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Semiotical and Hermeneutical Approach to Undiagnosed Rare Diseases

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Sociotype is a concept that allows a more comprehensive understanding about biosociology of undiagnosed rare diseases (URD). Sociotype is related to a genotype and a phenotype and it is an expression of the individual life world in society. In this paper, semiotic and hermeneutic analysis of papers published and selected about URD is developed. The perspective followed in this research is aligned with the works of Barbieri and Peirce. Papers with the most social content have been selected and those with a more biomedical content have been rejected. The semiotics analysis has been divided in genotypic, phenotypic and sociotypic, and related to the hermeneutical perspective. It has been possible to understand the basis of semiotics elements of URD. The general conclusion is that URD is a particular sociotype with a determined set of social characteristics. This paper opens research on the biosemiotic and hermeneutic perspective about URD.

Keywords: rare diseases, undiagnosis, biosociology, hermeneutic, sociotype, Peirce

INTRODUCTION

The *sociotype* is a socioecological construct that let us to organise the biological determinants according to the effects of these ones in the psychosociological context. In this sense, the sociotype is a framework synthesis of the factor that determines an individual resilience across the life of persons (Peng et al. 2018). This frame is made up of three domains: intra-personal, inter-personal and socioecological. The first one is related with the biological and psychological factor of each person. The second operates according to psycho-sociological and symbolic interactions. And the last is related to multiple factors of the social and ecological (biological) context. Then, the human being is a product of interaction between a genotype, a phenotype and also a sociotype, or – if preferred – between the intra-personal, the inter-personal and the socio-ecological.

Greeks were aware that the human being is a social being. Anaximander considered that characteristics of nature were not immutably fixed (Barnes 1982). According to Plato (2016),

the social environment of the polis is crucial for an individual. According to Aristotle (2013), the human being in his(her) very nature is *zoon politikon*, political being. The sociotype, as the reader will have imagined, is aware of the Greek idea of the human being as a social being, but expands this conception by linking the social with the biological. In addition, the sociotype construct needs more time to be configured and it was close to disciplines like paleo-anthropological, social networking and 'social physics' studies (Marijuán et al. 2017). According to Marijuán et al. (2017), it was Bogardus who used this term in order to show the situations (behaviour) of each person in society. Recently, the sociotype has been used related to biomedical fields (Berry 2011; Berry et al. 2017) and also has been used in a socio-evolutionary meaning (Marijuán, Navarro 2020). Consequently, this concept has an epistemological advantage, since, in addition to helping to study human society as a whole thanks to its differentiation by logical groups, it also allows us to understand the biosocial process of sociality in humans and also in other animals.

An ecological perspective is essential in any theory of evolution, and in our biosocial perspective. In this sense, interaction among social and biological knowledge has been shown to be truly relevant to understand the triad *gene-culture-coevolution* (Gintis 2011; Ross, Richerson 2014). The coevolution among gene and culture leads to the understanding that humans are biological beings (sometimes social sciences forget it, for example, when sociobiological knowledge is neglected). Moreover, human behaviour is conditioned by social factors as well as by our own cultural constructions. For this reason, it could be argued that human beings are complex organisms, framed in bio-socio-culture contexts, in which biological and social determinants are important equally.

Biosemiotics focus – which successfully used for research the triad mentioned above – concluded that because biological and cultural evolution is produced by their named *life's agency*, then relationship between cultural and biological evolution must be symmetric (Kleisner, Tureček 2017). According to Laland (2017), these authors expose that biology and culture share a common origin, and the difference among a genotype, a phenotype and a sociotype are in their degrees of modification. In this sense, the philosopher J. von Uexküll (2010) showed the interrelation, cognitive and operative, between living being, namely animals, and its environment. This author considers that every species develops a unification of its stimuli at an intra-organic level and with its external reality in a wide diversified *sociobiological phenomenon*.

The aim of this paper is deepening in this biosociological frame in order to analyse if it is feasible to talk about undiagnosed rare diseases as a sociotype category. Our research starts with a documental analysis of literature about rare diseases undiagnosed. The term 'undiagnosed rare diseases' (URD) has been searched in WOS (Web of Science) without using quotation marks, and 2,077 results were found on 9 September 2021. The year 2021 is incomplete, for this we consider that it is necessary to exclude 178 documents of 2021. Then, we found 1,899 papers. This search has a lot of documentary noise, so it is necessary to select the texts according to three basic criteria: period, subject matter and methodology.

25 papers were published before 1975 (1913–1974). These are articles where there is no concept of 'rare diseases' but unusual cases were studied. The unusual case concept mentioned a wide spectrum of specialties, many of them in relation to infectiology and parasitology. Then, according to the first criterion, these 25 papers were excluded. After excluding texts from 2021 (incomplete year) and those prior to 1975, it was decided to enter the qualitative term in the search. 10 results with which it was possible to work in a more selective way

were obtained. Also, we then decided to narrow the search using quotation marks. A simple search without time restriction with the following topic 'undiagnosed rare diseases' has been performed. This search returned 14 results. Once these 24 articles were obtained, we focused on reading their content in order to establish semiotics categories that help us to comprehend this semiotics context.

In selected papers, the basic semiotics elements of the hermeneutic exposed by families and illness have been determined. The way in which the scientific community deals with this problem has also been determined. All this will allow us to establish gaps in knowledge that will help to establish future research. The basic structure of the biosemiotics analysis starts with the idea of triple configuration of our nature: genotype, phenotype and sociotype. In this sense, our methodological intention is not to show the elements exposed in the analysed articles, but to determine the factors that condition semiotic (biological and sociologial) elements operating in the social group under study.

STRUCTURE OF A BIOSEMIOTICS APPROACH TO UNDIAGNOSED RARE DISEASES (URD)

According to the search of *Web of Science* undiagnosed pathologies are related with medical issues. Most articles explain a new biomedical method, network, molecule, technic, etc. that allow a faster and more efficient diagnosis. But there are few papers that consider the social reality of persons affected by rare diseases. On the other hand, philosophical papers have not been found in researching.

Undiagnosed rare diseases* (URD) raise a biosemiotics challenge to comprehend transfer of information among the three determinants of biosemiotics: genotype, phenotype and sociotype. In this chain of significance, each determinant incorporates new information as it increases the complexity of biological signs. This triad configures a triadic relationship, and a triadic biosemiotics.

Biosemiotics of Genotype

McConkie-Rosell et al. (2019) show that genomic sequencing (whole-exome and whole-genome sequencing) has yielded elusive diagnoses. In fact, around 40% of molecular diagnosis is wrong (Baynam et al. 2016; McConkie-Rosell et al. 2019). Genes have been considered as the main cause of anomalous traits of phenotype, but this causality phenomenon is conditioned by different factors. First, by the existence of genetic segregate variants, by multiple alleles of genes who give a similar phenotype, and by the existence of a wild-type gene that rescues the phenotype (Gal et al. 2017). Then, the causality of genotype in a biomedical context is probabilistic and rarely deterministic (Gal et al. 2017).

Noble (2008) indicated that the original notion of a gene was closely linked to the cause of phenotype characteristics. Then, genotype was the cause of phenotype but the causality has become more complex. Nowadays, genes are identified with a particular sequence of DNA which could generate a phenotype modulated by the environment, behaviour and society. The great problem is that genetics code is uninterpretable outside the cellular context in which they can be read and so generate functionality (Noble, 2008). Then, causality as a *cause* → *effect* → *treatment* lineal process is much more complicated.

* We prefer to use the term *undiagnosed rare disease (URD) instead of syndromes without name (SWAN)* because the first one is a broader denomination and includes not-syndromic illness.

Rare diseases are a set of pathologies with a similar typology often chronically debilitating, incurable, or in some cases, life-threatening (Anderson et al. 2013; Germeni et al. 2018) which in some cases has a syndromic characteristic or a complex pathology with physical, intellectual or neurological disabilities associated (Anderson et al. 2013).

One of the most important approximations to knowledge of rare diseases, and obviously to undiagnosed rare diseases, is the genetical approach. Wright et al. (2018) exposed that in the most of history, clinical genetics was based on two types of tests: highly focused high-resolution molecular single-gene tests and low-resolution genome-wide cytogenetic tests. In the first one (single-gene molecular tests), a particular gene is selected genotyping according to the diagnostician medical act, that is the clinical presentation of patients. These types of tests are suited in order to diagnose rare diseases caused by one or few genes. Wright et al. (2018), by contrasts, indicate that the low-resolution whole-genome approach let to diagnose common trisomies and segmental aneuploidy. Both anomalies in karyotype could help to diagnose if these variances of genotype appear together with developmental disorders that are caused by rare recurrent or unique large imbalances of chromosomal material. The sensitivity of this technic is low compared with that of new technics. In fact, only ~10% of patients with a rare pediatric disease can be diagnosed using these approaches (Sagoo et al. 2009).

In the recent years, tests based on next-generation sequencing have been generalised. This clinical diagnostic technic has the virtue to sequence different types of regions of genetic material. This technique let to the discovery of many novel rare-disease-causing genes (Boycott et al. 2013) and it has two variations: 1) sequencing whole single genes, panels of genes or sequencing all exons ~4,000 genes and 2) sequencing all ~20,000 protein-coding genes by WES and entire genomes by WGS are essentially non-targeted tests (Wright et al. 2018). Wright et al. (2018) suggest that the testes in parallel generate more data and increase the sensitivity, but its specificity decreases, and both the logistical and ethical challenges increase.

The previous exposition of genetical diagnosis let us to affirm that this one is a biosemiotics phenomenon. The reason of this assertion is based on the concept of code as a set of rules with meaning character (Barbieri 2015; 2019). Now, a code can be a mental entity if the code functions among different mental objects or it can be an organic entity if the code operates among organic molecules (Barbieri 2003; 2015; 2018). Also, according to Barbieri (2008; 2015; 2019), the genetic information could be correlated semiotically with the *metaphor of mechanism*. The metaphor of the mechanism is reminiscent of the Renaissance and the importance that artifacts played in industrialisation. But Barbieri uses this metaphor from a more complex hermeneutic. In fact, this idea presents some virtues based on the next facts: mechanism is not reductionism, not determinism, not physicalism, and mechanism is made of models (Barbieri 2015). But, as Barbieri says, the idea of genetic as a mechanism starts in the thought of Descartes who affirms that the body of human being is a machine. For this reason, the problem of the *metaphor of mechanism* is that this idea does not allow the relation of the variation of genes with the natural evolution or with the plasticity of nature.

Meloni (2019) shows interestingly that actually the gene is not experimented and represented as an informational medium. The variation of the genome and the epigenome let us comprehend these biological structures as metaphors of plasticity in which an imprinting and marking mechanism operates. But the metaphor of plasticity is neither a modernistic plasticity, related directly with the mechanistic Cartesian, nor a postmodernist celebration of potentialities (Meloni, 2019). Dobzhansky and Wallace (1954) already spoke years ago about the idea of genetic plasticity in order to explain the deleterious mutants in the evolutionary

phenomenon. According to these perspectives, it could be reasonable to understand gene mechanisms of evolution as a set of evolutionary plasticity.

It is possible to understand the gene as a biological mechanism of informational transmission (according to the classical biological idea) and also as a mechanism of imprinting and marking. We consider that the analyses of Barbieri and Meloni show complementary descriptions particularly useful to biosemiotics research. Both ones converge in a semiotic metaphor of gene as a plasticity mechanism in which the information and rules of understanding are transmitted. In this sense, Barbieri (2008) has advocated by the terminology of *code biology* to comprehend the semiotic reality of biology. Barbieri (2019) affirms that a code is a set of rules that let *link* the *sign* and the *meaning*. The ontology of this interaction centers its semiotic relevance in the determinate set of possibilities of informational combination or translation. These determinations let to comprehend the alteration of the genetic code (information or rules) as pathology.

Romanini (2014) – in accordance with Peirce – exposes that the semiotic relationship can be analysed based on the triadic relation among objects, signs and interpretants. This triad is complemented by the code model of semiosis (Barbieri 2015) in which it is affirmed that a semiotic system is a set of *signs*, *meanings* and *codes* that are produced by agents with the same *codemarkers*. This semiotic system (in this context) can be denominated as genotypical biosemiotics and it let us to interpret the genetical diagnosis in a double sense: into the biomedical code or into the biosocial code. In both genotypical-biosemiotic processes, genes are the fundamental signs which express possibilities of meanings according to one hermeneutics of normality or other of abnormality. The significances of these signs (genes) operate in a socioecological and in a biomedical context differently. In both contexts, genes are semiotics signs with a *normative* character or a character of *legisign*, according to the terminology of C. S. Peirce (1931–1958). But in a socioecological context, the *legisign* will be *symbolic*. In turn, in the biomedical context, genes operate as *iconic* and *rhematic legisigns*. For physicians, a genotype is a diagram of the human biology, a *decodemarker* of a biomedical reality which later will be treated. For families, a genotype is also a *decodemarker*, but in this case this sign decodes a socioecological reality and a set of futures possibilities.

Semiotic of Phenotype

Phenotype encompasses the morphological aspects of organisms which are determined by their genotype and modulated by their environment and society. This interrelation between internal and external elements requires a code that makes sense of this relationship. Phenotype, in summary, is a set of codes with information about morphological (visual) characters and it is caused usually by the Mendelian inheritance. Mendelian genes, thus, generate Mendelian phenotypes which are quite unknown (Chong et al. 2015). Then, the determination of phenotypic variation (and thus the phenotypic diversity) is a great objective to the scientific community. For that, nowadays whole-exome sequencing (WES) and whole-genome sequencing (WGS) data are crucial to this objective. Also a gap in our knowledge exists in order to comprehend the biomedical definition of normal versus abnormal.

The problems of elusive dates and clinical overlap in genotype analyses undoubtedly happen. There are studies which have detected clinical overlaps in patients co-diagnosed with a Mendelian disease and complex disease (Bastarache et al. 2018). Also, the possibility of overlap between immunodeficiency genes and complex inflammatory disease has been detected (Fodil et al. 2016). For that, some authors research the phenotype of undiagnosed rare

diseases as a possible solution to these problems. They have focused in phenotype to detect possible descriptors of the genetic reality (Bastarache et al. 2018). However, philosophy has shown us that form is one of the elements to be taken into account and, therefore, we cannot forget the other aspects that make up the human being. This is not to say that phenotyping studies are not important and do not offer solutions. For this reason, the phenotypical effects in patients and families with characteristic and often severe phenotypes were studied at first (Bastarache et al. 2018).

Hennekam and Biesecker (2012) exposed that next generation sequencing (NGS) is a new paradigm of biomedicine because it allows creation of phenotypical categories (based on genetic knowledge) to determinate possible effects of genetic abnormality or identify mutations causing disorders. NGS let to construct sets of phenotypical groups of persons with similar phenotypic characteristics. This epistemic phenomenon, among other things, generates biomedical initiatives to create a phenotypic ontology which let to do the comparison of patients (Hennekam, Biesecker 2012). The base of this genotypic-phenotypic process is increasing the possibilities to contribute to a faster and more accurate molecular diagnosis.

For these reasons, some institutions related to rare diseases and undiagnosed diseases create communication networks among parents and physicians in order to improve the genetic counselling and the empowerment of families (Baynam et al. 2016; McConkie-Rosell et al. 2019; Taruscio et al. 2015; Tifft, Adams 2014). Tifft and Adams's (2014) exposition that in the NIH program, only 7,000 genes were associated with any disease among 23,000 genes suggests that many genetic disorders remain unknown. This process modifies the typical direction of the biological code, which considers that information starts in the genotype, modifies the phenotype and finally conditions the sociotype. In turn, as in URD the code genotype-phenotype-sociotype is ignored, it was necessary to subvert the transit of signs in biosemiosis and star in sociotype in order to focus the searching of information. We will talk about the sociotype in the next section.

Going back to the phenotype, it is relevant to show that this code has two ways: a biomedical way and a biosocial way. In the first one, the phenotypic code operates as a Peircean *legisign*. Besides, within the *legisign* and in the context of the attempt to contribute to diagnosis it could be determined as a *dicent indexical* sign. Also, it could have the function of a *symbolic sign* in the same biomedical context. That is to say, the phenotype operates as a normative code – a *legisignical code* (integrating the terminology of Peirce and Barbieri) with possibilities to indicate – as the frame to search for the genetic problem, and also as the designation of biomedical problems. In fact, phenotyping has been defined as the analysis of biomedical phenotypic (observed and described) dis-normalities (Gainotti et al. 2018).

But the phenotype also operates within biosocial codes. The phenotype could be understood as manifestation of a biological problem and this one could origin a phenomenon of social exclusion. In fact, the social exclusion has evolved in our less developed ancestors as a means of responding to danger from a deterministic consideration of the world (Allman 2013). Rare disease without diagnosis is a set of sick people affected by an indeterminated biomedical semiosis but affected by a biosocial semiosis. The last semiosis could be positive (understanding positively by the social context) or negative (understanding negatively). In this sense, people with psychiatric and morphological phenotypical manifestations of diseases are affected by social exclusion (Nading et al. 2009; Anderson et al. 2013).

The social biosemiotics of the phenotypic code related to URD can be positive or negative depending on the evaluative understanding of the phenotype. In positive social biosemiotics,

the phenotype is interpreted as an element that defines the person in society. Thus, if a subject is short, tall, has skin blemishes, or presents some differentiating element, then he or she may be excluded. In this sense, the body is a symbolic expression of illness and of the possible affectation of others. In contrast, in the first case, in which the code is negative, the phenotypic manifestation is not so symbolically relevant. In this case, the phenotypic code of understanding operates as dichotomous and symbolic signs that facilitate the incorporation of affected persons. That is, the phenotype will be an encoder of a positive socio-emotional understanding, and will facilitate understanding and help to the affected persons.

But the URD configure an unusual social reality in which there is no possible conventional social semiotics. Affected individuals may have difficulty being conceptualised in social normativity and institutionalised or at least generalised semiotic codes. This is because, as we have seen, there is a kind of 'circle of ignorance' around them. People know that they or their family members are affected by some entity that makes them ill, but they cannot describe or name what it is. They are people in permanent search of something that allows them to name themselves in front of others. They live in a social context of uncertainty where their social normativity is ignorance.

Then, the phenotype operates as a *codemaker* of the semiotic of reject. This semiotics of rejection is based on the hermeneutics of exclusion or separation. Then, people affected by URD are not understood and they are excluded from the social structure. This phenomenon of exclusion is based on the process of social incapability (Bynner 2000) due to diagnostic odyssey, the inexistence of drugs (Kole, Faurisson 2009; Taruscio et al. 2015) and the impossibility to construct a social biosemiotics of their illness.

For that social process, families affected by URD feel necessity to have an identity in order to have possibilities to construct a code of their identity. In that case, people affected tend to claim a genetic identity. In this sense, it is appropriate to show that genomic sequencing configures new *technoscientific identities* (Clarke et al. 2010; Sulik 2011) different to the social identity. In this regard, it is very necessary to consider that the organic meaning is *objective-but-not-measurable* entity (Barbieri 2008b). Then, the social identity meaning is wider than the genetic code. Molecular tools of searching for mutations allow the identification of genes that cause pathologies. Once the causal gene has been identified, it is easier to determine the effect, which may be a variant of an existing disease or a new pathology. However, there is a risk that the technoscientific identity may become a defining element of the person containing the mutation. In other words, the presence of a mutation in a person's genome does not imply that the phenotypic and sociotypic manifestation of a person is determined. The problem is that people find it difficult to handle non-deterministic information; hence it is easier to think that if I have the mutation, I will have the disease or it will manifest itself in the most aggressive way.

Finally, it can be affirmed that phenotype operates as an intermediate code among the genotype and the sociotype. But code up (phenotype-sociotype: *ps code*) and down (genotype-phenotype: *gp code*) are different. In the last code (*gp code*), families affected claim open the broken code in order to have a *biosemiotic genotypic identity*. In the other code, named *ps code*, it actually seems that there are no possibilities to construct a social identity of people affected by URD. In summary, families cannot give meaning to the sociotype because there is a breaking off in the chain of the biological code. Individuals and families affected by URD have broken some of the most frequent codes of the genotype-phenotype-sociotype triad. Evidently, we could consider that these codes are not broken, they have simply been modified.

However, the fact that there is an alteration in the conventional mechanisms of information transmission means that there is a certain rupture in the bio-socio-semiotic phenomenon. Then we need to generate other mechanism to generate the biosocial meaning about their unknowledge condition.

BIOSEMIOTICS OF SOCIOTYPE

The sociotype is a conceptual construct, specifically a summary ecological construct, which implies three epistemic domains: individual, relationships and context (Berry et al. 2017; Peng et al. 2018). This concept adds to intra- and inter-personal inputs an ecological layer. Thus, the sociotype is concerned with the environmental influences on phenotypic responses (Peng et al. 2018). Now, we consider that according to the biosemiotics research, the human sociotype is a more complex concept than a mere consideration of a phenotypical response. The sociotype is a much more complex logical-type than the previous ones. The fact that it is based on relationships and interactions introduces a great element of variability. However, the determination of the characteristics of a sociotype in comparison with a non-existent and ideal normotype, allows us to study and understand the limitations or possibilities that a given sociotype may have.

The sociotype has a great virtue in terms of its operability, but it downplays the importance of external factors. That is, it focuses its interest on the social behaviour of the logical type to be described, but leaves aside the environment. In other words, the concept of the socio-type does not describe the interactions carried out by individuals in the environment, which, of course, condition the behaviour of the members of the socio-type in question. Now, if we broaden the concept of the sociotype and consider that the phenomenon of *codepoiesis* (Barbieri 2015) is essential in its structure, it will be easier for us to establish relationships of an ecological nature in its determination. In this sense, Laland et al. (2016) exposed – from a biological perspective – that organisms modify their environment in a non-random way and these alterations also affect the development of populations. This idea of Laland et al. (2016) helps us to conceive a sociotype framed in an ecological environment or niche, which also affects it.

From a social perspective, we could ask ourselves whether the processes of social exclusion are part of the niche of the sociotype of people affected by URD. The rupture of the social code that we have previously discussed reduces the possibility of sociality for those affected and their families. From this perspective, it is essential to establish alternative social mechanisms for society to understand this reality. In addition, it is essential that those affected are not too limited in their ability to interact with others and with their own environment. To this end, it is essential to consider the development of inclusive social environments. This potential phenomenon of social inclusion would enhance the possibility that the socio-type of people with rare diseases may have greater agency in the social structure. From a more semiotic perspective, one could say that inclusion would allow social scaffolding in this group that we are talking about.

URD has biological, intrapersonal and interpersonal factors whose part is unknown. Thus, the persons concerned are subject to an unidentified code and the *codepoiesis* of this phenomenon moves in an unstructured social locus. For this reason, biological factors operate in cells, tissues and organisms, but the social code has not yet been established. Social and ecological environments generate codes that are socially interpreted. For this reason, it is essential to maintain or encourage the generation (*poiesis*) of codes that increase the behavioural diversity of social groups. RD are part of the dis-normality of what Archer (2012)

named the social structure or the social morphology. Code of normality is configured as a biosocial factor of normal *codepoiesis*, a *legisign* of determination of the normal in human society. URD, in turn, is a broken-normality in which there is no object to design and then sociosemiotics is broken. Now, biosemiotics continues to operate in a socially invisible way from the genotype. The interpersonal frame continues the unknown reality and the *codepoiesis* unstructured. Therefore, it is important for society to pay attention to biosocial conditioning factors in order to increase the possibility of generating alternative socio-semiotics codes. This idea is close to the position taken by Heiskala in his semiotic proposal. According to this author, and starting from a neostructuralist approach, there is an 'immediate interpreter' and an 'immediate structure'. The immediate interpretant is defined 'as the range of possible interpretants of a given sign at a given time' (Heiskala 2003: 217). In turn, 'immediate structure' can be defined as the sum of the possible interpreters of a sign at a given time (Heiskala 2003: 218f). Indeed, Heiskala (2003) argued that society is a stratified totality of articulations of meaning. In other words, it is important to ensure that the social system develops different semiotic codes, for different socio-types, without this implying that exclusion phenomena occur and, therefore, that social scaffolding is allowed. To this end, it is essential that people at greater risk of exclusion and with more limited semiosis capacities find their possibilities of code generation and their socio-semiotic possibilities facilitated.

In short, URD shapes a certain socio-type and affects the relationship of individuals with their social environment. In fact, individuals often modify their behaviour in response to the experience in their society (Saltz et al. 2016). The main problem is that individuals with URD may have their fitness diminished by a process of social competition for semiotic resources. This competition plays against URD because there is a different capacity to generate semiosis and new codes. In this sense, people affected by URD have no possibility of *codepoiesis* because their basal semiotics is broken (as we have already indicated) and is also poorly controlled in the absence of social mechanisms that favour the agency of this social group. Then, this inability of *codepoiesis* seems to coerce affected persons to try to have a biosocial control mediated by biomedical information. This control is centered on the mechanisms of technoscientific identity (Sulik 2011).

CONCLUSIONS AND FUTURE DIRECTIONS ABOUT BIOSEMIOTICS OF UNDIAGNOSED RARE DISEASES

We have been studying how certain basic semiotic elements are produced in people affected by URD. Our premise was that subjects are conditioned by their biology (since it establishes, after all, their pathology). These conditioning factors end up affecting the social sphere, sooner or later.

In this paper, it has been showed that URD could be considered as a sociotype with a set of conditioning factors related to interrelation between its biosemiosis and its sociosemiosis. These boundaries are crucial to comprehend persons affected by URD and interactions of this collective with social niche. However, the semiotic processes and the social factors that limit them are still not fully understood. Then, it is necessary to increase the knowledge in these ways. We have seen that people affected by URD have limited capacity for social semiosis and code generation (*codepoiesis*). This is due to the fact that the conditioning factors of their condition and the biological determinants that identify their disease are not yet known. These factors are configured as limiting elements in their socialisation. It is therefore essential for

social systems to generate mechanisms to enable these people to overcome the socio-semiotic limitations we have mentioned.

Finally, we would like to conclude this investigation by exposing some highlights about questions generated in this emerging theme:

- How does social niche generate determinants to people affected by URD?
- What biosemiotics mechanisms operate in this sociotype?
- How do social and biological semiotics operate in social niche?
- What challenges can philosophy take on in studies on the reality that affects this socio-type?

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Semiotinis ir hermeneutinis požiūris į nediagnozuotas retas ligas

Santrauka

Sociotipas yra sąvoka, leidžianti išsamiau suprasti nediagnozuotų retų ligų (NRL) biosociologiją. Sociotipas susijęs su genotipu ir fenotipu ir yra individualaus gyvenimo pasaulio išraiška visuomenėje. Straipsnyje pateikiama semiotinė ir hermeneutinė paskelbtų atrinktų straipsnių apie NRL analizė. Laikomasi perspektyvos, pateiktos Marcello Barbieri'o ir Charleso Sanderso Peirce'o darbuose. Buvo atrinkti sociologinio turinio straipsniai, o biomedicininio turinio – atmesti. Semiotikos analizė buvo suskirstyta į genotipinę, fenotipinę ir sociotipinę bei susieta su hermeneutine perspektyva. Siekta atskleisti NRL semiotikos elementų pagrindą. Bendra išvada tokia – NRL yra tam tikras socialinis tipas, turintis nustatytų socialinių savybių rinkinį. Šis straipsnis padeda tyrinėti biosemiotinę ir hermeneutinę NRL perspektyvą.

Raktažodžiai: retos ligos, nediagnozuotos ligos, hermeneutika, sociotipas, Peirce'as