Drosophila Biology in the Genomic Age

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ABSTRACT

Over the course of the past century, flies in the family Drosophilidae have been important models for understanding genetic, developmental, cellular, ecological, and evolutionary processes. Full genome sequences from a total of 12 species promise to extend this work by facilitating comparative studies of gene expression, of molecules such as proteins, of developmental mechanisms, and of ecological adaptation. Here we review basic biological and ecological information of the species whose genomes have recently been completely sequenced in the context of current research.

IF most biologists were given one wish to facilitate their research, many would opt for the fully sequenced genome of their focal taxon. Others might ask for a diverse array of genetic tools around which they could design experiments to answer evolutionary, developmental, behavioral, or ecological questions. With the recent completion of full genome sequences from 12 species, Drosophila biologists are now in an unprecedented situation: they have both wishes—and more. Not only does the Drosophila model afford researchers full genome sequences and cutting-edge genetic tools, but also more is known about nearly every aspect of the biologies (genetics, development, ecology, phylogenetic relationships, and life history) of these species than of any other eukaryote. Furthermore, because of the comparative genomic framework of the 12 species, discoveries made in one taxon can immediately be placed in a larger evolutionary context.

While most researchers are well aware of the utility of *Drosophila melanogaster* and its close relatives to studies of genetics and developmental biology, few realize that several of the remaining species in this genus have been studied by ecologists and evolutionary biologists nearly since the time that Morgan picked up his first bottle of flies. For example, *D. pseudoobscura,* described by FROLOVA and ASTAUROV (1929), is well known from the classic evolutionary studies of Dobzhansky, his colleagues, and their students (ANDERSON *et al.* 1991; POPADIC and ANDERSON 1994). *D. virilis,* in addition to being a genetic model system in its own right, has also been used to study speciation and chromosome evolution (MCALLISTER 2002; CALETKA and MCALLISTER 2004).

The genus Drosophila contains >2000 described species (MARKOW and O'GRADY 2005, 2006), as well as

several hundred taxa that await description. Most of these taxa belong to one of two major subgenera: Sophophora and Drosophila. Figure 1 shows the phylogenetic relationships and divergence times of the 12 species for which whole-genome sequences are now available. The 12 species with sequenced genomes represent a gradient of evolutionary distances from *D. melanogaster,* including taxa diverging within the past 1 million years to those species who last shared a common ancestor with *D. melanogaster* >30 million years ago (Figure 1). This range was selected to take advantage of the power of multiple, related genomes to discover conserved regulatory motifs, enhance gene prediction, and improve annotation of the *D. melanogaster* genome (BERGMAN *et al.* 2003; BOFFELLI *et al.* 2003). Eight of the newly sequenced species are closely related to *D. melanogaster* and belong to the subgenus Sophophora. Five of these, *D. simulans, D. yakuba, D. erecta, D. sechellia,* and *D. ananassae,* are included in the *melanogaster* species group; 2, *D. pseudoobscura* and *D. persimilis,* are placed in the *obscura* group, sister to the *melanogaster* species group; and another, *D. willistoni,* is in the *willistoni* group, a basal clade within Sophophora (O'GRADY and KIDWELL 2002). The remaining 3 species belong to the subgenus Drosophila, the sister taxon of Sophophora. *D. virilis,* a sap flux breeding species, and *D. mojavensis,* a cactophilic taxon, belong to what is referred to as the *virilis–repleta* radiation (THROCKMORTON 1975). *D. grimshawi,* a large, spectacularly patterned species, represents the Hawaiian Drosophila radiation, a closely related clade to the *virilis–repleta* species.

Selection of the species to be sequenced thus was based on two criteria: (1) their degree of relatedness to *D. melanogaster* and (2) the likelihood of discovering new genes and new pathways. In the case of the first criterion, it was important to densely sample species closely related to *D. melanogaster* as well as successively more distantly related taxa to discover and annotate conserved regulatory

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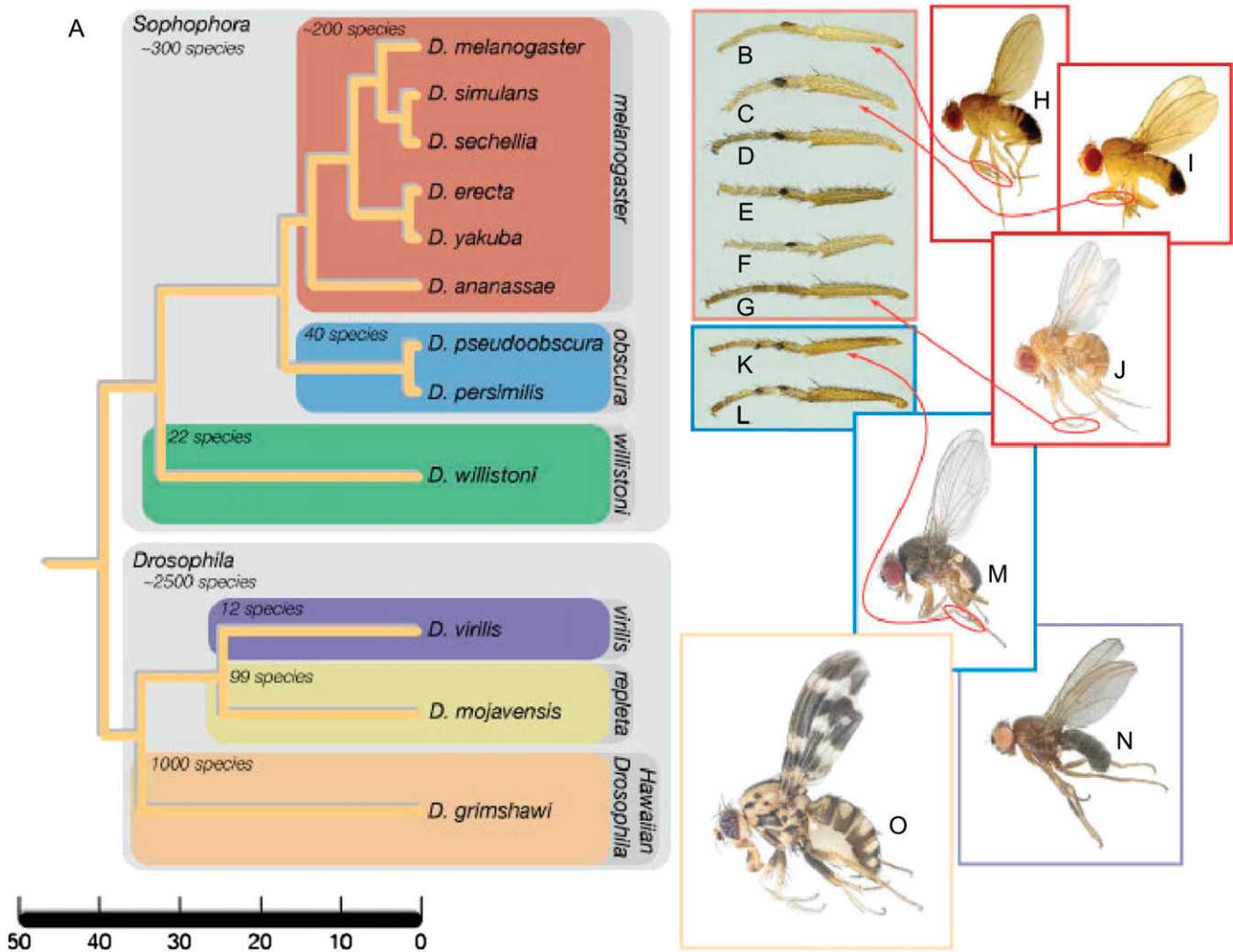
FIGURE 1.—(A) Phylogenetic relationships of the 12 fully sequenced Drosophila species, along with a timescale for evolution in this group (after RUSSO *et al.* 1995). Species-level diversity in the containing subgenera and species groups are shown (MARKOW and O'GRADY 2005a and references therein). (B–G) Sex combs in the *melanogaster* species group: (B) *D. melanogaster,* (C) *D. simulans,* (D) *D. sechellia,* (E) *D. erecta,* (F) *D. yakuba,* and (G) *D. ananassae.* (H) Adult male, *D. melanogaster.* (I) Adult male, *D. simulans.* (J) Adult female, *D. ananassae.* (K and L) Sex combs in the *obscura* species group: (K) *D. pseudoobscura* and (L) *D. persimilis.* (M) Adult male, *D. pseudoobscura.* (N) Adult male, *D. virilis.* (O) Adult male, *D. grimshawi.*

regions via phylogenetic shadowing (*e.g.,* BOFFELLI *et al.* 2003). The dense sampling within the *melanogaster* subgroup (*simulans, sechellia,* and *yakuba*) and inclusion of the more distantly related *D. erecta* and *D. ananassae* has yielded a much more detailed picture of the *cis*-regulatory regions than comparisons between *mela-nogaster* and *obscura* (MOSES *et al.* 2006; POLLARD *et al.* 2006). Some of the species were selected because they are behaviorally and ecologically diverse and would yield either novel biochemical pathways or unique variations on already known networks of gene interaction. This avenue has proved particularly relevant for the evolution of the olfactory and gustatory receptor genes in *D. sechellia,* a taxon that oviposits only in the rotting fruit of *Morinda citrifolia,* a highly toxic substrate (MCBRIDE 2007). Another taxon selected on the basis of this criterion is the cactophilic species *D. mojavensis,* in which novel

genes appear to be associated with the use of toxic cactus hosts (MATZKIN *et al.* 2006) as well as with their mating system (KELLEHER and MARKOW 2007).

The first Drosophila species, *funebris,* was described by J. C. Fabricius in 1787 and moved into the genus Drosophila by C. F. Fallen in 1823. Meigen described *D. melanogaster* in 1830 (MEIGEN 1830). The number of species described in this group rose slowly throughout the latter half of the 19th century. It was not until the early 1900s, however, after *D. melanogaster* was established as a model organism for understanding genetics that the rate of Drosophila species descriptions increased dramatically. Alfred H. Sturtevant, in addition to his contributions to Drosophila genetics, also produced early taxonomic treatments of Drosophila (STURTEVANT 1916, 1919, 1921, 1939, 1942) and described species such as *D. simulans, D. willistoni,* and *D. virilis.* In the late 1930s Th. Dobzhansky

began to use *D. pseudoobscura* and its sibling species, *D. persimilis* and *D. miranda*, in studies aimed at understanding the population genetic basis of species formation. Also around this time, extensive collections by J. T. Patterson and W. S. Stone's group at the University of Texas (Austin, TX) discovered hundreds of new species, mainly from the southwestern United States, Mexico, and Central and South America (PATTERSON 1943; PATTERSON and MAINLAND 1944). Subsequent efforts in Hawaii during the 1960s and the 1970s, the result of a collaboration between the University of Texas group and D. Elmo Hardy at the University of Hawaii at Manoa, discovered an immensely important radiation of Drosophila that numbers close to 1000 species (SPIETH 1981). This work led to the popularization of several species as model systems for ecological, population, and behavioral genetics (KAMBYSELLIS 1968; CARSON 1992; DESALLE 1992). Other groups, including those led by Lachaise, Tsacas, David, and Bock, worked throughout the 1970s, 1980s, and 1990s describing many taxa in Africa, Australia, and the South Pacific (BOCK and PARSONS 1981; OKADA 1981; TSACAS *et al.* 1981).

> For many problems there is an animal on which it can be most conveniently studied.   AUGUST KROGH

According to the Krogh principle, for all biological phenomena there is a perfect model system that can be used to formulate questions and test hypotheses. For example, *D. melanogaster,* popularized by T. H. Morgan and his students in the first half of the 20th century, is one of the premier model systems of modern genetics. Investigations into the ecologies, life histories, and genome features of the 12 fully sequenced species of Drosophila demonstrate that each of these flies can be viewed as a model system to address specific biological questions.

In spite of all the work that has been done, what do we really know about the biology and ecology of these 12 species? What makes them compelling models to study interesting questions? What biological questions are each uniquely suited to address? The facility of rearing and manipulating so many diverse but related species of Drosophila has fueled the expansion of experimental studies. Several recent reports have reviewed the wealth of research that has been done using Drosophila (POWELL 1997; MARKOW and O'GRADY 2005, 2006; ASHBURNER *et al.* 2006). Here, we discuss several areas where the combination of full genome sequences and comparative life history data may help redefine ecological and evolutionary studies.

Distributions and ecological associations: Choices about where to feed and oviposit are critical to the survival and fitness of all Drosophila species. However, the genetic pathways involved in host plant selection are largely unknown, as are the determinants that make some species specialists and others generalists. In spite of our current lack of understanding about these genes and how they might interact with the environment, they are of great interest to evolutionary biologists as they may be involved in driving the process of diversification at both the micro- and macroevolutionary levels. Related to host selection and selectivity are those factors (environmental, behavioral, population genetic, and otherwise) that allow some taxa to exist as widespread or cosmopolitan species, while the ranges of others are very narrowly defined. Range maps for Drosophila species are given in MARKOW and O'GRADY (2005, 2006). Some species are known to be constrained by host plant distribution and geographic factors, but the ranges, or the bases for the ranges, of others are less well understood.

The 12 species with sequenced genomes display a great diversity in both geographic distribution and ecological association. Some species, such as *D. melanogaster* and *D. simulans,* are cosmopolitan and have spread beyond their ancestral distributions as a result of their commensal association with humans and their ability to breed in a wide variety of rotting fruits. Some close relatives of these generalist species also oviposit in fruit, but are more narrowly distributed and highly selective in their choice of substrate. For example, *D. sechellia* is endemic to the Seychelles and has specialized on the fruits of *M. citrifolia,* a resource toxic to other Drosophila (R'KHA *et al.* 1991). Another case of specialization occurs with *D. erecta,* which breeds in species of Pandanus in the Ivory Coast of western Africa (LACHAISE and TSACAS 1983). *D. yakuba,* also restricted to Africa, is a generalist fruit breeder (LACHAISE and TSACAS 1983), but has not become a cosmopolitan species like *D. melanogaster* and *D. simulans. D. ananassae,* another fruit breeding species that is widespread throughout Asia and the Pacific, is used extensively by some researchers as a genetic model (TOBARI 1992). This species has spread beyond its initial distribution through its association with humans and the fruit trade and is now considered sub-cosmopolitan (SINGH 2000).

The sibling species pair of *D. pseudoobscura* and *D. persimilis* is mainly distributed in western North America, although a small population of *D. pseudoobscura* is located in the mountains near Bogotá, Colombia (DOBZHANSKY *et al.* 1963). During the summer months, both species are abundant in mid- to high-elevation forests, especially those dominated by Ponderosa pines. As temperatures at these sites become colder, populations move to lower elevations and both taxa can be found in or near desert habitats throughout their ranges during the winter. These habitats are not available to these species during the hotter months of the year. Although few breeding records for either species exist, *D. pseudoobscura* has been reared from slime fluxes, domestic fruits, cacti, and agave (POWELL 1997), suggesting that it may be an opportunistic species that can utilize a number of different host types. This would certainly agree with the almost complete lack of overlap in potential host plants between their summer (mountain) and winter (desert) ranges.

D. willistoni, a species that breeds in a wide range of rotting fruits, is probably one of the most numerous and broadly distributed drosophilids in the New World and can be found from southern South America to southern North America and throughout the Caribbean (AYALA 1971; DOBZHANSKY and POWELL 1975). Although *D. willistoni* can be readily found in association with humans and the fruit trade within its traditional range, it has not yet been reported outside of the New World.

The three species in the subgenus Drosophila that have been sequenced also show a diversity of distributions and ecologies. *D. virilis*, a Holarctic species, has also been reared from fruits in urban settings, but naturally breeds in the fluxes of willows and other decaying parts of trees (THROCKMORTON 1982). *D. mojavensis* is found in the deserts of North America where it breeds in the necroses of several species of cacti (HEED 1978). This species and its relatives have evolved to tolerate not only the toxic compounds found in its hosts, but also the high desiccation conditions of the Sonoran Desert (STRATMAN and MARKOW 1998; GIBBS *et al.* 2003; MATZKIN *et al.* 2006). Although most species of Hawaiian Drosophila are highly specific to a single host plant, *D. grimshawi*, a charismatic picture-winged species, is considered a generalist. It utilizes the decaying bark of over seven families of endemic Hawaiian plants (MAGNACCA and O'GRADY 2006).

Behavioral evolution: Variability in behavior has been reported for a great many Drosophila species, although measures have rarely been made in the same way. Genetics of nonreproductive behaviors for the genus have recently been reviewed by SISODIA and SINGH (2005). Data exist on several of the sequenced species for behaviors such as pupation site preference, locomotor activity, phototaxis, and geotaxis. Far more is known of reproductive behaviors. SPIETH (1952) was the first to categorize the elements of courtship behavior and to describe interspecific variability in these elements. Courtship behaviors of the 12 sequenced species differ in the relative roles of the particular sensory modes in mating: visual, chemical, and auditory (MARKOW and O'GRADY 2005, 2006). For example, *D. melanogaster* and *D. pseudoobscura* will mate equally well in the light and the dark, while mating in their respective sibling species, *D. simulans* and *D. persimilis*, is repressed in darkness. Males of *D. grimshawi*, with their patterned wings, provide elaborate visual displays not seen in males of *D. virilis* or *D. mojavensis*, which tend to focus their courtship activities behind the females. Chemical profiles, or pheromones, differ in close relatives, both within and between species and between the sexes of a given species (FERVEUR 2005). For example, *D. melanogaster* and *D. sechellia* possess long chain dienes not seen in *D. simulans* or *D. erecta*. The longest chain hydrocarbons are seen in *D. mojavensis*. These chemical differences predict that the olfactory and odorant binding receptors of these species would also be different. Finally, species such as *D. virilis* and *D. mojavensis* exhibit both male and female

courtship songs, while in the other 10 species, only the males appear to sing (MARKOW and O'GRADY 2005, 2006; HOIKKALA 2006).

Life-history evolution: Ecologists and evolutionary biologists now have the ability to use genomic information and genetic dissection tools to understand the heritable factors contributing to the dazzling array of life-history strategies observed in the genus Drosophila. This is an exciting avenue of research that will probe the selective forces that the environment exerts on the genome over evolutionary time. Several developmental and reproductive traits are currently being investigated. For example, there is a clear relationship between body size and egg-to-adult development time: the biggest flies require the longest time to develop (Table 1). Egg-to-adult development time is shortest in *D. melanogaster*, *D. simulans*, and *D. ananassae*, all of which require ~10 days at 24°. The longest development time is in *D. grimshawi*. Development from egg to adult requires nearly a month.

Interspecific differences in reproductive biology represent some of the most interesting features of the 12 species. Few species of Drosophila are ready to mate the moment they emerge from the pupa case. In those species in which flies are sexually mature upon emergence, the opposite sex typically requires several days before sexual maturity is achieved. Reproductive maturity times of the 12 species (Table 1) reflect the number of days after emergence by which 80% of flies of a given sex successfully mate with a sexually mature conspecific. Within the subgenus Sophophora, adult males tend to mature earlier than females, while in 2 species of the subgenus Drosophila, *D. virilis* and *D. mojavensis*, males require two to three time longer to reach sexual maturity. Female *D. grimshawi*, on the other hand, require at least 3 weeks to become sexually mature, almost three times longer than males. Proximate explanations for these differences appear to lie in the relative complexity of either gametogenesis or reproductive tract maturation in one sex or the other. An astounding 15-fold difference in sperm length exists among the 12 species, with *D. persimilis* having the shortest and *D. virilis* the longest sperm. Those species in which males mature before females tend to produce short sperm relative to those in which males mature much later than females (Table 1). In the case of *D. mojavensis*, whose sperm is similar in length to that of *D. melanogaster*, male accessory glands produce relatively large amounts of seminal fluid, the derivatives of which are taken up by females and incorporated into female somatic tissues and developing oocytes (MARKOW and ANKNEY 1984).

The development time in *D. grimshawi* may be related to egg development, rather than sperm formation. *D. grimshawi* females must produce eggs with immensely long chorionic filaments. Kambysellis and his collaborators have shown that the chorionic filament length is adaptive and correlated with the length of the female ovipositor, the type of oviposition substrate, and the depth to

TABLE 1

Biological characteristics of the 12 sequenced species

Species	F-thorax length (mm)	M-thorax length (mm)	Sexual dimorphism[a]	Egg to adult (days)	F-sexual maturity	M-sexual maturity	Female remating	Ovariole no.	Sperm length
D. melanogaster	0.99[a]	0.88[a]	Y[b,c]	10[a]	4[a]	2[a]	5[a]	43[a]	1.91[a]
D. simulans	0.97[a]	0.87[a]	Y[b,c]	10[a]	3[a]	1[a]	5[a]	40[a]	1.14[a]
D. sechellia			Y[b,c]	12[a]				16[d]	1.60[e]
D. yakuba			Y[b,c]	11[a]				28[e]	1.6[g]
D. erecta			Y[b,c]	12[a]				27[e]	1.2[g]
D. ananassae	0.94	0.87	Y[b,c]	10[a]			7	30[e]	3.3[g]
D. pseudoobscura	1.09[a]	1.01[a]	Y[b,c]	13[a]	3[a]	1[a]	4[a]	34[a]	0.36[a,f]
D. persimilis	1.06[a]	0.93[a]	Y[b,c]	13[a]	4[a]	0[a]	4[a]	36[a]	0.32[a,f]
D. willistoni	0.83[e]	0.79[e]	N	13[a]	3[e]	2[e]	4[e]	36[e]	
D. mojavensis	0.96[a]	0.89[a]	N	12[a]	5[a]	8[a]	1[a]	26[a]	1.90[a]
D. virilis	1.33[a]	1.27[a]	N	18[a]	3[a]	9[a]	3[a]	34[a]	5.70[a]
D. grimshawi	2.12[e]	2.23[e]	N	27[a]	21[e]	7[e]	Rarely[e]	28[e]	1.19[e]

Columns 2–9: female (F)-thorax length, male (M)-thorax length, presence of sexual dimorphism, egg-to-adult development time in days, age in days at which 80% of females are sexually receptive, age at which 80% of males are sexually mature, number of days before female remates, female ovariole number, sperm length (mm).

[a] Markow and O'Grady (2005a) and references therein.
[b] Sexual dimorphism for color.
[c] Sexual dimorphism for morphology: male sex combs.
[d] Coyne *et al.* (1991).
[e] T. A. Markow (unpublished data).
[f] Sperm length dimorphism, Snook (1997).
[g] Joly and Bressac (1974).

which the egg is inserted (Kambysellis 1993; Craddock and Kambysellis 1997). As the genetic pathways underlying life-history characteristics are elucidated, biologists will be able to better understand the complex interplay between the genome, development, behavior, and the environment.

Speciation genetics: Biologists have long been interested in the genetic changes leading to the formation of new species. Much research has centered on the generation of partial or complete reproductive isolation, both in terms of premating and postmating barriers to the production of viable or fertile offspring. Genetic dissection techniques have been successful in implicating specific chromosomal regions or candidate genes (Ting *et al.* 2004; Brideau *et al.* 2006; Moehring *et al.* 2006), but the sequenced genomes will allow for finer-scale speciation genetics studies.

Most of the species sequenced have close relatives and have been the subject of intensive studies of speciation genetics involving both interspecific mating experiments and studies using nucleotide variation to examine cases of natural hybridization. When *D. melanogaster* females are crossed with males of either *D. simulans* or *D. sechellia*, the result is the production of sterile females and no males, in accordance with Haldane's rule—meaning that when hybrid inviability or sterility is observed it typically affects the heterogametic sex most profoundly (Haldane 1922; Coyne 1985; Wu *et al.* 1996; Orr 1997). The reciprocal crosses, however, are counter to Haldane's rule in that they produce sterile males and no surviving females (Lemeunier *et al.* 1986). Hybrids never have been

obtained between *D. erecta* and any of its relatives, including its closest relative, *D. orena*, but this is not surprising given the great divergence times between these taxa. In the laboratory, *D. ananassae* produces fertile, viable hybrids in reciprocal crosses with its sibling species *D. pallidosa*, but in nature, sexual isolation, specifically differences in courtship song, prevent the two from interbreeding (Yamada *et al.* 2002).

Speciation genetics of the *D. pseudoobscura*–*D. persimilis* sibling pair began as early as 1929 (Lancefield 1929). Reciprocal crosses produce sterile male hybrids. With *D. pseudoobscura* mothers, however, ∼25% of the F$_1$ females also are sterile, while the reciprocal cross produces fully fertile females (Dobzhansky 1936; Orr 1987). Sequence comparisons of mitochondrial and nuclear genes reveal evidence of recent introgression in different parts of the genomes of these two species (Machado and Hey 2003).

The sophophoran most distantly related to *D. melanogaster* is *D. willistoni*. While *D. willistoni* has been reported to inseminate and be inseminated by, at very low levels, its relatives such as *D. equinoxialis* and *D. paulistorum*, its reproductive isolation from these species is effectively complete and no hybrids are produced (Burla *et al.* 1949). Reproductive barriers also exist within *D. willistoni*. A population of *D. willistoni* collected west of the Andes near Lima, Peru, shows hybrid sterility with *D. willistoni* from the rest of South America, leading Ayala (1972) to designate the Peruvian strains as a separate subspecies, *D. willistoni quecha*.

In the subgenus Drosophila, *D. virilis* is able to cross with many of the other species in the *virilis* group. Not

all crosses produce fertile or abundant progeny, however (THROCKMORTON 1982). This suggests that the barriers to reproductive isolation, and therefore the boundaries of what defines a species, in this group may be significantly different from those acting in the subgenus Sophophora. The cactophilic sibling pair *D. mojavensis* and *D. arizonae* have become a popular model system for speciation studies because they display a continuum of reproductive isolating mechanisms in interspecific crosses from various populations (MARKOW and HOCUTT 1998). These include premating, postcopulatory–prezygotic, and postzygotic isolation. In addition, the distribution of *D. mojavensis* is bisected by the Sea of Cortez and populations from different regions exhibit signs of incipient speciation (MARKOW and HOCUTT 1998).

Over 95% of the known Hawaiian Drosophila species are single island endemics. *D. grimshawi* is unusual in that it occurs on Maui, Molokai, and Lanai. Two of its closest relatives, *D. craddockae* from Oahu and Kauai and *D. pullipes* from Hawaii, are found on the remaining islands and thus the three species are allopatric. Crosses between *D. pullipes* and either *D. craddockae* or *D. grimshawi* produce some viable F_1 progeny, but few males have motile sperm (OHTA 1980), indicating that *D. pullipes* is a distinct species, in spite of only subtle morphological differences. Crosses between *D. grimshawi* and *D. craddockae* produce fertile F_1 progeny, but show a marked reduction in F_2 fertility in reciprocal backcrossess, suggesting evidence for postmating breakdown (KANESHIRO and KAMBYSELLIS 1999). Furthermore, *D. grimshawi* is undergoing differentiation itself, genetically, morphologically, and ecologically, on the different islands it inhabits (PIANO *et al.* 1997).

The evolution of genome size and rearrangement: On the basis of comparative cytological studies of metaphase chromosomes, PATTERSON and STONE (1952) suggested that the ancestral karyotype in the genus Drosophila is composed of one dot and five acrocentric, or rod, chromosomes (MULLER 1940; STURTEVANT and NOVITSKI 1941; PATTERSON and STONE 1952). All other chromosomal configurations are derived from this basic ancestral state via Robertsonian (ROBERTSON 1957), or centromeric, fusions. It was MULLER (1940) who first hypothesized that the genic content of these six different elements would remain relatively conserved over time because of the rarity of transposition events and the highly deleterious nature of pericentric inversions. The six chromosomal building blocks are lettered A–F and are referred to as Muller's elements. The *D. melanogaster* karyotype of one acrocentric, two metacentric, and one dot chromosome can be generated by two fusion events, one between Muller's B and C and another between Muller's D and E.

Following their role in demonstrating the chromosomal basis of inheritance, Drosophila have continued to be a model for studies of genome evolution and rearrangement. Genome sizes (BOSCO *et al.* 2007, accompanying article in this issue; GILBERT 2007) and karyotypes

TABLE 2

Genome sizes from assembled sequences, from flow cytometry (propidium iodide), both in megabases, and chromosome number for each species

Species	Genome size assemblies	Genome size flow cytometry[d]	Chromosome no. (*n*)
D. melanogaster	117[a]	178 ± 16	4
D. simulans	138[b]	165 ± 2	4
D. sechellia	167[b]	172 ± 4	4
D. yakuba	166[b]	187 ± 11	4
D. erecta	153[b]	146 ± 4	4
D. ananassae	231[b]	206 ± 9	4
D. pseudoobscura	156[c]	188 ± 4	4
D. persimilis	188[b]	188 ± 5	4
D. willistoni	236[b]	209 ± 7	3
D. mojavensis	193[b]	143 ± 0	6
D. virilis	206[b]	313 ± 11	6
D. grimshawi	201[b]	216 ± 5	6

[a] CELNIKER *et al.* (2002).
[b] GILBERT (2007): http://insects.eugenes.org/species/.
[c] RICHARDS *et al.* (2005).
[d] BOSCO *et al.* (2007), accompanying article in this issue.

(Table 2) are quite variable. Gain and loss of heterochromatin are likely explanations for the interspecific differences in genome size (BOSCO *et al.* 2007; GILBERT 2007), while the basic Drosophila karyotype of five rods (acrocentric) and a dot chromosome differs among species primarily owing to centromeric fusions.

Conclusions and prospectus for future research: The biological diversity of the 12 species provides unparalleled opportunities to address pressing questions about genome evolution, development, behavior, physiology, and species formation. Furthermore, the benefits of the genome sequences are not restricted to the 12 species: for each sequenced taxon, there are multiple related, biologically interesting species for which these genomes will prove a useful and informative springboard to future research. A century after its debut as a research organism, the Drosophila model now enters a new era as an even more robust tool for discovery.

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