Behaviour genetics in the post-genomics era: From genes to behaviour and vice versa

Amitabh Joshi

Evolutionary Biology Laboratory, Evolutionary and Organismal Biology Unit, Jawaharlal Nehru Centre for Advanced Scientific Research, Jakkur P. O., Bangalore 560 064, India

Approaches to understanding behaviour in an evolutionary context can be grouped into two broad categories: behaviour genetics and behavioural ecology. In this paper, I briefly discuss the development of these two fields, to highlight some serious shortcomings in their focus and/or approach to understanding behaviour. These shortcomings have been pointed out by numerous researchers before, but it seems to be an opportune time to revisit this issue because present day methods are making it increasingly likely that some of these gaps in our understanding of behaviour can now be addressed experimentally. Early behaviour genetics essentially led to neurogenetics due to its focus on single-gene mutations affecting behaviour, which were often mutations affecting the nervous system. This line of work, consequently, diverged considerably from the study of behaviour per se and, although it contributed a great deal to our understanding of how the components of the nervous system work, it did not really shed much light on behaviour at the organismal level. More recent approaches in behaviour genetics include quantitative trait loci (QTL) mapping, which is an attempt to go beyond the black box approach of classical quantitative genetics and to track down loci mediating behavioural differences among individuals. Behavioural ecology provided a counter point to traditional behaviour genetics by explicitly focusing on ultimate causes, and trying to understand behaviour in terms of its adaptive (fitness) value. However, behavioural ecology too has at its core a conceptual lacuna, which is the absence of knowledge of the genotype-to-phenotype mapping for most behavioural traits. This conceptual lacuna is serious, and it affects not just behavioural ecology but most attempts to understand the evolutionary dynamics of complex and composite phenotypes that are, in terms of gene expression, far removed from the genome. What I have to say, therefore, applies broadly to attempts to understand the evolutionary shaping of complex phenotypes, and not just to studies of behaviour. I suggest that we really need a new and enlarged conception of, and approach to, behaviour genetics; an approach that will utilize recent advances in genetic technology, but yet be rooted in a holistic, organismal weltanschaung. I briefly describe some examples of this approach that I believe highlight the potential that this new behaviour genetics has to enrich and round off our understanding of behaviour from an evolutionary perspective.

Keywords: Adaptive evolution, genome-to-phenome mapping, natural selection, phenomics, reverse genomics.

BEHAVIOURS, like many other traits exhibited by organisms, can be understood at different levels of causation, from the absolutely proximal to the ultimate, or evolutionary. For example, Alcock[1] distinguishes two kinds of sub-levels within both proximal and ultimate cause explanations: genetic-developmental and sensory-motor mechanisms at the proximal level, and identifying historical patterns and selection pressures at the ultimate level. There are, of course, other ways of slicing up this conceptual pie. For example, Tinbergen[2] classified questions pertaining to behaviour into four categories: those related to function (fitness), causation (in the proximal sense), development (ontogeny) and evolutionary history (phylogeny). Understanding of the genetics and ontogeny of behaviours related to fitness is at present very meagre. Yet, such an understanding is crucial to a more complete evolutionary understanding of behaviour.

In this paper, my focus will be on the evolutionary understanding of behaviour. I shall make my own background and bias explicit at the outset: I am an evolutionary geneticist and I primarily study life-histories, not behaviours. However, behaviours are an important subset of life-history related traits and the two share in common the attribute that they tend to be complex and composite traits quite far removed from the primary expression of the genome. My main point of interest here is the link, or rather the lack of it in most work so far, between two of the sub-levels in Alcock's[1] scheme, one at the proximal and the other at the ultimate level of explanation. I will use the term behaviour genetics to encompass studies primarily aimed at understanding the genetic-developmental mechanisms responsible for the ontogeny of behaviours, and the term behavioural ecology to refers to studies aimed at understanding selection pressures acting on different behavioural phenotypes. The principal point I wish to make is that behaviour genetics and behavioural ecology are necessarily complementary

e-mail: ajoshi@jncasr.ac.in

approaches if one wishes to understand behaviours from an evolutionary perspective; alone, each discipline can lead to interesting, satisfying, even plausible adaptive explanations for this or that behaviour, but not too much more. Unfortunately, however, behaviour genetics and behavioural ecology have historically developed more or less in isolation, a state of affairs now begging for change. I hope to provide a convincing, though brief, re-statement of the case that the merger of behaviour genetics and behavioural ecology is not only desirable but necessary, and that the new technologies available in the post-genomics era offer us at least a rudimentary ability to empirically study the biological processes linking genes to behaviours and to fitness. My discussion is focused throughout on multicellular sexually reproducing organisms and their assemblages (populations), although most of the concepts here are applicable, with minor modifications or caveats, to unicellular or asexual organisms.

A fundamental recursion in biology

From an evolutionary point of view, the fundamental problem in biology is to understand the recursive process(es) whereby the transition is made from a distribution of phenomes in one generation to the corresponding distribution of phenomes in the next (phenome is being used here in the sense of the composite, whole-organism set of trait phenotypes). In the course of adaptive evolution, the phenomic composition of a population changes over generations, largely due to the action of natural selection. However, phenomes do not transmit themselves to subsequent generations; that is done by the underlying hereditary endowment, or the genome. Thus, there are three major aspects of living systems to consider when thinking about their evolution: the genome, the phenome, and the environment, in the sense of the ecological context within which the organism leads its life (Figure 1). Briefly, the information in the genome largely directs the formation of a phenome, although this process – development – is also affected by feedback from the phenome itself, and by the environment[3,4]. The phenome can, moreover, influence the environment, which consists of both the physical environment as well as other individuals of the same or different species. Sub-disciplines like physiology and behaviour address what phenomes 'do' and 'how' they do it. However, organisms live their lives in a specific physical and biological context, and phenomena like behaviour and physiology are, therefore, best understood in the context of the organism's environment; this interface of phenome and environment (the horizontal solid line in Figure 1) is the domain of ecology.

A major consequence of the interaction between a phenome and the environment is that some individual phenomes, themselves a reflection of their underlying genome and environmental conditions during their lifetime, are better able to make a living, find mates, and produce offspring in the particular environment they experience, compared to other contemporaneous phenomes: some phenomes are more fit than others. Neither phenomes nor the underlying genomes, however, get transmitted intact to the next generation. The meiosis–fertilization cycle that characterizes the haploid–diploid alternation of generations chops up and reconstitutes multi-locus diploid genomes. The multi-locus diploid genome is first cut up during meiosis along two axes: between as well as within chromosomes. What is then transmitted to the next generation are newly shuffled combinations of alleles at various loci, reconstituted into multi-locus diploid genomes by fertilization. Understanding and quantifying the consequences of this shuffling for the genetic composition of populations is the domain of population genetics. To go back to the more fit phenomes, it is basically the alleles making up their genomes that get transmitted to the next generation to a greater degree than those of the other, less fit, phenomes. A widely accepted present heuristic representation of living systems, thus, visualizes the dynamics of life in the form of three transitions or mappings, underpinned by a somewhat simplistic metaphor of information transfer. Development maps genomes to phenomes, ecology maps fitness onto phenomes, fitness is ultimately refracted through the genome-to-phenome map in reverse, to be mapped onto underlying genomes, and, finally, reproduction (heredity) maps an array of breeding genomes – via the cycle of

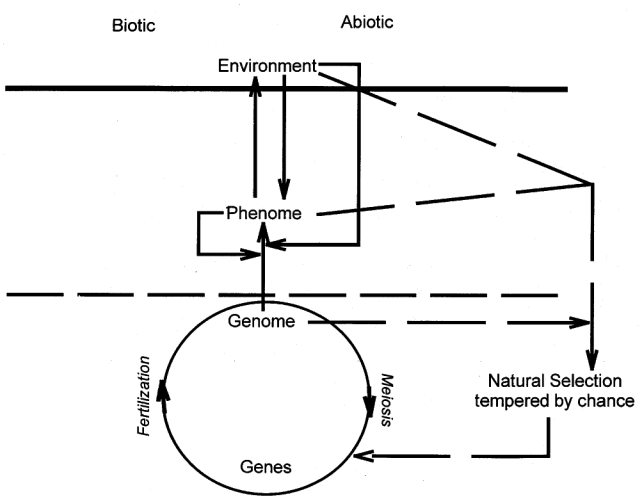

Figure 1. A schematic depiction of the major details underlying the recursion between phenomic distributions in successive generations (the depiction is with diploid organisms in mind, but the general issues are the same for haploids as well). Below the dashed horizontal line is the genetic domain, and the circle at the bottom represents the haploid–diploid–haploid cycling of genetic material through the alternation of meiosis and fusion, splitting up and recombining genes into genomes. The solid arrows in the centre of the figure represent influences that play a role in the lifetime of an individual, whereas the dashed arrows to the right of the figure represent influences on the evolution of the population of individuals.

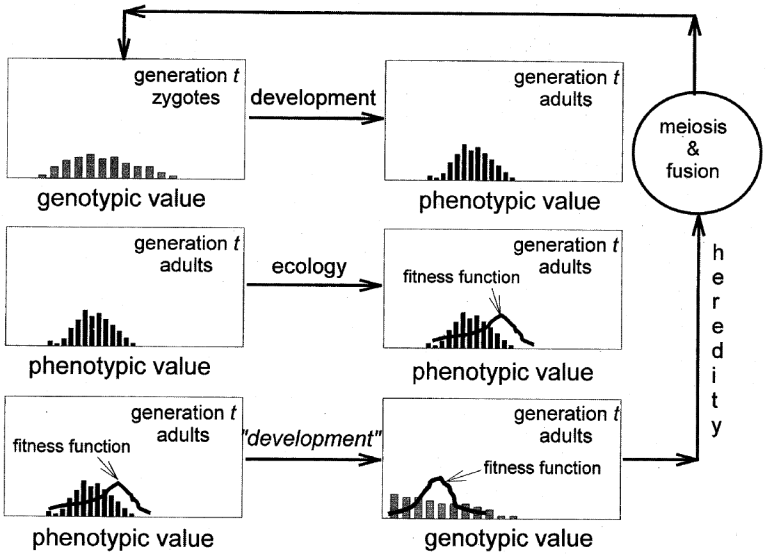

Figure 2. A representation of the recursion between phenomic distributions in successive generations in terms of three transitions (for details, see *A Fundamental Recursion in Biology*).

meiosis-fusion and the laws of Mendelian inheritance – onto an array of zygotic genomes that starts the next generation (Figure 2). Development is metaphorically seen as a process in which information that is largely genomic manifests itself over time as a phenome, which then must face the filter of natural selection wherein interactions between phenomes and environment determine fitness. In the context of this heuristic, evolutionary ecology focuses on how and why particular fitness functions are defined on the distribution of phenotypes in a population by its ecology, while population genetics addresses how the distribution of genotypes in a population changes from one generation to the next, under the influence of a given fitness function acting on it. Clearly, these two approaches are complementary if one is trying to understand a complex phenotype from an evolutionary viewpoint.

Black boxes, behaviour genetics and behavioural ecology

Of the three major mappings in living systems described above, two have been extensively studied; the third has essentially been pragmatically circumvented[3–6]. Evolutionary ecology focuses on the second transition depicted in Figure 2, whereas population genetics addresses the reproductive transition (heredity) in Figure 2. Clearly, connecting these two transitions that reflect, respectively, causes and consequences of natural selection, requires extrapolating a fitness function defined on a distribution of phenotypes to the corresponding underlying distribution of genotypes, and this requires a detailed understanding of the genome-to-phenome mapping (the first or development transition in Figure 2), an area in which little was known for much of the twentieth century. Let us now examine how the lack of knowledge of genome-to-phenome mapping was historically circumvented in the narrower domain of behaviour studies.

A good frame of reference here is that of two major aspects of genomes: they are expressed, and their constituents recombine. The chain of events leading to a phenome arising from the expression of the genome embodies a series of explanations, increasingly proximate to the final phenotpye(s) of interest. In this domain, to identify a gene(s) specifying a trait is to provide an ultimate explanation, whereas various forms of epigenetic causal explanations of how the trait comes about form a set of proximate explanations[4]. Historically, the rise of biochemical and, later, molecular genetics led to an increasing tendency to treat development as a black box in attempts to understand the formation of phenotypes; this, in turn, also had the consequence of divorcing mainstream developmental biology – a field with its own rich history of proximate explanations of living forms – from the Neo-Darwinian Synthesis in the mid-twentieth century[4]. Quantitative genetics, too, is essentially a pragmatic way of by-passing the genome-to-phenome map, and using the statistical properties of phenotypic distributions to make evolutionary inferences[7,8], although how useful this classical approach actually is remains somewhat controversial[5,9–11]. Unfortunately, while developmental genetics and developmental biology have made great advances in more recent decades[4], this black box still exists at the core of most heuristic models of the dynamics of biological systems[3,4], especially with regard to behavioural traits. Developmental genetics has hitherto focused on the genome-to-phenome mapping for morphological traits, leading to increased understanding of the ontogeny of form[12]. What has been lacking is an understanding of the ontogeny of

behaviour (function) in meaningful ecological contexts, an approach termed developmental evolutionary biology (devo-evo, as contrasted with evo-devo)[6]. With a few notable, and recent, exceptions that I shall come to later, behaviour genetics studies, too, have largely been restricted to a few broad categories. Classical mutagenesis-based studies have been helpful in elucidating molecular details of the neural bases of some behaviours[13], whereas QTL studies have confirmed that several behaviours are under polygenic control even though classical methods had revealed single genes of major phenotypic effect[14]. In some cases, the genetics component of an adaptive interpretation of among-population behavioural differences consists largely of demonstrating that the differences are heritable[15].

A second black box is apparent when we turn to the recombinational aspect of genomes, or transmission genetics. Behavioural ecology essentially ignores the reverse genome-to-phenome mapping required to extrapolate a fitness function defined on a distribution of behavioural phenotypes onto the underlying distribution of multi-locus genotypes, as also the reconstitution of multi-locus diploid genotypes during sexual reproduction[16]. This black box is largely due to lack of knowledge of the genetic control of most ecologically relevant behavioural traits, but has, nevertheless, given rise to much controversy – and also some attempts at finding common ground – between the proponents and opponents of optimization approaches in evolution[17–21]. It seems clear that a better integration of behaviour genetics, developmental neurobiology, and behavioural ecology will be helpful to a fuller understanding of behaviour.

A new behaviour genetics?

One major reason for the non-integration of behaviour genetics, developmental neurobiology, and behavioural ecology is that – partly because they address questions at different levels of the proximal-ultimate continuum – practitioners of the respective fields have tended to use different organisms and approaches, with the biggest gap being between behavioural ecology on the one hand, and behaviour genetics and developmental neurobiology on the other. The latter two disciplines have used tractable laboratory systems, and tended to focus on behaviours that are easily defined and often not too relevant to fitness in the natural environment. The gap between disciplines is further exacerbated by the fact that behavioural ecology is focused on trait differences, often quantitative, that are likely to play a role in adaptive evolution, whereas the tools and approaches of modern genetics and neurobiology are better suited to dissecting genetic and epigenetic pathways underlying large and dramatic phenotypic differences[12,22], that are unlikely to play a role in the evolutionary fine-tuning of the relevant phenotypes[23,24]. This particular aspect of the gap between traits examined by those with evolutionary versus developmental interests – a gap due to differences in the contrast class of explanations[4] – is evocatively expressed by Gilbert *et al.*[25], 'Genes could determine the number of bristles on the fly's back, but they could not determine how the fly constructed its back in the first place'. Since molecular genetics tools are suited to find genes of major effect, whose mutation typically causes a drastic phenotypic change, it is not surprising that these tools usually yield genes of the 'back construction' type. It is also not surprising that genes of major effect typically are not too sensitive, in terms of their phenotypic manifestation, to gene-by-gene interactions (henceforth G × G) in the form of epistasis, or to gene-by-environment interactions (henceforth G × E). Indeed, during an education in genetics, G × G and G × E interactions are encountered as deviations of some kind from a 'normal' (simple Mendelian) scenario wherein genotypes should have a simple one-to-one relationship with phenotypes. Integration of G × E interactions in developmental genetics studies is presently in an extremely rudimentary state, even though G × G interactions have been addressed to a considerable degree. Similarly, G × G and G × E interactions are also largely left out of most applications of the optimization approach to evolutionary questions that are so common in behavioural ecology. Thus, behavioural ecology models are typically framed purely at the phenotypic level with an implicit assumption of underlying genetic simplicity of behavioural traits. The common cause for this inability to incorporate G × G and G × E interactions into studies in both developmental genetics and behavioural ecology is that the same black box – the genome-to-phenome mapping – appears in two fundamental transitions at the heart of developmental genetics and behavioural ecology, respectively (Figure 2).

A serious new behaviour genetics will have to work out ways to incorporate G × G and G × E interactions in both development and evolution into studies of behaviour from an evolutionary perspective. QTL mapping studies of fitness components in both *Caenorhabditis elegans* and *Drosophila melanogaster* have revealed pleiotropy, G × G and G × E interactions to be ubiquitous[26–28]. Studies on *Escherichia coli*, too, clearly show that new mutations at single loci often result in new G × G and G × E interactions, in addition to mere trait changes in a single phenotype[29,30]. Experimental evolution approaches utilizing forward and reverse selection experiments in well characterized and relatively simple laboratory environments have also provided a lot of evidence for the ubiquity and importance of G × G and G × E interactions in the dynamics of adaptive evolution[6,17,19,20,31]. At a more general level, one of the particularly striking major findings of genomics studies is that species differences at the genome sequence level seem to be quite inadequate to explain phenomic differences between species. An obvious, though speculative, inference to be drawn from this

observation is that the unique identity of species, and the differences between them – the very differences that evolutionary biology tries to explain – are likely to reside in the specific patterns of G × G and G × E interactions that ultimately specify the developmental (epigenetic) rules that constitute the genome-to-phenome mapping for that species or population[6].

It seems clear that a new behaviour genetics that is to form a complete and meaningful complement to behavioural ecology needs to pay more attention to the expression aspect of genomes, not just in terms of the basic patterns of gene expression and their regulation, but also in terms of the functional architecture of the epigenetic (neural and otherwise) pathways and networks that result from and, in turn, affect the expression of the genome. We need an integration of genomic, neural, hormonal, environmental and social explanations of behavioural traits that appear to be of some adaptive significance; to paraphrase Houle[5], we need a behavioural phenomics to bridge the conceptual and methodological chasm between behaviour genetics and behavioural ecology. This integration is necessarily going to involve stepping beyond parochial biases and sub-disciplinary chauvinism[32]. I will next discuss briefly the three most important issues on which I believe a change of mindset is required; in many cases the change in mindset will also underscore the need for changes in methodology.

Genetic studies of complex traits relevant to adpative evolution need to focus more on genes of minor and cumulative effect, and on G × G and G × E interactions. In a sense, what is needed is for epigenetics to again be recognized as an integral part of genetics[4,5], as expressed in the traditional definition of genetics as the study of heredity and variation. The marginalization of epigenetics in studies of heredity has been an unfortunate side-effect of the advances in molecular genetics and it is time the balance of importance between genome and phenome, and the mapping linking them, was restored. It is to be hoped that future developments in this direction will go some way toward rooting quantitative genetics not just in multilocus population genetics theory[9], but also in an emerging evolutionary epigenetics[5]. One practical corollary of a focus on G × G and G × E interactions in genetics is the importance of controlling for genetic and environmental backgrounds in genetic manipulation experiments, an issue being recognized in the design of some evolutionary genetics studies[33], but one that is yet to percolate broadly into the genetics community.

In developmental biology, the time now seems to be ripe for at least beginning to address questions about the ontogeny of function, in addition to ontogeny of form[6]. To extend the metaphor of Gilbert *et al.*[25], it is time we also began to understand the ontogeny of bristle number differences among individuals, all of whom have a back. At the level of gene expression, the impact of ecologically relevant environmental variables on genome-wide patterns of expression needs to be studied. Similarly, the role of environmental variation in affecting epigenetic processes – in some cases, specifying alternative developmental paths[34] – also needs further experimental study. In behavioural ecology (or, more generally, evolutionary ecology), there is need for a wider appreciation that an extremely simplistic view of genome-to-phenome mapping is implicit in treating optimization models as predictors of what will evolve, rather than what is optimal in the context of a given set of constraints that, typically, includes no genetic or epigenetic constraints at all[6,17]. Most optimization models espouse a phenotypic equivalent of one-locus thinking in population genetics: the inferences drawn from such thinking are shaky in both fields, and tend to be reliable only under *ceteris paribus* assumptions that, empirically, are practically never met. The repeated inability of experimental evolutionists to accurately predict what traits are optimal and what traits evolve under relatively well defined selection pressures in the simplified ecology of *Drosophila* cultures[6] should, at the very least, strike a cautionary note to those who routinely make such predictions about natural populations.

From genes to behaviour and vice versa

One reason why this is an opportune time to start discussing a possible integration of behaviour genetics, genomics, phenomics and ecology is that we now seem to have sufficient basic knowledge of development, and a number of tools for studying the primary structure and expression of genomes, to feel that we can at least begin to try and peer into the black box of the genome-to-phenome mapping, a black box that is largely responsible for the lack of inter-disciplinary bridges in the attempts to understand the biology of behaviour. There are many studies, both theoretical and experimental, that are now increasingly at least reconnoitering – from both sides – the chasms between evolutionary genetics, development, and evolutionary ecology[19–21,27,28,31,35–47]. Many of these studies are not explicitly about understanding behaviour, but their existence should provide an impetus for students of behaviour to begin their own series of reconaissance patrols and intelligence-gathering forays as a prelude to planning a comprehensive campaign for a broader understanding of the biology of behaviour. One approach that is likely to prove especially fruitful is that of combining selection experiments with follow up studies of behavioural, physiological, transcriptional profiling and genomic sequence divergence between selected and ancestral (control) populations, an approach sometimes referred to as reverse genomics. Some elements of this approach have already yielded important insights into the subtlety of the processes of life-history evolution, and of adaptation to various biotic and abiotic stresses[6]. An ongoing integration of molecular, genetic, developmental and ecological studies in the laboratory

and the field has, similarly, greatly enhanced our understanding of thermal adaptation[48]. In the remainder of this section, I will summarize a few studies that exemplify how such integrative approaches – however tentative and preliminary – can lead towards more holistic understanding of behavioural phenomena from an evolutionary perspective.

A good example of a line of investigation leading from genes to developmental network to behaviour to evolutionary trend is provided by a comparative study of expression of different genes involved in the development of insect wings in queens and males (winged) and workers or soldiers (wingless) in four different species of ants[40]. The details of the gene network underlying insect wing development were originally worked out in *D. melanogaster*, and seem to be widely conserved across insects[49]. Abouheif and Wray[40] found that the expression pattern of six of these genes in winged castes of the four ant species was similar to that found in dipterans and lepidopterans. However, despite a consensus, based on phylogenetic arguments, that wing polyphenism probably evolved only once, the wing development gene network was found to be inactivated at different points in the wingless castes of these four species, and it was not possible to correlate these genetic events with observed differences in the anatomy of vestigial wing discs in larvae[40]. While a complete explanation for these observations is not yet available, the results suggest that regulatory gene networks and anatomical structures in development can perhaps respond to evolutionary forces like selection and drift in different ways[40].

An example of the reverse path of investigation, from behaviour to genes, is provided by studies on foraging path length in *D. melanogaster* larvae (reviewed in ref. 23). Bimodal distribution of distance moved by larvae in a given time interval on an agar plate overlaid with a yeast suspension led to the designation of two alternative phenotypes: rovers and sitters. Studies of foraging path length in natural populations of *D. melanogaster* showed that they tend to be polymorphic for these two phenotypes. Genetic analyses revealed the trait rover/sitter to be controlled largely by a single major gene *for*, with some effects of minor genes as well. The rover allele for^R is dominant over the sitter allele for^r. The *for* gene itself encodes a cGMP-dependent protein kinase, whose activity level in the heads of rovers is only 12% higher than that in sitters. Selection experiments further revealed that populations maintained at high larval densities for many generations tend to evolve a higher frequency of the rover phenotype, suggesting that density-dependent selection may be partly responsible for the maintenance of polymorphism at the *for* locus in nature[50]. Interestingly, the *for* gene is known to have pleiotropic effects on various aspects of development and behaviour[35], and the gene can be alternatively spliced to yield several different transcripts. A separate study has shown that rover phenotypes decrease drastically in frequency over ~ 50 generations of strong directional selection for rapid development in *D. melanogaster*[51], suggesting that the epigenetic pathways affected by the *for* gene might be involved in determining the balance of energy assimilated and expended during foraging which, in turn, is a trait that is likely to show strong G × E interactions with regard to fitness.

Interestingly, a somewhat similar contrasting pair of foraging-related behaviours is also seen in *Caenorhabditis elegans*, in which the difference between solitary versus social foragers seems to be largely due to allelic variation at a single locus *npr*-1, expressed mainly in the head and nerve cord[52], that bears homology to a nueropeptide Y receptor known to be involved in regulation of food intake in mammals[53]. More recently, it has been shown that the expression of another nueropeptide Y homologue, *D. melanogaster* neuropeptide F (*npf*), is correlated with feeding-related behaviour. Third instar *D. melanogaster* larvae that are reaching the cessation of feeding prior to the onset of wandering behaviour as a prelude to pupariation show greatly reduced levels of *npf* mRNA as compared to the levels seen in younger larvae still in the active feeding phase[41]. This finding is of considerable interest because the timing of cessation of feeding in last instar larvae has manifold potential effects on the life-history through its effects on resource assimilation[6]. There are several more such examples of interesting studies linking some sub-set of genetics, development, physiology, behaviour, ecology and fitness that could be described, but space constraints preclude me from doing more than provide a brief tag to some of the literature[6]. Trade-offs between larval competitive ability and resistance to parasitoids in *Drosophila* have been linked to the immune response and developmental processes of haemopoiesis and morphogenesis of cephalopharyngeal musculature[46]. The evolution of body size in *Drosophila* in response to temperature – a trait for which perhaps the best documented clinal variation exists – appears to proceed via different genetic and developmental mechanisms in different populations[54–56], and seems to be likely to involve genes of the insulin signalling pathway[57], which are also implicated in mediating lifespan, and lifespan related life-history trade-offs[58].

Conclusion

My main purpose in this paper was to re-state the argument that a broader view of behaviour genetics that includes epigenetic phenomena relevant to the development of behaviour in ecologically meaningful environments is required to bridge the conceptual chasm between behavioural ecology and behaviour genetics. This argument is not new, and has been made repeatedly over the past few decades[2,3,5,11,34,45,59–61]. However, it is only in recent years that methodological approaches to bridge that chasm in our understanding are beginning to become available, and

thus the argument acquires some urgency. Due to constraints of space, I have tried to briefly lay out what I feel is a useful conceptual basis for focusing on development as a bridge between more genetically versus more ecologically oriented approaches to studying behaviour, or for that matter evolution, and support the argument with a few illustrative examples. The composition of the reference list reflects this decision; I have tried to refer largely to reviews and books rather than providing a comprehensive guide to the primary literature. My intent in writing this article has been to provoke thought and, hopefully, introspection. Unfortunately, conceptual and methodological chasms between disciplines all too often end up becoming demarcating lines between academic territories, guarded vigorously, and often viciously, against intrusion from neighbours[4,62]. This is not, however, conducive to the advancement of science. Hopefully, this small effort will be received as being one among many other such attempts to move towards a common market behavioural biology, free of check-points and border controls. Developing such holistic research programmes in behavioural biology will, of course, be an extremely challenging task, especially for experimentalists. Yet, such challenges and hardships are part of the attraction of organismal functional biology. As Mirza Ghalib succinctly said over a century ago:

> '*ragon mein daudte phirne ke ham nahin qaayal*
> *jab aankh hi se na tapkaa to phir lahu kya hai*'

(Dissatisfied am I with wandering through the arteries and the veins: no virtue accrues to the drop of blood undistilled into tears)

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ACKNOWLEDGEMENTS. I thank Sutirth Dey, N. G. Prasad and Mallikarjun Shakarad for many interesting discussions and arguments that helped shape and focus many of the ideas expressed here, as well as two referees for helpful comments on the manuscript. My work is supported in part by funds from the Department of Science and Technology, New Delhi.