

# Project Description

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## Objectives and expected significance

That biologists use many different but closely related concepts of the gene is a truism amongst biologists as well as amongst historians and philosophers of biology. The fundamental aim of this project is to study the pattern of this conceptual variation and to relate it to the sorts of work that takes place in different biological fields. The study is emphatically not designed to establish a single, correct definition of the gene. It is not concerned with 'definitions' at all, in most of the common senses of that word. Historians and philosophers have put forward several theories concerning variation in the gene concept across biological disciplines and have used these theories to support further claims about the gene concept. These include claims about: 1.How the concept and its variation contribute to biological research, 2.How it limits or distorts biological research, 3.How conceptual differences affect communication between biological fields and, 4.How they affect communication between biological science as a whole and the broader community. Building on earlier work, this project will test some of these claims using questionnaire data obtained from populations of working biologists and analyzed using standard statistical methods. The project aims at collective ownership of the data by the research communities in history and philosophy of science and in related fields, both in the sense that the design of the study will involve extensive consultation with leading researchers and in the sense that the data will be made freely available (subject to constraints required by subject anonymity).

The project will lead to progress in understanding how various gene concepts contribute to the forms of biological research in which they figure. The current literature on the concept of the gene, outlined below, contains many exciting and innovative proposals concerning the conceptual structures that underlie the varied patterns of usage of 'gene' and of related terms like 'allele' across the range of biological disciplines. These proposals have been supported by relatively ad hoc argumentation, drawing mainly on authors' experience as participant/observers in biological research and on the history of genetics. While these two sources of insight are indispensable, they have various limitations (see below, Design of Study). Furthermore, supplementing the existing theoretical research tradition with an experimental tradition that challenges theories and forces their modification will cause the progressive refinement of those theories and thus benefit the field as a whole.

The project will assess the widespread view that there are deficiencies in current conceptualizations of the gene. As discussed in the next section, some researchers have

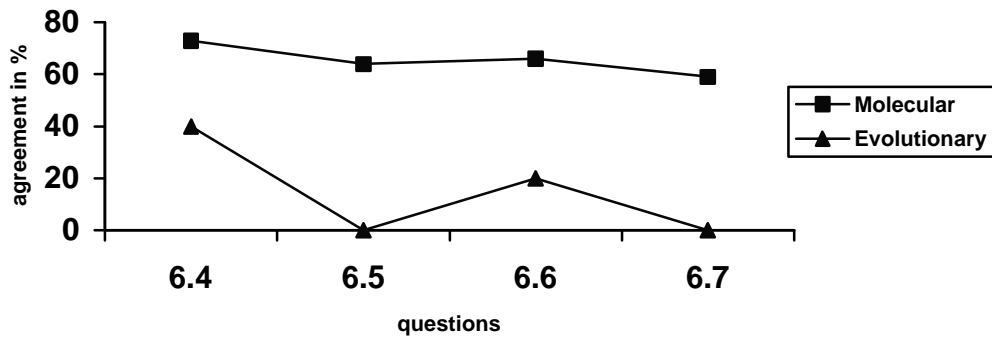
suggested that certain well-known gene concepts play no genuine cognitive role in biological research and that the use of these concepts obscures the real significance of genetic research. Others have suggested that findings made using one concept of the gene are illicitly imported into research contexts in which a different conceptualization of the gene is being used, leading to fallacies of ambiguity in scientific reasoning. If borne out, these suggestions might be of direct value to biologists (see below, Date Storage and Sharing). They would also have implications for science communication, bioethics, law, and public policy, fields which involve taking claims made in a specific research context and thus with a specific conceptualization of the gene, and applying those claims in a very different context (see below, Date Storage and Sharing). Finally, the project will have methodological significance, as social science research methods have not previously been used in HPS to address questions about conceptual diversity across scientific fields.

## **Relationship to Existing Knowledge in the Field**

The concept of the gene has undergone several important transformations since its introduction at the beginning of the last century. This has been critical to the continuing theoretical utility of the concept. It is widely agreed that this process of conceptual change is continuing and accelerating. The editors of one recent collection of essays on the gene concept go so far as to say that 'The gene has become a curiously intangible object, defying any straightforward definition' (Beurton, Falk, & Rhineberger, 2000: i). Some authors have concluded that the term 'gene' no longer has any very determinate meaning. The historian of genetics Raphael Falk has written that: "Today the gene is not *the* material unit or *the* instrumental unit of inheritance, but rather *a* unit, *a* segment that corresponds to *a* unit-function as defined by the individual experimentalist's needs." (Falk, 1986: 169, italics in original), a conclusion echoed by the biologist Thomas Fogle (Fogle, 2001). Indeed, according to some, the concept has finally outlived its usefulness as a theoretical construct in molecular biology (Keller, 2000). Others argue that there is a 'Kuhnian revolution' in the making in molecular biology and that the current fragmentation of the gene concept across sub-disciplines presages the emergence of a radically new consensus concept (Strohman, 1997). Still others have proposed new conceptualizations of the gene that allow the adequate representation of empirical data and that challenge assumptions implicit in existing definitions (Griffiths & Neumann-Held, 1999). Finally, some researchers have argued that existing conceptualizations have sufficient flexibility for current needs (Moss, 2001; Waters, 1994). To support this perspective, however, these authors make controversial (and competing) claims about existing conceptualizations of the gene.

Many of these proposals will be tested as part of the current project. For example, Kenneth Waters, who has agreed in principle to participate in the project workshops, sees the different concepts of the gene found in molecular biology as unified by a "fundamental" gene concept, namely, "a gene for a linear sequence in a product at some stage of genetic expression." (Waters, 1994: 178). The fundamental concept plus the scientist's research focus determines which DNA sequences count as genes. In effect, Waters proposes that the different uses of the term 'gene' in molecular biology correspond to research interests along a continuum of more or less distal stages of gene expression. Since that variable can be controlled experimentally, either by questioning biologists who work on a specific stage of expression or by asking biologists to think about processes involving that stage of expression, Water's view is an obvious candidate for test

and will be assessed as part of this project. The empirical tractability of such questions was demonstrated by earlier work conducted by the PI in Australia (see below, Relationship to PIs Ongoing Research). Part of the research instrument used in this earlier study asked biologists to assess whether various pairs of DNA sequences were ‘the same gene’. In successive questions, subjects were told that the gene products from the two sequences diverged at successively earlier stages of gene expression. Answers from pure molecular biologists differed significantly from those of evolutionary biologists (Figure 1). This is consistent with Waters’ hypothesis, given that evolutionary biologists are concerned with the distal, phenotypic effects of the genes whereas molecular biologists are concerned with the proximal, molecular products of the gene.



**Figure 1.** Biologists were asked whether the following pairs of DNA sequence were ‘the same gene’. 6.4. Two transcription units of identical nucleotide sequence leading to the same functional protein. 6.5. Two transcription units of identical nucleotide sequence, which are translated into the same polypeptide chain, regardless of how it is folded. 6.6. Two transcription units of identical nucleotide sequence, which produce the same final transcript, regardless of what happens to this transcript. 6.7. Two transcription units of identical nucleotide sequence, which produce the same primary transcript, regardless of what happens to this transcript. . Associations between agreement and group membership for the four questions are significant at levels ranging from 0.01 to 0.05 (Stotz & Griffiths, In preparation).

More recently, Lenny Moss has argued that both current and historic conceptualizations of the gene make use of two different ways of classifying DNA sequences, taxonomic schemes that he labels Gene P and Gene D. The Gene P concept identifies genes by their predictive statistical relationship to phenotypic traits in some population or populations. Gene P is not defined by any specific DNA sequence, nor in terms of the developmental pathway that connects the gene to a phenotypic trait. Prime examples of the Gene P concept occur in medical genetics where several developmentally impaired forms of a gene can be counted as the same allele (e.g. ‘the gene for cystic fibrosis’), even in cases where different impairments affect different parts of the developmental pathway leading to the trait. Although the Gene P concept was originally

introduced in the context of classical genetic techniques and the tracing of pedigrees it remains equally applicable in the contemporary context when correlations between gene and trait are established using molecular probes. In contrast to Gene P, the Gene D concept identifies genes by their specific molecular template capacity, with no commitment to any specific developmental or phenotypic effect. To be an example of the N-CAM (neural cell adhesion) gene is: "...to contain the specific nucleic acid sequences from which any of 100 potentially different isoforms of the N-CAM protein may ultimately be derived... N-CAM molecules are (despite the name) expressed at many tissues, at different developmental stages, and in many different forms." (Moss, 2001: 88). The concept of Gene D finds its home in molecular developmental biology and in basic research in molecular genetics, fields in which the emphasis is on the elucidation of molecular mechanisms and particularly on basic mechanisms that will be encountered in many different cellular and organismic contexts. Moss's claim, like that of Waters, suggests dependent and independent variables whose relationship could be investigated as part of this project. Moss has agreed in principle to take part in the project workshops.

The most widely used concept of the gene in the wider community is undoubtedly the informational gene concept. A gene is a packet of developmental information, or an instruction for development. Sahotra Sarkar, who has agreed in principle to take part in the project workshops, has argued that this "is little more than a metaphor that masquerades as a theoretical concept and ...leads to a misleading picture of possible explanations in molecular biology". (Sarkar, 1996: 187). The formal coding relation between DNA and polypeptides is unconnected to most of the other informational language used in molecular biology ( (Godfrey-Smith, 1999; P. E Griffiths, 2001), but see (Maynard Smith, 2000) for a contrary view). That other, loose 'information talk' may be harmless when the focus of research is actual molecular gene products and their interactions and when Gene P notions are being applied to that level of gene expression. At that level there are tight connections between what genes do (Gene P) and their intrinsic molecular nature (Gene D). Furthermore, contextual factors like the post-transcriptional processes discussed above are the actual focus of research and unlikely to be systematically overlooked. Critics of the informational conception of the gene allege, however, that when the focus is on higher levels of biological organization, and particularly when results are reported to the wider community, loose information talk almost inevitable leads to the conflation of Gene P and Gene D. Whether this is in fact the case should be able to be assessed as part of the current project.

## **Relationship to PI's ongoing research**

The PI has published a number of papers on the gene concept and on the conceptual framework of developmental biology, working in collaboration with several biologists and philosophers of science (P. E Griffiths, 2001; Griffiths, In Press 2002; Griffiths & Gray, 1994, 1997; Griffiths & Knight, 1998; Griffiths & Neumann-Held, 1999). Previous research conducted under Australian Research Council Large Grant A-59906145 in collaboration with Karola C. Stotz surveyed 81 post-PhD researchers who use molecular genetic techniques at the University of Sydney, Australia. The intention was to explore the feasibility of questionnaire based research in this field and to attempt to test some of the claims made in the theoretical papers cited above. Subjects were asked to perform a variety of free and forced choice tasks with respect to definitions of key terms, including 'gene', and to statements about the gene drawn from the current literature. They

were also given a list of pairs of DNA sequences and asked to judge if each pair was 'the same gene'. Responses to these questions were cross tabulated with responses concerning subjects' training, research experience and current research activity and tested with standard statistical procedures based on a contingency table to identify the existence and strength of an association. A draft paper and copy of the research instrument is accessible from the PI's website <<http://www.pitt.edu/~pauleg/genes>>. It proved possible to identify statistically meaningful groups of subjects by grouping them into 'developmental', 'evolutionary' and 'molecular' groups based on their answers to questions about their training and research. Membership of these groups correlated with specific patterns of answers in a way consistent with a series of hypotheses advanced on the basis of the theoretical literature.

This preliminary study had several major shortcomings. Despite this, it produced many results that were both statistically significant and theoretically interesting, some of which feature in this project description. The fact that such crude criteria for group membership as discipline of undergraduate and postgraduate degree and self-report of current area of research nevertheless produced statistically significant patterns of answers suggests that the variation in the gene concept across biological fields is both extensive and structured. This is extremely encouraging for future research of this kind. This project would remedy the following shortcomings in the previous study: 1. Groups would be defined using questions about subject's current lab techniques, subjects' degree of attention to different journals; membership of professional societies and meeting attendance and other measures designed to better resolve groups; 2. Greater resolution would be obtained with the larger numbers of subjects made possible by not restricting the study to a single campus; 3. The research instrument will be significantly better designed than that used in the first study, both as a result of learning from the preliminary study and as a result of drawing on relevant expertise on the Pitt campus to help with the design. The existing links between the Department of HPS and the Program in Rhetoric of Science, Department of Communication have proved particularly valuable in this respect (See below, Design of Study). In particular, we expect to use more 'indirect' questions - questions about how to describe specific genes and their behavior - and less 'direct' questions which ask for responses to explicit definitions and general statements; 4. This project will aim at collective ownership of the results by the research community. The concept of collective ownership of results has three main aspects. First, the research questions will be determined in collaboration with other leading researchers in the field, ensuring that the study targets issues of interest to them. Second, these researchers will have input to the complex task of operationalizing the relatively abstract claims in the theoretical literature. This will ensure that the data generated is seen to have a genuine bearing on the research questions. The proposed workshops thus are an integral part of the design of the study and will greatly increase the benefits gained from the survey. Thirdly, the data will be made freely available to the research community (see below, Data Storage and Sharing).

## Design of the study

The methodologically innovative element of the proposed research is the integration of empirical research methods with the traditional philosophical task of analyzing key concepts and elucidating their role in scientific reasoning.

### Philosophical Presuppositions about Conceptual Analysis

While the aim of the project is to produce results that are accepted as valid by as wide a range of researchers as possible, its basic conception necessarily embodies some philosophical presuppositions about the nature of conceptual analysis. The project builds on ideas about category concepts in the life sciences developed by PI in his book *What Emotions Really Are: The Problem of Psychological Categories* (Griffiths, 1997) and elsewhere (Griffiths, 1999; P.E Griffiths, 2001). Drawing on work by Richard Boyd and Ian Hacking (Boyd, 1991, 1999; Hacking, 1991b, 1995) the PI has argued that conceptual change in science can be understood by treating concepts as ongoing projects in which both the extension and intension of concepts are changed by the scientific community in an attempt to obtain categories with maximum explanatory and predictive power. Whilst accepting Hacking's claim that conceptual change is often driven by pragmatic and normative, as well as epistemic projects (Hacking, 1991a), the PI has argued for the value of an idealized model of conceptual change in which only epistemic considerations play a role. This idealized case, he has argued, is useful for understanding the difference between those radical changes in what scientists believe about the referent of concept that nevertheless allow conceptual continuity with earlier science (e.g. "The old theory of the gene is false root-and-branch") and changes of the same apparent magnitude which appear to create a conceptual rupture (e.g. "There *are* no genes in the old sense"). The resulting picture of conceptual evolution in science has some similarities to Rheinberger's proposal that there exist 'epistemic objects' - names are introduced into language as targets of research rather than to designate objects with which we are acquainted (Rheinberger, 1997, 2000). The PI's treatment differs critically from Rheinberger's however, in that the PI takes scientific language to have an important referential aspect. Thus, the philosophical perspective that informs the design of this study is one in which scientific categories are conceived as ongoing - and possibly ramifying - projects of deriving empirical generalizations of increasing scope and reliability by adjusting both the extension of theoretical categories, so as to encompass sets of instances with as much in common as possible, and the intension of those categories, so that statements involving the category change their modal status in a way that reflects the centrality of certain beliefs to current theory. A flagship example of this sort of change of intension, of course, is the changing modal status of the claim that biological taxa are descended from a common ancestral population (Griffiths, 1999; Hull, 1976; Wilson, 1999).

One corollary of this approach to scientific concepts is that conceptual analysis should not make unrestricted use of the 'method of possible cases' - the traditional philosophical activity of testing claims about concepts by offering outré examples and asking if the proposed analysis applies the concept to the example in an intuitively satisfying way. The philosopher John Dupré once attacked the modern, cladistic approach to species in this way, arguing that cladism implies that if some walnuts grew into birds exactly like chickens, these would be in the same genus as walnuts, not the same genus as chickens (Dupré, 1981). In reality, of course, all this example

proves is that in such a distant possible world, contemporary biology would be false root-and-branch and the classificatory practices of modern biology would be useless. Hence in contemporary philosophical semantics it has become common to distinguish two ‘dimensions’ of modality in order to explain the relationship between scientific definitions (i.e. water *is* H<sub>2</sub>O, species *are* lineage segments between speciation events, and so forth) and intuitions about how to apply concepts in bizarre counterfactual scenarios like that just discussed (Chalmers, 1996; Jackson, 1994, 1998). The ‘secondary intension’ of a concept is used to assess counterfactuals in the light of what we know about the actual world, e.g. “given what we know about chemistry, if people on other planets do not drink H<sub>2</sub>O, then they do not drink water”. In contrast, the ‘primary intension’ of a concept is used to assess counterfactuals in which knowledge about the actual world is bracketed off, e.g. “If Lyell’s speculations in the 1830s about cyclical nature of speciation and extinction had been true, then species would not have been lineage segments between speciation events”. Like many other philosophers (Hintikka, 1999; Hull, 1997; Lycan, 1996), the PI does not believe that *primary* intensions can be reliably constructed through the unrestricted use of thought experiments. Intuitions about possible cases are most reliable and easiest to interpret when the possible cases do not violate fundamental presuppositions of many of the other concepts that must be used to describe the example. However, irrespective of this criticism, it is clear that the conceptual truths that are of primary interest for the current study concern *secondary* intensions. The study is concerned to determine what biologists in certain fields take genes to be in the light of their biological knowledge, just as we might be concerned to find out what chemists take gold to be given contemporary physics and chemistry.

### **Special Difficulties Raised by the Study of Conceptual Variation**

Conceptual analysis has traditionally relied on the semantic competence of the individual investigator. In the case of scientific concepts it has always been recognized that the investigator needs to be more than a competent speaker of English - the investigator must also be recognized by the relevant expert community as a competent user of a specialized scientific concept. Nevertheless, given this precondition, the investigator can rely on their individual intuitions - there is no need to systematically survey the other members of the speech community. It is evident, however, that this traditional approach cannot be used to assess the claim that there is conceptual variation within some community. The current literature uses several, alternative methods to support such a claim about the concept of the gene. One is to examine the history of genetics and to discern changes in how the gene has been conceived at different periods and by different groups of researchers. This approach is extremely valuable and must form part of the background to any work on the concept of the gene. However, molecular genetics is a field in a state of explosive growth, and conceptually challenging empirical findings are an almost weekly occurrence. The pace of conceptual change in the last two decades makes it necessary to attend to current work in the field as well as to the history of the discipline. Another prevalent method is the researcher having ‘participant-observer’ status in the molecular biological research community. However, no individual can be equally well acquainted with the whole spectrum of contemporary biological research. It is also plausible that the biologists who choose to collaborate with philosophers or to participate in philosophical debates are unrepresentative of the research community as a whole. The introduction of empirical research methods makes it possible to evaluate competing accounts of the gene concept and its variants in a more rigorous and systematic way.

One inspiration for the preliminary study was research on conceptual change in childhood in cognitive developmental psychology. The psychologist Frank Keil, amongst others, has explicitly compared the changes in extension and intension that accompany conceptual development in children to conceptual change in the history of science (Keil, 1989). Conversely, Susan Carey has used ideas about ‘incommensurability’ in science to understand the different ways in which children and adults understand the words in their common language (Carey, 1991). The so-called ‘theory view of concepts’ (Medin, 1989) interprets conceptual change in children as the result of changes in the child’s explanatory theory of the relevant cognitive domain. Children’s naive biology, for example, is taken to be the source of their concepts of species and of higher taxa such as ‘plant’ and ‘animal’. Children of different ages correspond to groups of scientists with different theoretical orientations to one and the same field. Whether or not this theory is correct as an account of cognitive development in children, the extensive efforts to provide experimental evidence for and against it provides a valuable source of experimental paradigms for the study of conceptual variation. The PI is actively seeking workshop participants with experience in this field of research with the aim of developing better ‘indirect’ (see above) methods of eliciting responses that provide evidence for and against claims about conceptual structure.

## **Phases of the Project**

### *Phase 1. Initial workshop*

The proposed research would begin with the organization of a workshop involving leading contributors to the literature outlined above. A working session of this kind has an optimum size of around twenty participants. It would nevertheless be possible to include expertise in history and philosophy of genetics, molecular and developmental biology, bioethics and biotechnology law, statistics and research instrument design. This would be facilitated by the existence of individuals with multiple areas of expertise. Amongst those US researchers whose attendance would be sought and who would be supported from the budget are philosophers Kenneth Waters (Minnesota), Kenneth Schaffner (GWU), James R. Griesemer (Davis), Evelyn Fox Keller (MIT), Philip Kitcher (Columbia), Sahotra Sarkar (Austin) and Richard Burian (VPI), philosopher and former molecular biologist Lenny Moss (Notre Dame), biologists Scott Gilbert (Swarthmore) and Thomas Fogle (St Mary’s), and molecular biologist and statistician Robin D. Knight (Colorado). We are seeking support in the budget for 13 researchers from other US institutions. In addition, some leading overseas researchers, such as Raphael Falk (Tel Aviv), Hans-Jörg Rheinberger (MPI Berlin) and Jason Scott Roberts (Dalhousie) would be invited and separate funding sought for this purpose. Considerable expertise is available on the Pittsburgh campus, including other members of the Department of HPS, particularly the historian of genetics Robert Olby, and members of the Center for Bioethics and Health Law, notably bioethicist Lisa Parker and biotechnology patent lawyer Sean O’Connor. Pitt’s Program in Rhetoric of Science, Department of Communication is another valuable resource where Donald Egolf has valuable expertise in questionnaire design and questionnaire-based research. We are discussing the form of possible collaboration with him and his students. Both Pittsburgh and CMU have faculty with expertise in cognitive developmental psychology (see previous subsection), but we have not yet found a specific local collaborator and we are also actively seeking collaborators in this discipline from further afield.



At the workshop, tractable research questions would be identified and guidelines laid down for the design of the research instrument. As described above, the workshop is designed to ensure the collective ownership of the research instrument and to maximize the value of the data collected to the research community. We would hope to convene the workshop in Fall of the first year of the project and consultation with workshop participants would continue throughout the ensuing work on the research instrument.

### *Phase 2.*

In the second phase of the project, the research instrument would be completed and agreement sought from learned societies such as Society for Cell Biology and Society for Developmental Biology to contact their membership and invite them to access the research instrument over the internet (alternatively, facilities could be provided at society meetings for attendees to complete the research instrument). It is estimated that this phase, and the actual administration of the questionnaire would occupy the middle twelve months of the project.

### *Phase 3.*

The third phase of the project would involve formatting and analyzing the data in preparation for a second workshop at which the data would be presented and discussed and plans made for publication. We would hope to convene this workshop in either Fall or early Spring of year two of the project. The remainder of the project would involve preparing publications and undertaking the wider dissemination of the data discussed in the section immediately below.

## **Data storage and sharing**

Original questionnaires would be stored and eventually destroyed in accordance with the applicable ethical guidelines covering human subject research. Copies of the research instrument, along with the collected quantitative data would be made available to all researchers via a dedicated website linked to the sites of relevant professional organizations, such as the Philosophy of Science Association, History of Science Society, International Society for the History, Philosophy and Social Studies of Biology and the scientific societies involved in the study (see above, Design of Study). The data would be available formatted for SPSS 10.1 and also as simple, printable tables. The website would also serve as a source of materials and a discussion site for workshop participants during the period of the study.

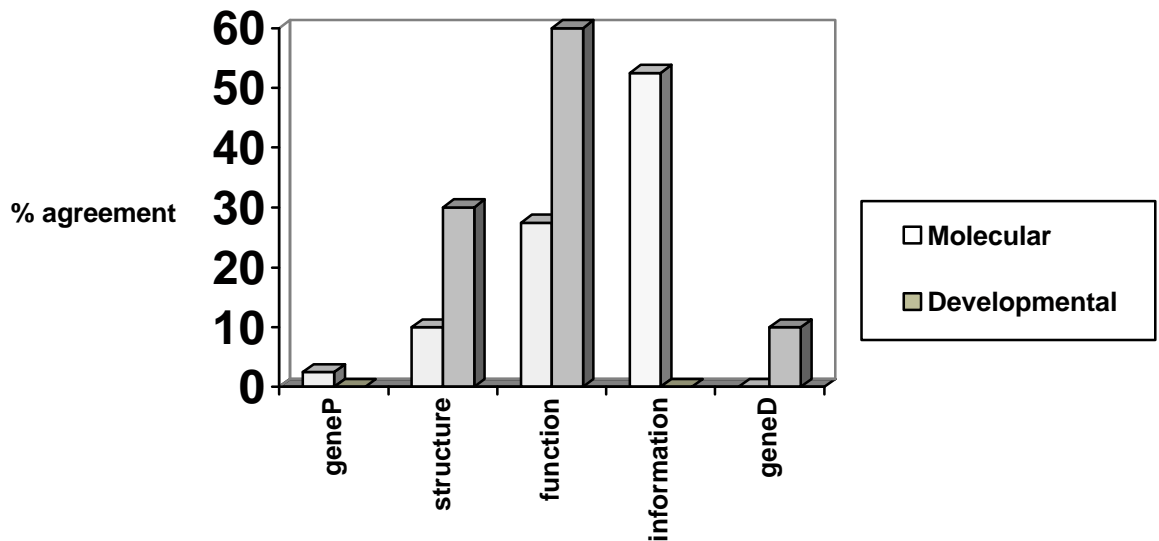
It is anticipated that the data would form the basis of a series of papers by the PI and research associate, probably in collaboration with other participants at the workshop as well as for independent papers by overlapping collaborations by other participants in the workshop. One part of this publication effort would take place in professional HPS journals, whilst a second would be targeted at the scientists who participated in the study via the journals of the professional associations involved in the study. A third part of the publication effort would be directed at bioethicists, genetic counselors, lawmakers and policymakers and would draw on expertise available through the University of Pittsburgh's Center for Bioethics and Health Law. Information about the study would also be communicated to the general public through the release of information concerning the project's findings to the media. This part of the project would draw on expertise available from Pittsburgh's Program in Rhetoric of Science, Department of Communication.

## Broader Impacts of this Research

An adequate conceptualization of the gene is an essential part of public understanding of findings of molecular biology and a prerequisite of meaningful reflection on the social and ethical aspects of biotechnology. Many of the current contributors to the history and philosophy of genetics are also involved in debating social and ethical questions raised by biotechnology and in explaining these issues to the wider public. Philip Kitcher's *The Lives to Come: The Genetic Revolution and Human Possibilities* (Kitcher, 1996) is a notable example of a leading researcher in the field contributing to debates in the public arena. Similarly, Michel Morange related his scholarly work in *A History of Molecular Biology* (Morange, 1998) to problems with the public understanding of genetics in his book *The Misunderstood Gene* (Morange, 2001). On a smaller scale, the PI has appeared to discuss similar themes on Australian public radio. As discussed above, the project may also uncover inadequacies in current conceptualizations of the gene and systematic problems in translating ideas about the gene in one research field into other fields or into more popular discourses. The third phase of the project is designed to ensure that the results are interpreted and presented to as wide an audience as possible in a number of targeted publications.

One specific example of the likely benefits to be derived from the project is with respect to the literature on the persistence of unjustified genetic determinism in the reporting of molecular biology to the wider public. The discovery of genetic involvement in the development of some human traits is commonly taken to imply that: 1. The prevalence of the trait in the population can never be reduced below the proportion of variance in the trait correlated with genetic factors, 2. The development of the trait will be insensitive to environmental factors in development in rough proportion to 'how genetic' the trait is (i.e. the percentage of variance due to g), 3. Interactions between different genes and between genes and environment are roughly additive, so that a given genetic change will make roughly the same difference irrespective of the values of other developmental parameters. It is widely agreed that these inferences are rarely justified, but there is considerable disagreement as to why they remain so attractive. Susan Oyama has argued that genetic determinism is inherent in the way we currently represent genes and what genes do. She claims that as long as genes are represented as containing *information* about how the organism will develop, they will continue to be regarded as determining causes no matter how much evidence exists to the contrary (Oyama, 2000a, 2000b). Kitcher, however, has strongly disputed Oyama's view, arguing that the persistence of genetic determinism is explained not by any conceptual problem in current representations of genetic causation, but by two much simpler facts: the universal human preference for simple explanations over complex ones and the sheer difficulty of communicating complex science to a wider audience (Kitcher, 2001). This is an important debate for those hoping to improve the public understanding of molecular biology and this project should translate at least some aspects of that debate into empirically tractable questions and provide data relevant to those questions. For example, if Oyama is correct then there should be an association between using the informational concept of the gene, in which genes are type-identified by the developmental information they contain, and neglect of the role of contextual factors in gene expression. The preliminary study conducted in Australia suggests that such an association is worth testing for. In that study, biologists with training and experience in developmental biology were much less likely to endorse the informational gene concept than those with backgrounds in biochemistry and pure molecular genetics (Figure 2). Other results suggested that developmental biologists view DNA sequences in the light of contextual factors that affect the expression of gene products. Prospects for operationalizing the claim that the

informational gene concept has a distorting effect on either research itself or the interpretation of research results would be discussed at the first workshop.



**Figure 2.** Molecular and developmental biologists were offered a list of ‘short definitions’ of the gene and asked which they would endorse if forced to choose only one:

1. That which makes the difference between two phenotypes [gene P]
2. A nucleic acid sequence with a certain characteristic structure [structure]
3. A nucleic acid sequence with a certain characteristic function [function]
4. A carrier of heritable information [information]
5. A resource for development [geneD]

Association 0.553; Significance 0.008.

## **Appendix: Information on Postdoctoral Associate**

Dr. Karola C. Stotz, the designated postdoctoral researcher for the project, completed her Masters in Human Biology (including Human Genetics) and in the Social Sciences at the University of Mainz in Germany in 1993. She completed her PhD in the Philosophy of Science at the Department of Philosophy and Moral Sciences at the University of Ghent, Belgium, in 1999, after a three-year research scholarship at the Konrad Lorenz Institute for Evolution and Cognition Research in Austria, and a two-year appointment in Ghent within the ‘Complexity and Evolution’ research group. In Vienna she also worked for the Institute for Empirical Research (IFES) and the Office for the Organization of Applied Social Research (BOAS). Her most important project was for an Austrian electricity company (Energieverbund Österreich) under the title “The Use of Nature: Psychological Experience and Ecological Reality”, in which she tested the impact of power poles and lines on public perception of landscapes. Her interdisciplinary training as a scientist, sociologist, and philosopher renders her exceptionally suitable for conducting research that requires expertise in genetics/molecular biology, in social scientific techniques of empirical research, and in the traditional philosophical task of analyzing key concepts and their role in scientific reasoning.

Dr. Stotz collaborated with the PI on the preliminary research related to this project and described in the application. She was employed as a Postdoctoral Research Associate on an Australian Research Council grant, a position for which she was designated in the grant application. This collaboration continuing under a Steven D. Manners Faculty Development Award from the University Center for Social and Urban Research, University of Pittsburgh. This funding was used to reanalyze the existing data from the preliminary study to extract information relevant to the present project. These results will be valuable in preparing participants for the first workshop (see Design of Study). Her involvement in these two projects makes Dr Stotz exceptionally well qualified for this postdoctoral associateship.

### **Relevant Publications**

Callebaut, W. & Stotz, K. (2000). Lean Evolutionary Epistemology. *Evolution and Cognition* 4 (1): 11-36.

Griffiths, P. E. and K. Stotz (2000) How the Mind Grows: A Developmental Perspective on the Biology of Cognition. *Synthese* 122(1-2): 29-51

Stotz, K & Griffiths, P.E (In Press) Dancing in the Dark: Evolutionary Psychology and the Argument from Design. In *Evolutionary Psychology: Alternative Approaches*. Scher, S and M. Rauscher (Eds). Dordrecht, Kluwer.