mechanism of compensatory growth. [62] Specifically, there is solid evidence that across diverse taxa, that when one side is larger than the other, growth slows for the larger side and speeds up on the smaller – essentially correcting the previous subtle asymmetry.

There are mixed findings in the study of FA (although presumably no more than any other area of evolutionary ecology – see Møller and Thornhill). [63] These mixed findings may reflect the weakness of FA as a general measure of latent developmental instability, problems with measurement error or a combination of both. It has been argued that the effect size and heritability for FA is rather low, but not necessarily lower than any other trait studied in ecology. Nonetheless, developmental stability holds a special place in evolutionary biology since it rests at the fundamental core of how genes and the environment are intertwined during the ontogeny of phenotypes. Early FA researchers would refer to low FA individuals as displaying fitness indicators or perhaps displaying their "good genes" to the opposite sex. Generally such short-hand has subsided within the main literature as few studies have actually investigated the associations between FA and molecular loci. This has now begun to change with the increasing availability of molecular and cellular assays of healthy development. One example is the study of FA and heat shock proteins.

Heat shock protein (*Hsp*) activity under some circumstances may be a better assay of developmental buffering capacity than FA. [64] [65] [66] Heat shock proteins are an evolutionarily-conserved protein class important for the regulation of other proteins when exposed to stress. They are believed to be an important aspect of an organism's developmental buffering capacity. For example in one study of *Drosophila*, *Hsp90* chaperone buffering capacity was not correlated with fluctuating asymmetry, but in another study, Takahashi et al measured the activity of four different *Hsp* genes (*Hsp22, Hsp67Ba, Hsp67Bb, Hsp67Bc*), and found the predicted association (i.e., deletions of relevant *Hsp's* led to an increase in *Drosophila* bristle FA). [67] [68] So far there have been no studies testing the link between human FA and heat shock protein buffering capacity. However, given the recently reported positive association between human FA and oxidative stress -- a correlate of *Hsp* response -- by Gangestad, Merriman and Thompson, developing multiple assays of developmental buffering capacities at different levels of biological organisation, may be the best way forward for future research due to problems with effect size and measurement error in FA studies. [69]

CONFLICTING THEORY IN THE STUDY OF SYMMETRY

In some ways the study of FA has been part of the scientific pursuit to find an accurate assay for the developmental integrity of organisms (i.e., the unity of their component parts). In this sense the big questions in the scientific study of symmetry have not really diverged much from Darwin. How do our developmental integrity genes (presuming such entities exist) regulate symmetry in developing organisms facing environmental and genetic stressors? This outstanding question may be resolved in part by remembering that bilateral traits have one genotype, so any differences between sides are an epigenetic phenomenon. Modern epigenetics is defined as heritable changes in gene expression that do not change the underlying DNA sequence. Bilateral traits are analogous to monozygotic twins (i.e., they share the same genotype). Specifically when size and shape differences emerge between the left and right sides,

they may be caused by epigenetic forces that are only recently being addressed via molecular study (e.g., investigating mechanisms such as DNA methylation, histone modifications and microRNAs).

The remainder of this chapter will present a new theory of developmental stability specifically designed to address existing theoretical controversies surrounding the generality of the relationship between heterozygosity and FA. Heterozygosity is when two alleles on each strand differ from one another. There are two rival approaches regarding the emergence of developmental instability in nature each bolstered by contradictory empirical findings regarding the FA-heterozygosity association: (1) the co-adapted gene complex hypothesis (simply stated heterozygosity and FA are predicted to be positively related); and (2) the heterozygous advantage hypothesis (simply stated FA and heterozygosity should be negatively correlated). [70] It is proposed in the chapter that a reduction of genomic antagonisms may in part mediate the contradictory associations found with regards to the association between FA and heterozygosity.

DEVELOPMENTAL STABILITY: A GENOMIC ANTAGONISM APPROACH

Most scholars acquainted with the study of evolution are aware of Dawkins' idea that genes are selfish replicators, however as importantly pointed out by Strassmann, Queller, Avise, and Ayala, selfish genetic elements behave in particularly selfish ways, as their replication success often supplants the interests of the organism itself.[71] These ultra-parasitic elements have unique biochemical pathways which can be in conflict with other loci in the genome (Figure 1 illustrates different types of selfish genetic elements).

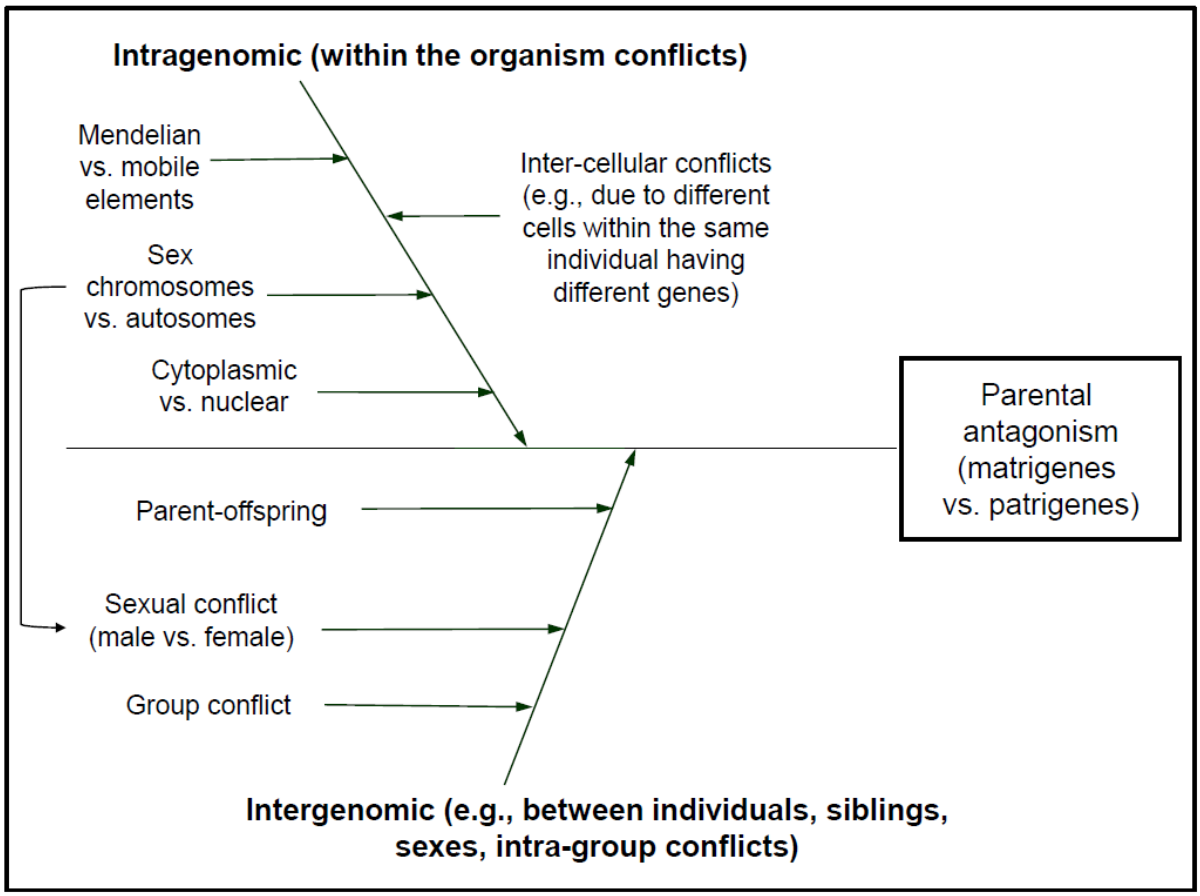

Figure 1. Types of intragenomic and intergenomic conflicts, modified from Werren.[72]

Werren hypothesized that selfish genetic elements are evolutionarily maintained by their selfish behavior, but the new chunks of DNA left throughout genomes can sometimes be co-opted, domesticated, or modified to cause some beneficial effect to the organism.[73] Figure 1 highlights the importance of parental genome conflicts, which mediated in part by epigenetic molecular tags of shared recent ancestry.

Importantly we see that organisms in principle are not cohesive wholes. Within genomes there are sometimes conflicts. Intragenomic contest evolution or sexual antagonistic effects exist, also parental antagonisms between parentally-derived alleles within offspring. The idea that there is a quantifiable developmental integrity must deal with the presence of selfish genetic elements. Interestingly there has been little work on this for the study of symmetry (however there are notable exceptions to be discussed below).

Despite the diversity of selfish genetic elements in Figure 1, there are some general observations regarding their frequency in nature. [74] For example, the diversity of selfish genetic elements in a species is positively correlated with outbreeding rate. Indeed it is expected that sexual reproduction enhances the spread of selfish genetic elements, while inbreeding decreases it. [75] Heterozygosity decreases upon inbreeding and opportunities for transmission between genomes decreases in a population. Thus among inbred populations, selfish genetic elements have an increased chance of being paired with their homologue and the frequency of selfish behaviour would decline impairing spread of the element. Among inbred strains of yeast *Saccharoyces cerevisiae* a homing endonuclease gene -- considered to be a selfish genetic element – there was no significant increase in frequency of the selfish genetic element compared to outcrossed samples. [76] The work of Goddard et al provides convincing experimental evidence for the effect of inbreeding to dampen the spread of a selfish genetic element. [77] Importantly, this work provides evidence that host mating system plays a critical role in the population dynamics of a selfish genetic element.

Based on the above findings, the idea presented here (Table 1) is that the contradictory correlations between FA and level of heterozygosity may depend on the presence of selfish genetic elements within the genome. Specifically, when antagonisms are low (e.g., among some plants and ectotherms), a negative association between FA and heterozygosity will emerge; however the reverse will be true when genetic antagonisms are high (e.g., among social living organisms). In the latter case, social-living endotherms may benefit from homozygosity as it could weaken the effects of genetic antagonisms (e.g., conflict between parental genomes).

Table 1. Predictions derived from genomic antagonism reduction theory regarding FA outcomes by levels of heterozygosity and genomic conflicts.

	HETEROZYGOSITY		
GENOMIC ANTAGONISMS		LOW	HIGH
	LOW	↑ FA	↓FA
	HIGH	↓FA	↑ FA

Based on genomic antagonism reduction theory for developmental stability, a possible solution emerges for the contradictions between the genomic co-adaptation versus heterozygote advantage approaches to developmental stability (i.e., the latter predicts that low FA organisms will have high heterozygosity, while the former predicts the reverse pattern).

These contradictions may depend upon the degree to which social relations affect the spread of selfish genetic elements and underlying intragenomic antagonisms. Social conflicts with kin are caused by distinct species and life history factors (i.e., live bearing, heat sharing, internal gestation, postnatal care, relatedness asymmetries due to dispersal and mating systems etc). One way to re-conceptualise this problem is the development of a theory that takes into account the degree of intragenomic antagonisms for a given species or individual. Essentially when testing heterozygosity-FA relationships, one should consider species natural and life history background for the degree of genomic conflict. The cross-species FA-heterozygosity associations reported Vøllestad, Hindar and Møller indicate a pattern largely consistent with the genomic antagonism hypothesis, which is explored further in the following paragraphs. [78]

Vøllestad, Hindar and Møller found the predicted negative association between FA and heterozygosity (for within-population studies of ectothermic species only). [79] One reason for this association not emerging for endotherms may be due to the degree of parental antagonism among internal

gestating and heat-producing species. Indeed it appears that in Vøllestad, Hindar and Møller, among organisms with conditions ripe for genetic conflict (i.e., internal gestation, heat sharing in social contexts) the negative association between FA-heterozygosity reduces. [80] One may ask: why would heat production and sharing be important for the development of underlying genomic conflict? The driver is when heat is shared among littermates or others with varying degrees of genetic relatedness between heat givers and receivers. Essentially, once endothermia emerged evolutionarily, conflicts over heat generation and reception may occur. When paternal genomes benefit from withholding heat from others, at a cost to the maternal genome, maternal counter-adaptations are expected to evolve.

Endothermia is a classic example of developmental stability. That is, altering internal mechanisms of heat generation is a homeostatic response to environmental disturbance. In the case of nonshivering thermogenesis, there is now empirical evidence that maternal genomes are involved with heat sharing among litter mates, while paternal genomes are more selfish. [81] [82] [83] [84] Specifically, heat generated by huddling littermates is a collective good, and the empirical evidence suggests that there are two paternally expressed loci for reducing heat and one maternal loci involved with increasing heat to share with huddling littermates. [85] It stands to reason that endotherms are more likely to be engaged in intragenomic conflicts due to heat social exchange between rivals (e.g., thermoregulatory social conflicts mediated by brown fat or other mechanisms). Endotherms are unintentional temperature altruists. Once the evolution of endothermia emerged during evolutionary history, the context was set for the emergence of conflicts over sharing one's heat with others (e.g., huddling littermates). This hypothesis may seem far-fetched, however there is solid evidence that some endotherms with brown fat show the traces of an ancient intragenomic conflict of social origin. Specifically, genes for storing heat for oneself are paternally expressed, while genes for sharing heat are maternally expressed. Indeed simply being an endotherm (with brown fat), could be a rough indicator of genomic antagonism. It is also important to note the existence of behavioral-induced enothermia among ectotherms (known as facultative endothermy

in insects (e.g., the honeybee – see Kammer & Heinrich). [86] Indeed, some insect species are capable of maintaining higher than ambient abdominal temperatures using exercise behaviours. So, why do they? One hypothesis is to alter investment in kin and this will produce intragenomic conflicts over the muscle adaptations producing the behaviour. In these social ectotherms with facultative endothermy we would not expect the negative association between FA and heterozygosity. Indeed in the Vøllestad, Hindar and Møller'scross-species review report that there is a negative association between FA-heterozygosity among ectotherms, not ectotherms. [87] Eusocial insects are facultative endotherms (i.e., normally ectotherms unless they creat heat for the benefit of the colony) and may not fit the ectotherm pattern. As expected, the average association between FA and heterozygosity ($M = 0.003$, $SD = 0.095$) among fourteen studies of honeybees *Apis mellifera* (over 4,000 subjects), diverged from the ectotherm pattern (i.e., a significant negative association). That is, a one-sample t-test with a test-value of "0" revealed little association in honeybees between FA and heterozygosity: $t\ (14) = 0.108$, $p = 0.916$. A similar pattern emerged in ants *Iridomyrmex humilis*, although to my knowledge there is no evidence of facultative endothermy.[88] *Iridomyrmex humilis* do have multiple queen colonies, which would in theory increase genomic antagonisms. A genomic antagonism reduction approach would suggest that in the case of high genomic antagonisms, hetrozygosity may be more detrimental to developmental stability (i.e., higher FA) relative to homozygosity. Further work is needed on eusocial *Hymenoptera* to determine if they do in fact diverge from the negative relationship between heterozygosity and FA found in many ectotherms.

SYMMETRY, SELFISH GENETIC ELEMENTS AND CONFLICT RESOLUTION

One of the key premises of this chapter is that selfish genetic element elements will increase developmental instability. There is some evidence for this association. For example, Leamy, Meagher, Taylor, Carroll and Potts found that a selfish genetic element called the t-allele was associated with increased fluctuating asymmetry in house mice. [89] However, in a study of yellow-necked mice, *Apodemus*

flavicollis results were less straightforward.[90] Specifically, trait size variability (but not FA) was positively related to increasing B chromosome number (a well-studied selfish genetic element). Interestingly, the levels of the FA followed the changes in frequency of subjects with B chromosomes at the beginning of the mating season. Granted, it could be that unknown ecological factors influenced a disruption in developmental homeostasis and the frequency of animals with B chromosomes.[91]

Interestingly, Zeh and Zeh hypothesised that organisms may use mating strategies to avoid selfish genetic elements.[92] Specifically, when a selfish genetic element reduces the competitive ability of sperm in those that are carriers, females may use polyandry as a strategy to avoid carrier males as the fitness of their progeny would be more likely to be compromised if they inherit the selfish genetic element. Thus Zeh and Zeh theorized that polyandrous mating may be a tactic to reduce effects of genomic incompatibility caused by selfish genetic elements.[93] The antagonism reduction theory of developmental stability argues that when intragenomic antagonisms are reduced (e.g., low relatedness asymmetries, reductions in selfish genetic elements due to lower heterozygosity) individual organisms will have greater developmental stability. To indirectly test this hypothesis, Cuervo and Møller's cross-species avian FA data was categorised by whether there a species is polyandrous, socially monogramous, lekking or polygynous. Hasselquist and Sherman have shown that chicks from extrapair matings are twice as common in socially monogamous compared to polygynous passerines.[94] If polyandry is a strategy to avoid genetic incompatibility from selfish genetic elements as hypothesised by Zeh and Zeh, it may have effects on developmental stability of offspring.[95]

In 70 species of passerines, Cuervo and Møller provided useful data on FA differences by species, sex and mating system.[96] Species' mating systems were classified based previously published findings. Specifically "socially monogamous" was if a male and a female assortate for reproduction; "polygynous" was if approximately 5% of the males were reproductively associated with more than one female; polyandrous if at least 5% of the females was associated with more than a single male for reproduction,

and (4) lekking if males aggregated at communal display grounds where females arrived to make their mate choice. Presuming multiple paternity decreases the costs associated with selfish genetic elements, one would expect that socially monogamous / polyandrous species will have lower FA than polygynous / lekking species. [97] Such a finding could indicate that multiple paternity may increase offspring developmental stability via the reduction in incompatible matings due to selfish genetic elements. To test these hypotheses the published data from Cuervo and Møller were investigated. [98]

It was predicted that socially monogamous / polyandrous species of passerines will have reduced FA than non-monogamous species (e.g., lekking or polygynous). Counter-intuitively perhaps (as one could have predicted that where FA is sexually selected for low values then directional selection would have caused reduced FA in such species – the so-called Lek paradox), non-ornamental FA was significantly lower among monogamous / polygamous ($M = 0.53$; $SD = 0.28$, $n = 82$) compared to lekking and polygynous species ($M = 0.89$; $SD = 0.98$, $n = 53$): $t\ (57.55) = 2.59$, $p = 0.01$ (Figure 1). Note that between-group FA variances also significantly differed (Levene's test $p < 0.01$).

In contrast to non-ornamental FA (where the sexes did not significantly differ > 0.60), there were sex differences in ornamental FA, with males having higher FA ($M = 4.68$, $SD = 7.39$, $n = 61$) than females ($M = 2.20$, $SD = 3.00$, $n = 41$): $t\ (85.35) = 2.35$, $p < 0.05$. Males had significantly (Levene's test $p < 0.05$) greater FA variance than females. Finally, ornamental FA was not statistically different depending upon mating system ($p > 0.40$). This is indirect evidence for the genomic antagonism reduction theory of developmental stability and Zeh and Zeh's proposal that polyandrous matings reduce genomic incompatibly. [99] More generally it suggests that FA varies by mating system in passerines.

SUMMARY

It is the premise of this chapter, that when genomic antagonisms are minimized, developmental stability is expected to increase. This is a preliminary hypothesis and this review has just begun to unravel these

complex processes and interactions between the multiple levels of organization responsible for genomic conflict resolution and its possible role in developmental stability. The main findings were that: (1) The negative associations between heterozygosity-FA may be mediated by the degree of genomic antagonism. Specifically, species with reduced genomic antagonisms will receive developmental stability benefits from increasing heterozygosity and (2) Among passerines, polyandrous matings and mating systems may yield benefits for developmental stability.

There appears to be increasing amount of evidence suggesting that positive developmental outcomes are associated with the reduction of genomic antagonisms. Kawahara and Kono[100] have provided nice evidence for the general idea even though they did not measure morphological asymmetries. Specifically, in newborn mouse pups that were genetically manipulated in two regions -- the imprinting centres of *Igf2-H19* and *Dlk1-Gtl2* -- Kawahara and Kono found that that genetically manipulated mice (reduction in intragenomic conflict) lived 186 days longer than controls. [101] This extension of the longevity of progeny from bi-maternal genotypes in mice is consistent with models based on sex-specific selection of reproductive strategies causing differential effects on mortality. [102] It remains to be seen if such experimental manipulations of degree of genomic conflict reduce offspring FA. It is important to note that some of these mechanisms could well be mediated by behavioural adaptations. For example, mate choice and dispersal patterns. Future work needs to study how behavioural adaptations influence the degree of intragenomic conflict and optimise organismal developmental stability.

CONCLUSIONS

Organisms are integrated wholes but divided in principle.[103] This may appear contradictory for physiologists and organismal biologists not familiar with the concepts of selfish genetic elements (i.e., elements that harm the host for their own transmission advantage), parental (kinship theory of genomic imprinting) and sexual antagonisms (e.g, sexually antagonistic coevolution). Incorporating such genomic

antagonisms into our current views of developmental integrity of organisms could well help resolve debates surrounding the associations (and lack thereof) between FA and fitness outcomes. Essentially, like most work in evolutionary ecology, the natural and life history of organisms shifts the tradeoffs stable developers face. Essentially 'good genes' in one context may be 'bad genes' in another.

In conclusion we need to further explore the source and mechanisms mediating antagonism resolution, especially in terms of developmental integrity. It is the premise of this chapter, that upon the discovery of these regulatory mechanisms we will explain two puzzles simultaneously: (1) Contradictory findings regarding FA-developmental stability; and (2) why some organisms thrive with an abundance of selfish genetic elements (almost like a domesticated crop) and others do not.[104]

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