EDUCATION AND OUTREACH

Nature or Nurture? Heritability in the Classroom

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ABSTRACT

Understanding evolution is a necessary component of under-graduate education in biology, and evolution is difficult to explain without studying the heritability of traits. However, in most classes, heritability is presented with only a handful of graphs showing typical morphological traits, for example, beak size in finches and height in humans. The active-inquiry exercise outlined in the following pages allows instructors to engage students in this formerly dry subject by bringing their own data as the basis for estimates of heritability. Students are challenged to come up with their own hypotheses regarding how and to what extent their traits are inherited from their parents and then gather, analyze data, and make inferences with help from the instructor. The exercise is simple in concept and execution but uncovers many new avenues of inquiry for students, including potential biases in their estimates of heritability and misconceptions that they may have had about the extent of inference that can be made from their heritability estimates. The active-inquiry format of the exercise prioritizes curiosity and discussion, leading to a much deeper understanding of heritability and the scientific method.

Keywords: active learning, evolution, heritability, human biology, inheritance, pedagogy, quantitative genetics.

Introduction

Beginning with a seminal article by Arnold (1983), the perspectives and techniques of quantitative genetics (Falconer and Mackay 1996) began to enter physiological ecology. Within a decade, research aimed at estimating heritabilities of physiological and related traits had become a mainstream component of the new evolutionary physiology (Garland and Carter 1994; see also Feder et al. 2000). At present, estimating heritability (Hawks 2011; Brookfield 2012) is fairly common in the ecological and evolutionarily subfields of physiology (e.g., Dohm et al. 2001; Nespolo et al. 2003; Heideman et al. 2007; Sadowska et al. 2009; Careau et al. 2011; Bruning et al. 2013; Fuchikawa and Okada 2013; Mattila and Hanski 2014; review in Storz et al. 2015), as well as fields that are increasingly incorporating information from the physiological sciences, such as behavioral ecology (e.g., Dochtermann et al. 2014; Petelle et al. 2015). Heritability also remains a key topic in animal breeding (e.g., Velie et al. 2015), in the biomedical sciences (e.g., Wood et al. 2008; Fernández-Grandon et al. 2015; Ganjgahi et al. 2015), and indeed in the biological sciences generally (Visscher et al. 2008).

Students should have a working knowledge of the basics of heritability, given its broad usage and applicability in the biological sciences. Considerable research in educational pedagogy indicates that open-ended, active-inquiry exercises that require active engagement by students can be effective tools for conveying sophisticated concepts, especially those that require some degree of quantitative reasoning (Wood 2009). With this in mind, we have developed an exercise that offers students a chance to learn about the importance of nature and nurture in determining phenotypic differences among individuals by collecting data on themselves and their parents to estimate heritability. Guided by the instructor, students propose traits that can be easily and reliably quantified (measured) for both themselves and their parents. Students also develop their own hypotheses about how and why different traits have higher or lower narrow-sense heritability and factors that could affect empirical estimates of heritability. When students perform guided and structured analyses of their own data, the meaning of heritability—and of some of the statistical tools that can be used to estimate it—is more effectively presented. The lesson plan is freely available and hosted at IDEA (http://idea.ucr.edu), the University of California–Riverside (UCR) Institute for the Development of Educational Applications (http://idea.ucr.edu/documents/flash/heritability_in_the_classroom/Heritability_Exercise_v10.pdf).

Required Background Information

Students need to be familiar with the concepts and definitions of traits (or characters or characteristics), phenotype, and genotype. They should have had material related to inheritance and heritability. They should already have seen things such as graphs of offspring versus parental body height. The exercise involves making scatterplots and fitting least squares linear regressions, although typically the instructor would do the actual data analysis and students would learn to interpret results.

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At UCR we have used this exercise in two upper-division undergraduate courses: (1) Evolution and (2) Ecological and Evolutionary Physiology. In both cases, students have had lectures and readings on quantitative genetics before this exercise. In the latter course, they would also have had a lecture on individual variation, which includes consideration of measurement error and repeatability. We would consider some background on quantitative genetics as essential before attempting this exercise, whereas concepts related to measurement error and repeatability could be dealt with as they arise during the exercise.

Lesson Concepts

The following concepts should be conveyed by completion of the heritability exercise:

1. Traits can be defined as any aspect of the phenotype that can be measured with a reasonable degree of accuracy and repeatability. Examples of traits include a person's height, attitude toward social issues, intelligence, how many minutes it takes the person to run a mile, blood pressure, and blood hormone levels.

2. Some traits are referred to as "Mendelian" because they have a simple pattern of inheritance (e.g., affected by only one or two genetic loci and subject to few environmental influences). Quantitative traits, on the other hand, are usually polygenic, meaning that multiple loci affect the trait. Studying the pattern of inheritance is more complicated with polygenic traits, so we use the statistical methods of "quantitative genetics."

3. The variation of any trait within a population is a result of genetic differences among individuals ("nature"); the different environments each individual has experienced since conception ("nurture"), including even the environments experienced by their parents; and the interactions between genes and the environment.

4. Narrow-sense heritability ($h^2 = V_A/V_P$) is the measure of how much of the phenotypic variance in a population is caused by variance in additive effects of alleles segregating at all genetic loci that affect the trait in question. (a) Narrow-sense heritability of a trait indicates its potential to respond to selection (natural, sexual, or artificial), at least in the short term (over perhaps 10–30 generations in laboratory studies). (b) Narrow-sense heritability is used in the breeder's equation, $r = h^2s$, where $s =$ the directional selection differential and $r =$ the response to selection from one generation to the next.

5. Narrow-sense heritability of a trait in a population can be estimated as the slope of a least squares linear regression line of offspring average trait value on parental average trait value. (a) Regression analysis is used to describe the relationship between a dependent variable and one or more independent variables. The slope of a linear regression line measures how much the value of the dependent variable changes when a given independent variable is changed by one unit. (b) In this exercise, male and female offspring are analyzed separately to avoid statistical complications caused by sex differences (e.g., men are taller than women, on average).

6. Environmental factors (e.g., diet) shared between parents and their offspring often inflate estimates of narrow-sense heritability. (a) The study of heritability in human populations is complicated by this and by various practical considerations. (b) Whether explicitly acknowledged or not, many estimates of heritability reported for humans and for wild vertebrates are not narrow-sense but rather broad-sense heritabilities (ratio of all genetic variance divided by phenotypic variance) or something more complicated than either of these quantities (Plomin et al. 1990; Brodie and Garland 1993; Visscher et al. 2008; Wilson et al. 2010). (c) We can start teasing apart these issues by comparing the slopes of offspring regressed on their mothers with those regressed on their fathers. Often, the maternal slope will be steeper than the paternal slope, suggesting that mothers provide more in the way of shared environmental effects, which are one type of "maternal effects" (Falconer and Mackay 1996).

7. Some traits are more heritable than others (e.g., cf. figs. 1, 2; Plomin et al. 1990; Brodie and Garland 1993; Falconer and Mackay 1996; Visscher et al. 2008; Wilson et al. 2010).

8. Heritability is a characteristic of a population (i.e., a more or less freely interbreeding collection of individuals) in a particular environment, at a particular point in time. The same trait studied in two different populations, or even in different years within a single population, may show somewhat different heritabilities. Do the students and their parents satisfy these definitions?

Perspectives on the Lesson Concepts

Depending on the course, many other concepts could be brought into the pedagogy. For example, a genetics course that implemented this exercise might build on earlier lectures on Mende-
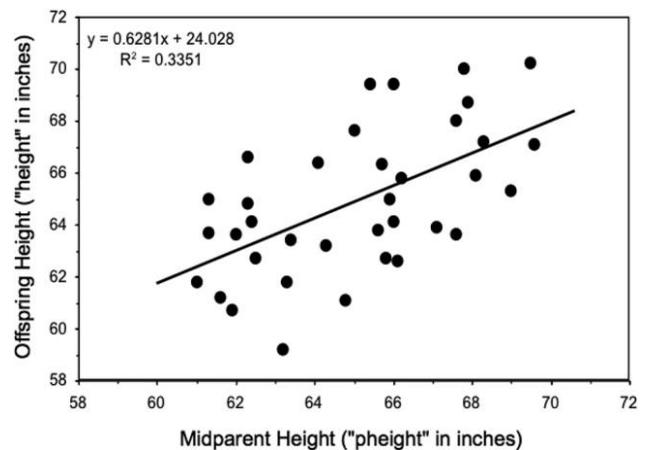

Figure 1. These data are representative of those that can be gathered in a college course. They do not represent actual values from students but instead have been created to resemble the patterns we have gathered from a college class. The plot shows the offspring-on-midparent regression of height. The data for this plot are also given in the teacher packet, found at http://idea.ucr.edu/courses.html. Midparent values are averaged from mothers and fathers. The equation of the regression line is on the top left corner of the plot, along with the coefficient of determination R^2 (the percentage of variance in the y variable that can be predicted by variance in the x variable). The slope of the regression, 0.6281, is the estimated narrow-sense heritability, or h^2. A statistical test would indicate that this slope differs "significantly" ($P < 0.05$) from zero.
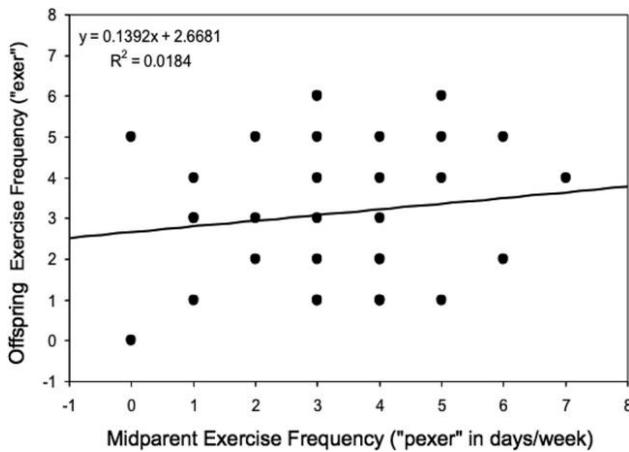
Figure 2. As for figure 1, except that this plot shows the offspring-on-midparent regression of exercise frequency (measured in days per week). The slope of the regression, 0.1392, is the estimated narrow-sense heritability. The estimate of the slope is not statistically significantly different from zero. In other words, we do not have much evidence that exercise frequency is heritable in this population of students and their parents.

lian genetics, Punnett squares, and so forth and might then move into finding quantitative trait loci, the concept of missing heritability (Edwards et al. 2014; Zuk et al. 2014), and estimating genomic heritability (de los Campos et al. 2015). Those concepts are beyond the scopes of the courses in which we have used the lesson plan.

Some students are surprised to know that we organismal biologists consider such a wide range of things as "traits" that we can study empirically. Some of these, such as "intelligence," may make them uncomfortable, but we have found that treating all potential traits (anything we can measure reproducibly) in a matter-of-fact way gets past any apparent discomfort.

Physiological and behavioral traits are generally more difficult to measure, for a variety of reasons, than morphological ones. This provides an opportunity to teach students about the complications involved with working on live animals, the use of sophisticated measurement techniques, and so on. It may also help them build an appreciation for modern physiology and biochemistry.

Our university is very diverse racially and socioeconomically, and many of the students are commuters. As a result, they hardly constitute a "population" in the sense of the word that is required for appropriate estimation of heritability (see point 8). We have often found rather high estimates of heritability, as compared with typical values found in the literature (Falconer and Mackay 1996; Visscher et al. 2008). If the students pick up on this point, then we can discuss it in terms of our data set being a mixture of multiple "populations," some of which probably differ, on average, with respect to some of the traits we are studying (e.g., body height). Thus, our sample of data is really mixing some among-population variation with within-population variation, which tends to inflate heritability estimates for both statistical and biological reasons.

Materials Required

Before undertaking this sort of exercise, instructors should determine whether collecting data from students would require approval from an organizational entity that reviews proposed human studies. Guidelines, requirements, and restrictions vary among institutions and among countries, so it is difficult to provide proscriptive advice here. On our campus, this sort of data-gathering exercise does not require human-subjects approval unless the data are intended for publication. Instructors should make clear that students may opt out from data collection for personal reasons, without being penalized. Students should still be required to fill out the form but can simply enter something like "−9" for numerical values (i.e., something that can easily be spotted as missing data).

We have students submit their data via Google Forms, which requires that they have access to an Internet-connected device and may require that they create a free Google account. We ask students to enter their names and student identification numbers, which allows us to track who has submitted their data and whether they were submitted on time. The data then end up in a Google spreadsheet, which we make accessible only to the instructors. Instructors could then, if they chose, remove the identifying information and share it with the students.

Instructors (and/or students) can analyze the data with whatever graphical/statistical software they choose. In the teacher packet, available online at IDEA (http://idea.ucr.edu/documents/flash/heritability_in_the_classroom/Heritability_Exercise_Teacher_Packet_v10.pdf), we provide instructions on how to do so directly inside the Google spreadsheet. Thus, all of the requisite data-gathering and analysis steps can be accomplished in free, cross-platform software.

Although not mandatory, we believe that this exercise is best accomplished in classrooms that allow projection of materials. This may be useful for presenting background materials in a discussion section or lab, such as graphs of offspring-on-parent regressions for various traits, taken from the literature (e.g., fig. 4 in Koch and Britton 2003; fig. 4 in Luttikhuizen et al. 2003; figs. 1, 2 in Roulin and Dijkstra 2003; Hawks 2011). Showing the Google form where data will be entered can also be useful. Most importantly, though, instructors will want to share graphs of the students' own data (e.g., see figs. 1, 2).

Evaluation

The main opportunities for assessment are (1) student participation in the discussions that lead to decisions as to which traits will be studied, (2) data collection, (3) data analysis (if appropriate for the course material and level), (4) writing a report on the activities, and/or (5) asking questions about the exercise on quizzes or exams. As noted above, we recommend that the instructor do the actual data analysis. However, some or all of this could easily be assigned to students. In the teacher packet, we provide suggestions for the structure of student reports, including the standard sections of Introduction, Methods, Results, Discussion, and Conclusions. Instructors may also want to ask for feedback to help improve future offerings. With respect to quiz

questions, it is easy to devise true-false, multiple-choice, or open-ended ones that pertain to either the details of the results obtained or the general principles involved (including procedures for data analysis).

Instructional Challenges

Undergraduates at many colleges and universities suffer from a lack of quantitative literacy; they routinely have trouble with exercises that involve graphs, numerical analyses, or statistics (Speth et al. 2010 and references therein). In this exercise, instructors can choose to create the graphs themselves or have students do so as a teaching opportunity.

Reading and interpreting graphs are difficult for students. When they see a scatterplot with no correlation, they tend to think of it as a "bad" graph—with errors or uninterpretable results. They think the exercise "did not work." Instructors should directly challenge this misunderstanding by walking students through each graph. A graph with no correlation shows an interesting result: that the two variables, which students might have hypothesized to be related, are in fact not. Instructors should also note that because some variables are discrete, points might overlap, making the overall graph look less strongly related than the correlation or regression indicates.

Some outliers are difficult to talk about, especially with body weight. Students may be uncomfortable or embarrassed by having their datum pointed out as an outlier. The instructor can simply delete the point before showing results to the class and mention that outliers were deleted. However, deleting the point may be more embarrassing for the student. The best route may be to talk to the student beforehand or otherwise gauge the group of students for the appropriate way to handle potentially embarrassing results. Other potential difficulties include individuals who know only one or neither of their biological parents. Make sure that students know that it is acceptable for them to complete the survey to the best of their ability (e.g., entering "−9" for any missing data values).

Beware of confounding variables when considering traits for this exercise. For example, one might want to see whether preference for coffee is heritable and may ask individuals to rank how much they enjoy coffee. Students may think this gets at the taste of coffee alone, but coffee is a complex substance and preference for it may involve some level of reward received from caffeine. Additionally, some people drink their coffee black, while others add cream and/or sweeteners. One way to make this type of question more reliable is to be more specific with regard to the question itself, such as "How much do you like black coffee?" or "How many cups of black coffee do you drink per day?" Further, students have pointed out that age or time of day might influence preferences (or other traits). As mentioned in the next section, use of covariates in statistical analyses is a possible extension for this exercise.

Extensions

This activity is open-ended in that the number of traits for which students could potentially gather data is virtually endless. Beyond this, data analysis offers many opportunities for extension to more sophisticated and/or closely related topics. For example, before regressing offspring values on parental values, residuals from regressions on such covariates as age or body height could be performed. In the courses where we have used the heritability exercise, students have already become familiar with the concept of statistical control via residuals, so this extension fits easily into the pedagogical flow of our courses. In any case, computation of residuals is a key aspect of analyses in many areas of comparative/ecological/evolutionary physiology (e.g., Clobert et al. 2000; Dohm et al. 2001; Sadowska et al. 2009; Careau et al. 2011; Mattila and Hanski 2014; Wone et al. 2015), and this exercise offers a hands-on opportunity for teaching this material.

Many of the behavioral and physiological traits likely vary in relation to time of day. This could be addressed by having students record values with respect to a certain time of day (e.g., "How much do you like to drink black coffee in the morning before school?") or perhaps record their scores over multiple times and report an average value.

Another direct extension is to consider genetic correlations between traits. Genetic correlations provide insights as to the causes of physiological trade-offs and constraints that have always been of interest to both evolutionary biologists and physiologists (Garland and Carter 1994; Storz et al. 2015). At its simplest level, analysis of genetic correlations involves relating the values for one trait in offspring to those of another trait in parents or vice versa. We have not tried to teach the various formulas for estimating a genetic correlation, instead leaving this at the intuitive levels of whether two traits tend to run together in families. This can be illustrated very simply by making scatterplots of offspring trait A versus parent trait B and vice versa. In any case, genetic correlations are a key topic in various studies of heritability and quantitative genetics (e.g., Dohm et al. 2001; Nespolo et al. 2003; Sadowska et al. 2009; Careau et al. 2011; Bruning et al. 2013; Fuchikawa and Okada 2013; Petelle et al. 2015; Storz et al. 2015; Wone et al. 2015).

In summary, the empirical study of heritability in the classroom, as outlined above, offers an opportunity to increase hands-on knowledge of some of the key concepts within modern evolutionary physiology and related fields. The focus is the estimate of heritability, but students are encouraged to think about many aspects (and potential sources of error) when quantifying and comparing morphological, physiological, and behavioral traits. The exercise also allows instructors to bolster the use of quantitative methods in biology education. Students learn how to estimate heritability, but, perhaps more important, they learn the broader lessons of using the scientific method to address their curiosities.

Acknowledgments

Literature Cited

Arnold S.J. 1983. Morphology, performance and fitness. Am Zool 23:347–361.

Brodie E.D., III, and T. Garland Jr. 1993. Quantitative genetics of snake populations. Pp. 315–362 in R.A. Seigel and J.T. Collins, eds. Snakes: ecology and behavior. McGraw Hill, New York.

Brookfield J.F.Y. 2012. Quick guide: heritability. Curr Biol 22: R217–R219.

Bruning A., J.D. Gaitán-Espitia, A. González, J.L. Bartheld, and R.F. Nespolo. 2013. Metabolism, growth, and the energetic definition of fitness: a quantitative genetic study in the land snail *Cornu aspersum*. Physiol Biochem Zool 86:538–546.

Careau V., D. Thomas, F. Pelletier, L. Turki, F. Landry, D. Garant, and D. Réale. 2011. Genetic correlation between resting metabolic rate and exploratory behaviour in deer mice (*Peromyscus maniculatus*). J Evol Biol 24:2153–2163.

Clobert J., A. Oppliger, G. Sorci, B. Ernande, J.G. Swallow, and T. Garland Jr. 2000. Trade-offs in phenotypic traits: endurance at birth, growth, survival, predation and susceptibility to parasitism in a lizard, *Lacerta vivipara*. Funct Ecol 14:675–684.

de los Campos G., D. Sorensen, and D. Gianola. 2015. Genomic heritability: what is it? PLoS Genet 11:e1005048.

Dochtermann N.A., T. Schwab, and A. Sih. 2014. The contribution of additive genetic variation to personality variation: heritability of personality. Proc R Soc B 282:20142201.

Dohm M.R., J.P. Hayes, and T. Garland Jr. 2001. The quantitative genetics of maximal and basal rates of oxygen consumption in mice. Genetics 159:267–277.

Edwards M.D., A. Symbor-Nagrabska, L. Dollard, D.K. Gifford, and G.R. Fink. 2014. Interactions between chromosomal and nonchromosomal elements reveal missing heritability. Proc Natl Acad Sci USA 111:7719–7722.

Falconer D.S. and T.F.C. Mackay. 1996. Introduction to quantitative genetics. 4th ed. Pearson, Harlow, England.

Feder M.E., A.F. Bennett, and R.B. Huey. 2000. Evolutionary physiology. Annu Rev Ecol Syst 31:315–341.

Fernández-Grandon G.M., S.A. Gezan, J.A.L. Armour, J.A. Pickett, and J.G. Logan. 2015. Heritability of attractiveness to mosquitoes. PLoS ONE 10:e0122716.

Fuchikawa T. and K. Okada. 2013. Inter- and intrasexual genetic correlations of exaggerated traits and locomotor activity. J Evol Biol 26:1979–1987.

Ganjgahi H., A.M. Winkler, D.C. Glahn, J. Blangero, P. Kochunov, and T.E. Nichols. 2015. Fast and powerful heritability inference for family-based neuroimaging studies. NeuroImage 115: 256–268.

Garland T., Jr., and P.A. Carter. 1994. Evolutionary physiology. Annu Rev Physiol 56:579–621.

Hawks J. 2011. Heritability and stature. John Hawks weblog. http://johnhawks.net/explainer/stats/heritability-and-stature/.

Heideman P.D., D.R. Broussard, J.A. Tate, and M. Avigdor. 2007. Number of immunoreactive GnRH-containing neurons is heritable in a wild-derived population of white-footed mice (*Peromyscus leucopus*). Physiol Biochem Zool 80:534–541.

Koch L.G. and S.L. Britton. 2003. Genetic component of sensorimotor capacity in rats. Physiol Genom 13:241–247.

Luttikhuizen P.C., J. Drent, W. Van Delden, and T. Piersma. 2003. Spatially structured genetic variation in a broadcast spawning bivalve: quantitative vs. molecular traits. J Evol Biol 16:260–272.

Mattila A.L.K. and I. Hanski. 2014. Heritability of flight and resting metabolic rates in the Glanville fritillary butterfly. J Evol Biol 27:1733–1743.

Nespolo R.F., L.D. Bacigalupe, and F. Bozinovic. 2003. Heritability of energetics in a wild mammal, the leaf-eared mouse (*Phyllotis darwini*). Evolution 57:1679–1688.

Petelle M.B., J.G.A. Martin, and D.T. Blumstein. 2015. Heritability and genetic correlations of personality traits in a wild population of yellow-bellied marmots (*Marmota flaviventris*). J Evol Biol 28:1840–1848.

Plomin R., J.C. DeFries, and G.E. McClearn. 1990. Behavioral genetics: a primer. 2nd ed. W.H. Freeman, New York.

Roulin A. and C. Dijkstra. 2003. Genetic and environmental components of variation in eumelanin and phaeomelanin sextraits in the barn owl. Heredity 90:359–364.

Sadowska E.T., K. Baliga-Klimczyk, M.K. Labocha, and P. Koteja. 2009. Genetic correlations in a wild rodent: grass-eaters and fast-growers evolve high basal metabolic rates. Evolution 63: 1530–1539.

Speth E.B., J.L. Momsen, G.A. Moyerbrailean, D. Ebert-May, T.M. Long, S. Wyse, and D. Linton. 2010. 1, 2, 3, 4: infusing quantitative literacy into introductory biology. CBE Life Sci Educ 9:323–332.

Storz J.F., J.T. Bridgham, S.A. Kelly, and T. Garland Jr. 2015. Genetic approaches in comparative and evolutionary physiology. Am J Physiol 309:R197–R214.

Velie B.D., N.A. Hamilton, and C.M. Wade. 2015. Heritability of racing performance in the Australian Thoroughbred racing population. Anim Genet 46:23–29.

Visscher P.M., W.G. Hill, and N.R. Wray. 2008. Heritability in the genomics era: concepts and misconceptions. Nat Rev Genet 9:255–266.

Wilson A.J., D. Réale, M.N. Clements, M.M. Morrissey, E. Postma, C.A. Walling, L.E.B. Kruuk, et al. 2010. An ecologist's guide to the animal model. J Anim Ecol 79:13–26.

Wone B.W.M., P. Madsen, E.R. Donovan, M.K. Labocha, M.W. Sears, C.J. Downs, D.A. Sorensen, et al. 2015. A strong response to selection on mass-independent maximal metabolic rate without a correlated response in basal metabolic rate. Heredity 114: 419–427.

Wood A.C., F. Rijsdijk, K.J. Saudino, P. Asherson, and J. Kuntsi. 2008. High heritability for a composite index of children's activity level measures. Behav Genet 38:266–276.

Wood W.B. 2009. Innovations in teaching undergraduate biology and why we need them. Annu Rev Cell Dev Biol 25:93–112.

Zuk O., S.F. Schaffner, K. Samocha, R. Do, E. Hechter, S. Kathiresan, M.J. Daly, et al. 2014. Searching for missing heritability: designing rare variant association studies. Proc Natl Acad Sci USA 111: E455–E464.