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Exploring the post-genomic world: differing explanatory and manipulatory functions of post-genomic sciences

Christina Holmes[a*], Siobhan M. Carlson[b], Fiona McDonald[c], Mavis Jones[a] and Janice Graham[a]

[a]*Technoscience and Regulation Research Unit, Department of Pediatrics, Dalhousie University, Halifax, NS, Canada;* [b]*Interdisciplinary Studies, University of New Brunswick, Fredericton, NB, Canada;* [c]*Australian Centre for Health Law Research, Queensland University of Technology, Brisbane, Queensland, Australia*

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Richard Lewontin proposed that the ability of a scientific field to create a narrative for public understanding garners it social relevance. This article applies Lewontin's conceptual framework of the functions of science (manipulatory and explanatory) to compare and explain the current differences in perceived societal relevance of genetics/genomics and proteomics. We provide three examples to illustrate the social relevance and strong cultural narrative of genetics/genomics for which no counterpart exists for proteomics. We argue that the major difference between genetics/genomics and proteomics is that genomics has a strong explanatory function, due to the strong cultural narrative of heredity. Based on qualitative interviews and observations of proteomics conferences, we suggest that the nature of proteins, lack of public understanding, and theoretical complexity exacerbates this difference for proteomics. Lewontin's framework suggests that social scientists may find that omics sciences affect social relations in different ways than past analyses of genetics.

Keywords: proteomics; genomics; public understanding of science

Introduction

This article considers why genomics and genetics garner significantly greater relevance to the general public than proteomics. For social scientists, the social relevance of science has been a key issue. While the concept of social relevance is open to a variety of interpretations, for the purposes of this article we refer to the creation of a narrative that enables the public to integrate basic understandings of a particular science into their accounts of themselves and the world that they live in and can imagine. Many scientific fields are highly socially relevant while others

*Corresponding author. Email: cpholmes@dal.ca

appear less so. In this paper, we examine two sciences: genetics/genomics, which we argue has been integral in our understandings of ourselves and the world around us, and proteomics – a post-genomics science – which has had, to date, less social impact. While social scientists have studied in detail sciences that have had strong societal impact, less attention has been paid to sciences that appear less socially relevant. We argue that sciences have social impact in a variety of ways, even if they do not have social relevance as we have defined it. We use Lewontin's concepts of manipulatory and explanatory functions of science to critically examine the current social relevance of each science and to analyze why one is, at least presently, more socially relevant than the other. Lewontin's work provides insights into how and why a science becomes socially relevant, why it may not yet be, and why it may never be.

We first define some key concepts and outline our methods, then we compare genomics and proteomics using Lewontin's framework. Table 1 provides a comparative overview. We conclude that explanatory and manipulatory functions are not fixed and that these categories can change as a science develops. The constantly developing technical and analytic complexity within the post-genomic sciences, dependent on an evolving array of new technologies, means that the reductionism of genetics and genomics has become more nuanced. Social scientists may find that omics sciences affect social relations in different ways from previous analyses of genetics.

Genetics, genomics, and post-genomic sciences

The science of genetics captured medico-scientific attention in the late twentieth and early twenty-first centuries, making a profound impact on society. Genomics, or the sequencing and study of all the genes in an organism, has continued genetics' social impact. While the words "genetics" and "genomics" are often used interchangeably, as both examine DNA, genetics involves the study of individual genes and their role in inheritance, while genomics is *the large scale* study of all genes and their environmental interactions involving large databases using new methods of computational biology. Genetics/genomics has provided new understandings of how and why our bodies operate and respond in certain ways; it has promised to create new frontiers in medicine. Understandings of the science of genetics/genomics are culturally interpreted unpredictably by individuals and communities. As a result, it has become part of the public imagination, the zeitgeist, transforming our understandings of self (Fujimura 1998; Lindee, Goodman, and Heath 2003; Nelkin and Lindee 1995; Taussig, Rapp, and Heath 2003).

Post-genomics[1] is the term that describes the group of omics sciences that emerged following the sequencing of the human genome, including nutrigenomics, metabolomics, transcriptomics, and others including proteomics, on which we focus. The term proteomics for the large scale study of proteins (Mishra 2011), was only coined in the mid-1990s (James 1997; Wilkins *et al.* 1996). Although

Table 1. Differences between genomics and proteomics.

	Genomics	Proteomics
Basics	• DNA is formed by a combination of four nucleobases which combine to make up nucleotide strands • 21,000 protein encoding genes in the human body • Essentially constant over time within an organism	• Proteins are formed by a combination of 20 amino acids, in addition to over 100 post-translational modifications, leading to a wide variety of structural differences • Number of proteins in the human body still unknown. Estimated between 250,000 and 1,000,000 • Changes over time and from cell to cell
Main method of study	• DNA sequencer (often now high-throughput)	• Mass spectrometry (variety of instruments) • Immunoassays (detection of antibodies, e.g. ELISA or Western blot)
Term coined	• "Genome" coined in 1920 and "genomics" in 1987	• "Proteome" was coined in 1994 and "proteomics" in 1997
Omics mapping projects	• Human Genome Project launched in 1990, completed in 2001	• HPP launched in 2002, re-launched in 2011

protein biochemistry has a long history, new high-throughput technologies using mass-spectrometers allowed the identification of many proteins at once, in contrast to older methods that focused on one protein at a time. Proteomics' historical foundation in biochemistry, recent technological innovations, and the complex scientific challenges specific to protein studies that are not present in the study of genetic DNA makes it a valuable case to compare with genomics. Ruth McNally has considered the history and role of proteomics in comparison to genomics (McNally and Glasner 2007) and in the context of intensive data flows (McNally *et al.* 2012), particularly within cyberspace (McNally 2005), and the role of standards in the making of proteomics has recently gained the attention of social scientists (Mackenzie *et al.* 2013).

Manipulatory and explanatory functions of science

Lewontin's ([1993] 2001) conceptual framework proposing that science has both explanatory and manipulatory functions is helpful for understanding the social

relevance of emerging genomics and proteomics. Writing before the completion of the Human Genome Sequencing project, Lewontin focused on genetics but his framework continues to be valuable in understanding the ways in which the new omics sciences possess and are socially organized around different explanatory and manipulatory functions.

The manipulatory function of science offers alternative ways of influencing the material world through the development of novel techniques, practices and innovative products (e.g. personalized medicines or gene therapies). While scientists commonly appeal to science's potential as well as actual end products in order to legitimate funding claims to pursue that science (e.g. to cure cancer, create targeted health technologies, etc.), science manipulates and changes the material world in important ways. Vaccines, for instance, cure before there is disease; they act preventatively, invisibly and to a large extent, effectively.

The explanatory function of science, the ability to explain why things are the way they are (e.g. in the omics sciences to expand our understanding of how the body works) also helps us to understand how the world works. Lewontin suggests that this happens at multiple levels and that science has taken over from the church that in the past explained and rationalized social hierarchy through concepts such as divine grace. Science, as an expert-driven universal truth, can be used as a type of ideological weapon to persuade people that the world they live in is equitable and fair to each and all of its biological citizens, or at least inevitable, given set circumstances. Represented by highly skilled authoritative experts, science and scientists are commonly recognized as standing above politics as a purer, rational and more evidence-based legitimating force.

Lewontin observes that these two functions are often independent of each other. Successful manipulation of the natural and material world is not necessarily dependent on a correct understanding of how that world works. Lewontin argues that genetics provides both a powerful explanatory function and social legitimation (e.g. in sociobiology's more infamous moments reducing and confabulating racialized inequalities with genetic intelligence (Gould 1996; Hernstein and Murray 1994). Lewontin suggests that this is only possible through social explanations that use reductionism and atomism.

Applying Descartes' notion of atomism that explains how the world works through powerful machine metaphors, Lewontin suggests that people often forget that it *is* a metaphor. Combining the tropes of atomism with reductionism: "the belief that the world is broken up into tiny bits and pieces, each of which has its own properties and which combine together to make larger things" (Lewontin [1993] 2001, 108), genetics is simplified into an acceptable social explanation that "genes make individuals and individuals make societies, and so genes make society" (Lewontin [1993] 2001, 14).

We will return to the impact of incorporating social interaction within scientific thought for the new omics sciences after considering the manipulatory and explanatory functions held by genetics, genomics, and proteomics. We suggest, however,

that the ability to explain why things are the way they are (an explanatory function) varies across scientific fields. Some have greater ability to move from theoretical inquiry to provide social relevance (legitimacy/explanation) and tangible results (manipulatory function).

Methods

We conducted 35 semi-structured interviews with proteomics scientists and regulatory scientists or clinicians and engaged in four years of participant observation at the annual Human Proteome Organization's (HUPO's) international conferences (2011–2015), as well as the Australasian Proteomics Association's annual conference (2012 and 2013). While the majority of the interviewees were based in Canada, the USA, and Australia at the time of interview, many had been trained or had worked in a wide variety of other countries. The HUPO is an international scientific consortium that was established in 2001 to promote proteomics (the Australasian Proteomics Society is a regional grouping of HUPO). One of HUPO's arguably most significant initiatives to date is the organization of the Human Proteome Project (HPP), modeled on the Human Genome Project, which aims to map human proteins to the genome. Our interviews focused on the role of standards and knowledge translation in the scientific process. The findings from participant observation and interviews have been triangulated (analytical comparison, augmentation and corroboration of interviews and participant observation with other documents) through examination of scientific editorials and reviews related to proteomics, standards, and clinical applications. The project received ethical approval from Dalhousie University's Research Ethics Board and Queensland University of Technology's Human Research Ethics Committee. Analysis for this paper is based primarily on transcripts of interviews.

Genetics, genomics and society: powerful explanatory narratives

Manipulatory functions

Both genetics and genomics have promised much but delivered little with regards to manipulatory functions. In the early days of genomics there was a great deal of optimism (some say hype) over its manipulatory potential, with advocates claiming that genetics and genomics research would result in significant advances in medical care and treatment that have largely been unfulfilled to date (Boycott *et al.* 2013; Caulfield 2000; Fleising 2001; Tutton 2012). Genetic testing, when available, usually elucidates one's level of risk (Boenink 2010) (e.g. BRACA-1 and BRACA-2) as a probability, garnering some criticism that such tests are no different from other cultural methods of divination (Lock 1998). While they can be diagnostic of a particular genetic condition, such as Trisomy 21 (Down's syndrome), particularly in the case of reproductive medicine (Rapp 2000), actual genetic treatments are rare and gene therapy is still largely experimental (U.S. National

Library of Medicine 2015). As Hedgecoe and Tutton (2013, 2) commented "The influence of genetics on day-to-day medical care is far more limited" (than its potential).

While genetics, and especially genomics, have promised much in terms of new medical advances, the science has not yet lived up to its many promises (Fortun 2008). In other spheres, notably criminal justice and agriculture, some of the promised potential of genetics and genomics has been actualized: in the criminal justice sphere, in forensic DNA; and in agriculture, the genetic engineering of plants and animals. In comparison to the myriad of hopes associated with genetics and genomics (Fortun 2008), however, genomics' substantive material (manipulatory) outcomes have been quite restrictive. This contrasts with the field's explanatory function.

Explanatory functions

The explanatory function of science, according to Lewontin, explains why things are the way that they are. Genetics, and by extension, genomics have a very strong narrative appeal. Genes are often used to explain everything from "why I look the way I look" to "why I did the things I did." Such individual explanations are often extended to the social to try to explain why people behave the way that they do. Genetics has been linked to a discourse around universal truth claims surrounding our understanding of who we are as a human species, our personalities, our flaws and our health and there has been a large body of social science literature that has critiqued the reductionism of genetic explanations (Fujimura 1998; Lindee, Goodman, and Heath 2003; Nelkin and Lindee 1995; Taussig, Rapp, and Heath 2003). Lewontin ([1993] 2001) argues that this social tendency toward genetic reductionism has reduced emphasis on the flexible nature of DNA and the structures it creates.

Nelkin and Lindee (1995) suggest that genetics has provided an ideal venue through which to blame economic-social-structural dysfunctions. By focusing on an individual's genetics to explain social phenomena such as criminality, poverty, and health problems, the "criminal" or disease-mutated gene, for example, perform the same work as the reductionist concept of original sin in the past. Genetic research that identified a rare mutation causing a deficiency in the MAO-A gene resulting in high levels of impulsive aggression, has been used to ascribe individual responsibility to violent crimes (Hunter 2010). Subsequent research establishing that environmental (nurture) factors, in particular serious maltreatment or abuse in early childhood, may trigger the genetic predisposition in only those with low variant MAO-A, did not prevent it being dubbed the "it's not my fault I have the criminal gene" defense in legal cases (Connor 1995; Hunter 2010). Recognition of the existence of the MAO-A gene has led to a dilemma for courts asked by prosecutors to consider this gene as evidence to justify a longer sentence on the grounds of risk. Defense lawyers, on the other hand,

submit "it" (the gene) as a mitigating factor to reduce sentence length or reduce murder to manslaughter. In short, this reduction to an entity of a sequencing process with wide variability in expression has contributed to debates about identity and individual responsibility that have personal, legal and political dimensions for individuals and populations.

Similar to genetics, genomics has a strong explanatory appeal, bolstered with powerful referential narratives, such as the "book of life," "code," "map," or "blueprint" (Stelmach and Nerlich 2015). Along with the critiques of genetics detailed above, genomics, in the 1990s at the start of the Human Genome Project, was criticized by many social scientists, historians and philosophers for its reductionism, genetic determinism, and hyperbolic promises (Richardson and Stevens 2015). Post-genomics' "emphasis on complexity, indeterminacy, and gene-environment interactions" may be less reductionist than the path traced through the genomics era "from a simplistic, deterministic, and atomistic understanding of the relationship between genes and human characters" (Stevens and Richardson 2015, 3). However, these researchers note that while post-genomics seems to move toward more holist approaches, reductionism has not entirely disappeared; genes and sequences still play a central role in post-genomic thinking. Indeed, epigenetics, a post-genomics science, has provided an explanatory "sense of empowerment" about the role of environment over heredity (Stevens and Richardson 2015).

Similar to Richardson and Stevens, we argue that reductionism has not disappeared, despite the fact that genomics incorporates complexity into its work and scientific explanations, including multidimensional computational and informatics approaches, new kinds of data, and systems-based frameworks and forms of genomic explanation. This may be particularly true in terms of the social impact of genes and genomics (i.e. its explanatory function). "The enthusiasm for genes and genomes appears to be as great as ever" (Richardson and Stevens 2015, 233). Thus, while genomic research may indeed include a complexity that eluded genetics, complex explanations do not filter into social explanations such as the role of gene and genome sequencing in self-identity, self-knowledge, and personhood. Thus, for the purpose of understanding social impact, much of the reductionism critiqued by social scientists and historians of genetics is still in play in the age of genomics, even if there have been significant differences in the way the scientific field of genomics is practiced compared to genetics.

Genomics and explanatory function: three examples

We consider three examples of popular social adoptions of the explanatory function for genomics or genetics[2]: direct-to-consumer genomic testing; advertising; and cult fiction. By no means exhaustive or exclusive, these provide illustrative counterpoints by their absence in proteomics discussions. We compare the presence of explanatory function in genomics against its relative dearth in other post-genomic sciences, in particular, proteomics.

An increasing number of genetic testing/genomic sequencing websites and "retail genetics" services (Richards 2010) offer to test individual genomes to provide information on health risks. Groves and Tutton (2013) more accurately refer to this as personal genomic susceptibility testing. When a gene to health connection is already scientifically complex and tenuous, making informed consumer choice difficult, this marketing vehicle simplifies the information (Curnette and Giuseppe 2012; Hennen, Sauter, and Van Den Cruyce 2010; Messner 2011; Richards 2010). While direct-to-consumer testing companies employ various strategies to create trust and credibility for risk information (Einsiedel and Geransar 2009), the precarious nature of genetic risk probabilities require seductive accounts that favor nuanced endpoints that address some general form of "feelings" and "knowledge" as a key selling points for direct-to-consumer genetic testing rather than definitive diagnosis. Curnette and Giuseppe (2012), for example, argue that websites for direct-to-consumer genetic testing present their information as personal knowledge in contrast to being for medical application. This personal information is presented as key to modern understandings of self. The websites use emotional responses to promote their product, linking it to a cultural need "to understand" for both personal and family benefit (Hiraki *et al.* 2009). The websites market their genetic tests as an important aspect of modern identity formation.

Taussig, Rapp, and Heath (2003) argue that genetic research has led to new technologies of the self and negotiations of identity against a genetic "normal," which they frame as a form of biopower. For example, by signing up to undergo a genetic test to access an array of particularly desired information, the consumer exerts a level of perceived self-agency that cannot be achieved through the limited and focused testing available in the clinical setting. Genetic testing creates an explanation for the way one is or will be. McGowan, Fishman, and Lambrix (2010) suggest that direct-to-consumer genetic tests are a kind of information technology that is being co-constituted by both lay experts/consumers and the companies marketing them to create new subjectivities and engagements with the future. Thus genomics as a whole is visualized as key to creating different kinds of "genomic futures" or socio-technical landscapes, all of which are significant, even if there is disagreement about where genomics will lead society (Webster 2005).

It could be argued, however, that direct-to-consumer genomic testing is a special case, one which only reaches a small percentage of people. To further demonstrate the widespread contemporary nature of the strength of the explanatory function of genomics and genetics, we turn to two additional examples, an ad campaign and a popular cult fiction book and television series.

In 2015 Land Rover ran an international media advertising campaign containing the text: "New Discovery Sport ADVENTURE. IT'S IN OUR DNA. #InTheDNA." In one commercial for their Discovery Sport Adventure vehicle,

they linked a desire for adventure (and therefore a need for their product) to "the adventure gene":

> If we have an overwhelming desire to explore, perhaps the reason lies in our DNA. There is a genetic variant known as DRD47R, carried by roughly $\frac{1}{4}$ of all humans. It is more commonly known as the adventure gene. It makes people more curious, less restricted by boundaries. They'll be more likely to take risks and may get a sudden urge to explore. But before you can act on the urge to explore, you'll need the tools to make that exploration possible. New Discovery Sport Adventure. It's in our DNA! (Land Rover 2015)

The advertising campaign humorously drew on genetics as an explanation for desire (social behavior), linking a genetic variant with a vehicle. Such a marketing campaign can only work by engaging consumers (Armstrong and Kotler 2015) in the presence of widespread popular acceptance of genetic explanations (in a reductionist form).

For our third example, we draw on cult fiction surrounding the transformation of werewolves. Cult fiction requires a level of audience engagement outside the observations from the simple confines of their living rooms (Abbott 2010; Cherry 2012; Mellins 2012; Ruddell and Cherry 2012). Recent years have witnessed a rise in the integration of gothic themes coupled with scientific innovation (Abbott 2010; Crow 2009; Martin and Savoy 1998; Goddu 1997). Stories of monstrous transformation incorporate scientific explanations of nature/culture hybridity that draw from explanatory disease models.[3] Early werewolves were "created" during much of the second millennium by a bite (e.g. transmission of bodily fluid). More recently, stories influenced by hereditary models of disease (or geneticization; Lippman 1992) are packaged in popular accounts to explain a fictional group's identity and reason for being. In the Sookie Stackhouse/*Southern Vampire Mysteries* novels written by Charlaine Harris (2006) adapted to screen in the *True Blood* series, shape-shifters are made by a bite or, with the right heritage, spawned. Genetics seeds ideas that once had other explanations:

> That didn't mean Jason's life as a shape-shifter would be worry free . . . if he married a regular human woman their kids would be normal. But if he married into the shifter community at Hotshot, I'd have nieces or nephews that turned into animals once a month. *Dead as a Doornail*. (Harris 2006, 4)

Similarly, in the television series *The Vampire Diaries* (Somerhalder *et al.* 2010, 2011), becoming a werewolf is genetically inherited. Genes alone, though, are not sufficient to trigger the transformation. The gene (or werewolf predisposition) is only activated/triggered if the carrier kills someone. We see here a popularization of genetic susceptibility which might be considered culturally "post-genomic," but only includes a limited amount of complexity in its explanation. We now turn to proteomics in order to consider *how much* scientific complexity can enter into a science's explanatory function.

Proteomics and society: more potential manipulatory, but less explanatory function?

In this section we apply Lewontin's concept of manipulatory and explanatory functions to proteomics, using data collected from research with proteomics scientists. Proteomics, like some other post-genomic "omics" sciences, such as nutrigenomics (Harvey 2009), builds upon an older science of protein biochemistry. It combines this earlier scientific field, which analyzes one protein at a time, with the comparatively newer computational biology and sequencing platforms of genomics and new techniques to analyze proteins, chiefly the mass-spectrometer, to analyze many proteins at once.

Manipulatory functions: "You need to get out of the blueprint and into the building"

Proteomics is similar to genomics, in that most of its potential for manipulation is still that – potential. However, there are some differences. Some clinical diagnostic tests already in existence rely heavily on protein analysis using older, more robust methods, such as enzyme-linked immunosorbent assay (ELISA) or more modern mass spectrometry methods. Unlike genomics, which accesses the "blueprint" of the body, proteins form the "building blocks" and action molecules. As one researcher who moved into proteomics after working in genetics put it, genes end up working through proteins:

> Over all the years I have done a variety of research, especially related to Eco genetics: the interaction of genetic and environmental factors. Proteins are sensors for agents of communication inside cells, so if you want to understand what the genome is expressing, you have to study the proteins and not just one at a time. (Dr A,[4] proteomics scientist)

In terms of the development of diagnostic tests, proteins have the potential to measure, not the *risk* of a disease, but its presence and severity. Therapeutic drugs target proteins in the body, rather than genes, so there is greater potential for the development of new drugs and personalized medicine (e.g. matching the appropriate drug to the proteins expressed by an individual within a specific tissue, or type of cancer, etc.). As one researcher put it, proteomics is more direct than genomics:

> There's lots of publicity about sequencing the human genome . . . But, as we all learned in school, the central dogma of molecular biology says that DNA makes RNA makes protein. And it's really the proteome then that is most proximal, that more directly gives rise to the phenotype and characteristics of a tumor. So there's the expectation that if we really are going to be using molecular signatures to define tumors and guide in their treatment, that signatures based on proteins might have a better readout of the biology and the therapeutic responses than something as indirect as genomics. (Dr B, proteomics scientist and MD)

Given the more direct nature of proteins in health or disease states, then, it is logical to suggest that proteomics may well turn out to have a more direct manipulatory function than genomics, even if both have predominantly only potential manipulatory function at this point.

Explanatory function: "You're studying proteomics? What's that?"

We argue that in spite of having better potential for manipulatory function than genomics, proteomics has not been able to generate narratives with the same strong explanatory function as genetics and genomics. So what would proteomics' explanatory capacity look like within our previous examples? Direct-to-consumer genomic testing, for instance, plays upon notions of identity that the public associates with genes, but not proteins. If proteomic related tests can be difficult for medical students to understand, as one researcher pointed out, would it be possible to market them directly to the public? An advertising campaign using protein-based references seems absurd rather than convincing: Would the slogan "Adventure – it's in our post-translational protein modifications!" sell cars? Finally, how would one incorporate a protein-centered method of monstrous transformation into a cult fiction or gothic storyline? Would people understand a werewolf transformation that hinged upon crucial protein changes, interacting with the genome, the metabolome, and the transcriptome?

We suggest that a key reason for proteomics' relatively weaker explanatory function is due to its complexity. Grappling with complexity is central to omics sciences and systems biology perspectives (Fortun and Fortun 2005; Fujimura 2005; Levin 2014). In the following section, we describe the complexity of explaining or translating proteomics to non-experts in three different areas: (1) the scientific nature of the protein, (2) a lack of public understanding of a protein, and (3) the increasing importance and use of a systems view within proteomics.

Proteomics and explanatory function: complexity

One of the key themes arising from our discussions with proteomics scientists was the increased level of complexity and number of proteins to be identified compared to genomics making both clinical application and the ability of funders and policy makers to understand the science more difficult:

> Proteomics is orders of magnitude more challenging [than what] we've solved [in] the human genome, we will never solve the human proteome. (Dr C., proteomics scientist)
>
> I think just in general that proteins are much more difficult molecules to work with. (Dr D., protein biochemist and MD)

Why is proteomics more complicated? Those we interviewed provided several reasons. Proteins are still difficult to isolate, so preparing a reliable sample of relevant proteins that do not degrade (thereby losing their structural shape),

presents a problem. Proteins have many more structural variations (i.e. shapes, which affect function) and components (i.e. amino acids as building blocks) than does DNA. There are approximately 21,000 protein encoding genes but the number of proteins that can encode upon these genes is still unknown, estimated at between 250,000 and 1,000,000 (National Cancer Institute, http://proteomics.cancer.gov/whatisproteomics). Genes are relatively constant but proteins change from cell to cell and time to time:

> Yeah, it's a much, much more complex problem. If you look at DNA, there are four bases and there's methylation, which is like an on/off switch, on the DNA. So that's five. With proteins there's 20 amino acids and 100 post-translational modifications, and there's a lot more structure to protein. And the structure – it's relevant with DNA but it's not as crucial as it is with proteins. So there's probably at least an order of magnitude maybe two orders of magnitude more complexity in proteomics. (Dr C., proteomics scientist)

Coupling the more complex nature of the protein with the still emerging nature of the technology (mass-spectrometers) used for analysis in proteomics (rapidly improving sensitivity and speed) and the continual development of quality control standards for those instruments, further complicates the ability to easily explain the field.

This brings us to the second important aspect of complexity that was raised: there is less public recognition of proteins than genes. A researcher used to communicating protein-related concepts to medical students, details the difficulties involved in explaining central concepts of the field to the public:

> Socially, you have to recognize that people, the vast majority of people don't have the scientific training that you or I have. Most people know what their genes are. They know that, "my cousin had sickle cell disease so I had better be careful". To understand what a protein is – that's a whole smaller segment of the population that really understand what a protein is. They might realize that, "certain proteins are found in disease and that's why they screen for PSA, to tell me if I have prostate cancer" – which is controversial right now, actually, whether that's a good test or not. You see what I mean? They might realize that these proteins are markers, but they don't really know what protein does. So the technology, in terms of how you fragment a protein and look at the pieces based on their mass, to not only identify proteins, but in two different samples to compare their levels . . . . it is very difficult to translate that to the public. Or even to medical students sometimes. (Dr D., protein biochemist and MD)

This researcher highlights three key factors in terms of translating proteomics to the public. First, understanding how the instruments analyze proteins is a challenge. Second, the interpretation of even widely publicized tests for protein markers, such as prostate-specific antigen (PSA) for prostate cancer, is not necessarily straightforward, making practical examples of protein tests complicated to explain. Third, the interaction between proteins and/or looking at a variety of proteins at once, does not

lend itself to a reductionist explanation. These factors make it more difficult to explain proteomics to funders and clinicians, let alone the public. This is very different from the long standing explanatory function of genetics that can draw on a history of biological reductionism and familiarity with the concept of heredity (Lewontin [1993] 2001). Proteomics, through a focus on the context and interaction of proteins, cannot rely on a background understanding, even if reductionist, of individual genes that contributes to the explanatory power of genomics in social situations. While this complexity does not necessarily prevent proteomics from making a contribution to science and medicine (and being funded to do so), it might be more difficult, at this time, for it to claim social relevance.

The third aspect of complexity that was discussed in interviews with proteomics scientists was the increasing importance of a systems view in the omics sciences. Proteomics is not considered a stand-alone science. It builds on the findings of genomics, as well as integrating with data from other omics fields, such as transcriptomics and metabolomics, etc., in order to get a total picture of what is happening in a particular cell, tissue, or body. The goal is that:

> . . . future advances in genomics and proteomics are expected to bring several revolutions in medicine and will make personalized medicine a reality. Advances in proteomics are expected to integrate the reductionist views of Watson and Crick into systems biology to show how molecular parts evolved and how they fit together to work as an organism. The latter is expected to provide the ultimate understanding of biology. (Mishra 2011, 3)

This sentiment echoes Lewontin's argument that reductionism does not sufficiently take into account the importance of interaction and interrelationships, although the importance of looking at individual parts is not discounted:

> . . . there is clearly truth in the belief that the world can be broken up into independent parts. But that is not a universal direction for the study of all nature. A lot of nature . . . cannot be broken up into independent parts to be studied in isolation, and it is pure ideology to suppose that it can. (Lewontin [1993] 2001, 15)

He suggests that neither an atomistic nor holistic world view heavy on mysticism (e.g. the Gaia hypothesis) is sufficient. Instead, he suggests a crucial third way for better understanding nature:

> one that sees the entire world neither as an indissoluble whole nor with the equally incorrect, but currently dominant, view that at every level the world is made up of bits and pieces that can be isolated and that have properties that can be studied in isolation. . . . In the end, they prevent a rich understanding of nature and prevent us from solving the problems to which science is supposed to apply itself. (Lewontin [1993] 2001, 15)

One interview captured this with a landscape metaphor. Instead of focusing on a particular plant (i.e. one protein), scientists now have the ability to zoom in and out from the plant to its landscape (i.e. community of proteins or proteome):

> I've got this picture of a landscape, I focus in on this fern, this one little plant in this landscape – and I say, "This will be a reductionist biology approach to looking at this system". You zero in on something that you are interested in and you find out as much as you can about it and that is extremely useful information. It gives you very high resolution around that one thing. But it doesn't necessarily mean you get a clear picture of how that one thing fits into or integrates very well under certain conditions with the rest of the system. And so then you zoom out to the whole landscape. And I say, "So you can see that this is in many ways a lower resolution view, but you get to see more of what is happening in the landscape and how different things are integrated and what different components of that landscape may influence others especially in a dynamic situation". (Dr X, clinical researcher who uses proteomics)

The future will involve contextualizing the particular within the broader system:

> So, you know, if you just take a single time point, you are only interested in – you are not going to get a very good view or feel of how things change over time, and today it is all about dynamics. It is about how things change over time – I think that is where we are going in the future. [. . .] That's why you have a look at the whole picture, so you can zero in on the things that you think look interesting. And so it is not to say we shouldn't be doing reductionist biology – absolutely. It's essential to be able to build resolution around individual areas, but what are the most important areas to be looking, you know? We can pick our favorite protein, or favorite gene, or favorite class of genes and investigate that to death and that's fine because it builds a lot of resolution around that. But is that the most important thing? I would not advocate saying we should just be doing systems biology type things, big data type things. I think you have to go back and be able to validate and look at things in much higher resolution. [. . .] It's all linked, it's all independent, so you do need to have a look at the whole thing – so I think these things can be much more integrated than what they are. (Dr X, clinical researcher who uses proteomics)

Proteomics deals with enormously complex data. A systems approach, drawing data from multiple sources (genomics, transcriptomics, metabolomics, proteomics) that lends understanding of how a single element in a body (e.g. a single protein) interacts in its wider context (i.e. the proteins which surround that protein) heralds significant potential. It rejects the sole focus on reductionism that Lewontin deplored, while incorporating its strengths. Translating this complexity and explaining its work to a wider audience, has proven elusive for proteomics, hindering its explanatory function.

Proteomics scientists employ various strategies to increase recognition (and gain popularity and funding) for the field and strengthen its social relevance. One of these strategies is the HPP. The original HPP, launched in 2002 with an organ and data standards focus (Mackenzie *et al.* 2013), was later re-launched by HUPO with a chromosome focus in an attempt to mirror the human genome project (Human Proteome Organization 2015). The HPP has two arms: one looking at mapping the proteins to chromosomes (C-HPP) and the other mapping the proteins in respect to disease states (B/D-HPP). While the scientific

rationale is to extend knowledge based on genomic sequencing (for example, by cataloguing proteins associated with certain chromosomes (C-HPP)), this also has the benefit of tying proteomics to the human genome mapping project, which had a high public profile. Another arm of this project is to focus mapping a particular tissue, or disease related proteins, in an attempt to work on avenues of investigation with potential translational scientific benefits (B/D-HPP). These strategies which tie explanations to clinical or biological functions, are not however a priority for all proteomics researchers who instead pursue a systems biology approach, for instance, even though they do not expect it to be widely understood. As Fortun (2015) has suggested, scientific interest is an important motivator for a research area; many proteomics scientists are intrigued with the wider possibilities for the future using a systems biology approach.

Conclusion

We have detailed how and why proteomics is deemed less relevant than genomics despite an equal or stronger potential for new techniques, practices, and products (see Figure 1).

We have suggested that this is due to the greater complexity inherent in protein analysis, which makes it difficult to translate to the public or reduce into a readily understandable mechanistic soundbite. What are the consequences of this complexity and perceived lack of social relevance in proteomics?

First, we suggest that the explanatory and manipulatory functions of a science are not fixed and can change. For example, even if the attempts by proteomics scientists to increase proteomics' ability to provide widespread explanations for the way the world works do not succeed, an increasing number of new applications from this science could gain it recognition. The field's ability to transcend its complicated subject matter and increase its presence within the social world could come with recognition of the disruptions its advancing discoveries bring to the everyday world. For example, Bell (2013) suggests that biomarkers for monitoring cancer survivors (e.g. PSA, etc.) are changing the way people visualize the internal body, shifting the gaze from a molecular (probability of disease risk) to a numeric

	Manipulatory function	&/or	Explanatory function	→	Social relevance
Genomics	Claims high potential Largely unrealized	&	High capacity to explain	→	Extensive social relevance
Proteomics	Claims high potential Largely unrealized	&	Low capacity to explain	→	Limited social relevance (as yet)

Figure 1. Differences between genomics' and proteomics' social relevance. Demonstrates current differences between the social relevance of genomics and proteomics using Lewontin's ([1993] 2001) division between the manipulatory and explanatory functions of science. Manipulatory function refers to the ways in which science affects the material world (e.g. application), while explanatory function refers to a science's ability to explain and understand the way the world works. We note that a scientific field's functions can change over time.

one (which quantifies disease along a continuum). Just as capacity for better explanation of proteomics may lead to more research funding and thereby produce more tangible (manipulatory) results, these recognizable outcomes of research may change the scientific field's ability to explain what is happening in the human body. Nevertheless, genomics shows us that manipulatory and explanatory functions are not necessarily aligned; a lack of high manipulatory function does not preclude the capacity for explanatory function.

Second, there is a widening gap between the complex scientific explanations present in the new post-genomics sciences and the genetic reductionism of the past. Post-genomics science includes increased complexities within large data sets and biological systems analyses. The reductionism that proved so persuasive in explaining past sciences is an uncomfortable fit with analysis of large, complex systems. This increasing complexity and lessened reductionism is well noted in the genomics and post-genomics literature (Bitsch and Stemerding 2013; Hauskeller, Sturdy, and Tutton 2013; Lappé and Landecker 2015; McNally and Glasner 2007; Richardson and Stevens 2015; Torgersen 2009), even though genomics is still tied to the gene and its accompanying reductionism. Indeed, tensions exist in scientific research arenas between the way in which genomic discoveries are reported in the media and the less deterministic way in which genes are contextualized (Torgersen 2009). The new omics sciences frame "the research object, namely living cells, as complex systems and no longer as simple machines" (Torgersen 2009, 84).

Finally, we suggest that the social implications of the new omics sciences (and therefore the attention of social science) may be found in newer arenas than those of identity which yielded rich analysis in the past. Hauskeller, Sturdy and Tutton, suggest that it is analytically important to remember "the power of material technologies and discourses of materiality to represent and realize social relations" when considering the impact of genetics on identity (2013, 884). Proteomics may, through the power of material technologies, *change* social relations, but at this point it looks less likely to *represent* social relations than genetics and genomics has in the past. As Harvey (2009) points out, while such new sciences draw on past scientific practice, they are not a simple continuation of these practices, and therefore the new omics sciences cannot be analyzed by reference to past social science understandings of genomics. However, while Harvey (2009) posits that the key question has shifted from "what makes us human" (e.g. with Human Genome research) to "what makes us different from one another" with the post-genomic sciences, following Lewontin we would argue that the explanatory function of past gene science has already been extensively used to naturalize differences between groups of people. Instead, we suggest that the relationship between explanatory and manipulatory functions will vary between post-genomic sciences. The post-genomic sciences may translate into new and interesting science and societal relationships for social scientists to explore in both their manipulatory, as well as their explanatory functions.

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Notes

1. Post-genomics is still a contested term in the life sciences for the stage of scientific research that followed the sequencing of the human genome, as it implies that genomic research consists only of gene sequencing (McNally and Glasner 2007). However the term is used in the social sciences to refer to the widespread transformations in the life sciences following the completion of major genome projects (Stevens and Richardson 2015).
2. There is some overlap in the examples we use as to whether they refer to a genetic or a genomic example.
3. Examples of werewolf transformation are drawn from Siobhan Carlson's Master's thesis analysis, which is reviewing key narratives within this cult fiction genre.
4. Pseudonyms used.

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