HETEROGLOSSIA (13)
Studia kulturoznawczo-filologiczne
www.wsg.byd.pl
Wydawnictwo Uczelniane Wyższej Szkoły Gospodarki, 2022

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DECODING THE VIRUS: BLENDING PATTERNS BEHIND THE NAME "SARS-CoV-2"

INTRODUCTION

The newly emerged, fast replicating coronavirus, initially referred to as "novel coronavirus" (2019-nCoV), received the name SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2) on the basis of the genetic affinity it shows towards the founding virus of the whole species, SARS-CoV. Therefore, the inclusion of the SARS part in the name of the virus did not result from the cause-effect relationship established between the newly emerged coronavirus and clinical manifestations of the SARS syndrome but from its genetic affinity with the SARS-CoV virus[1]. The fundamental difference between SARS-CoV and SARS-CoV-2 lies in replication efficiency[2]. This article attempts to reconstruct basic conceptual links between the

[1] Coronaviridae Study Group of the International Committee on Taxonomy of Viruses, *The species Severe acute respiratory syndrome-related coronavirus: classifying 2019-nCoV and naming it SARS-CoV-2,* "Nat Microbiol.", [online], 2020, 5(4), p. 536–544, retrieved October 12, 2021, from https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7095448/. Yuntao W. et al., *SARS-CoV-2 is an appropriate name for the new coronavirus*, "The Lancet", [online], 2020, 395, p. 949–950, retrieved November 7, 2021, from https://www.thelancet.com/journals/lancet/article/PIIS0140-6736(20)30557-2/fulltext. Simmonds, P. et al., Consensus statement: virus taxonomy in the age of metagenomics, "Nat Rev Microbiol.", 2017, 15, p. 161–68. Zheng J., *SARS-CoV-2: an Emerging Coronavirus that Causes a Global Threat*, "Int J Biol Sci.", [online], 2020, 16(10), p. 1678–1685, retrieved November 7, 2021, from https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7098030/. Gorbalenya, A.E. et al., *Severe acute respiratory syndrome-related coronavirus: The species and its viruses – a statement of the Coronavirus Study Group*, Preprint at "bioRxiv", [online], 2020, retrieved November 5, 2021, from https://www.biorxiv.org/content/10.1101/2020.02.07.937862v1.

[2] Wanbo T. et al., *Characterization of the receptor-binding domain (RBD) of 2019 novel coronavirus: implication for development of RBD protein as a viral attachment inhibitor and vaccine*, "Cellular & Molecular Immunology", [online], 2020, 17, p. 613–620, retrieved November 7, 2021, from https://www.nature.com/articles/s41423-020-0400-4#:~:text=The%20S%20protein%20mediates%20viral,membranes%20through%20the%20S2%20subunit.&text=SARS%2DCoV%20and%20

name SARS-CoV and the frame of fast viral replication in terms of the Conceptual Blending Theory.

This paper is based on preliminary research results presented in the article *Der Name 'SARS-CoV-2' als Integrationsnetzwerk. Ein Rekonstruktionsversuch* (*The Name 'SARS-CoV-2' as Conceptual Integration Network. A Reconstruction*), which has been accepted for publication in the series *Text-Satz-Wort. Studien zur germanistischen Linguistik* by the University of Rzeszów, Poland.

ORIGIN OF THE NAME "SARS-CoV-2"

As mentioned above, the newly emerged coronavirus, initially referred to as "novel coronavirus" (2019-nCoV), received the name SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2) on the basis of the genetic affinity it shows towards the founding virus of the whole species, SARS-CoV, which in turn caused a serious outbreak of disease in the years 2002-2003. The name was coined by the Coronavirus Study Group (CSG) of the International Committee on Taxonomy of Viruses (ICTV), specifically dedicated to the enveloped, single-stranded RNA coronaviruses infecting vertebrates, and first mentioned in their official statement published on February 11, 2020 in the preprint journal for biology bioRxiv.

As it comes to the genetic relationship between the newly emerged coronavirus and primary viral isolates from the family *Coronaviridae*, J. Zheng[3] states as follows:

> When compared with SARS-CoV and MERS-CoV, the nucleotide sequences of SARS--CoV-2 showed a higher homology with that of SARS-CoV while was relatively poor with that of MERS-CoV [19]. Despite some of the six major OFRs of SARS-CoV-2 genes share less than 80% identity in nucleotide acids to SARS-CoV, the seven conserved replicase domains in ORF1ab has 94.6% sequence identity in amino acids between SARS-CoV-2 and SARS-CoV [14], suggesting that these two viruses might belong to the same species.

From the perspective of radical structuralist semantics it seems that the form of the first expression constituting the name SARS-CoV-2 implies a close and direct link between the name as such and the severe acute respiratory syndrome. Nevertheless, the CSG definitely indicates that the use of "SARS" is not directly derived from the SARS disease but from the SARS-CoV virus which was found in humans in 2002. Therefore, the inclusion of the "SARS" part in the name of the virus did not result from the cause-effect relationship established between the newly emerged coronavirus and clinical manifestations of the SARS syndrome but from its genetic affinity

MERS%2DCoV%20RBDs%20recognize%20different%20receptors. V'kovski, P. et al., *Coronavirus biology and replication: implications for SARS-CoV-2*, "Nat Rev Microbiol.", [online], 2021, 19, p. 155–170, retrieved October 13, 2021, from https://www.nature.com/articles/s41579-020-00468-6.

[3] Zheng J., op. cit.

with the SARS-CoV virus[4]. This, in turn, follows from the formally approved taxonomic practice for the SARS species. According to the standardized formats for classifying viruses established by ICTV[5], "a newly emerged virus is normally assigned to a species based on phylogeny and taxonomy"[6]. Under these rules, the primarily assumed novelty of the virus emerged in 2019 was questioned and it eventually was recognized as a sister virus to the virus isolate essential for the whole species, SARS-CoV. Therefore, it must be concluded that "The use of SARS for viruses in this species mainly refers to their taxonomic relationship to the founding virus of this species, SARS-CoV. In other words, viruses in this species can be named SARS regardless of whether or not they cause SARS-like diseases"[7]. Relying on established taxonomy practice and phylogenetic profile of the virus, "the CSG recognizes this virus as forming a sister clade to the prototype human and bat severe acute respiratory syndrome coronaviruses (SARS-CoVs) of the species *Severe acute respiratory syndrome-related coronavirus*, and designates it as SARS-CoV-2"[8].

As has been shown above, the inclusion of the "SARS" part in the name of the virus does not allow to establish any conceptual link between the SARS disease and the severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2). This results from the fact that the "SARS" component does not refer to the SARS illness as its' expressive form might suggest, but it reflects the genetic affinity between the newly emerged virus and the primary viral isolate of the species, SARS-CoV.

BASIC ASSUMPTIONS OF CONCEPTUAL INTEGRATION

Formal complexity of compound expressions, such as SARS-CoV-2, results from the interplay of multidimensional conceptual operations that lead to their actual meaning. Considering names of scientific notions, the firmly anchored juxtaposition of two or more compound's formal elements is based on projection of selected conceptual components derived from different frames into the emerging conceptual blend[9]. Particular interrelations connecting these conceptual elements, manifesting themselves in specific situational and contextual conditions, lead to the emergence of a novel meaning, whose scope reaches far beyond the semantic value directly de-

[4] Coronaviridae Study Group of the International Committee on Taxonomy of Viruses, op. cit. Yuntao W. et al., op. cit. Simmonds, P. et al., op. cit. Zheng J., op. cit.

[5] Coronaviridae Study Group of the International Committee on Taxonomy of Viruses, op. cit. Yuntao W. et al., op. cit.

[6] Yuntao W. et al., op. cit.

[7] Tamże.

[8] Coronaviridae Study Group of the International Committee on Taxonomy of Viruses, op. cit.

[9] Fauconnier G., Turner M., *Jak myślimy. Mieszaniny pojęciowe i ukryta złożoność umysłu*, Warszawa, Biblioteka Kwartalnika Kronos, 2019.

rivable from any of the mental elements or their sum. The conceptual background of the compound's complexity is, therefore, implicitly reflected in its' formal shape at the linguistic level.

In order to capture the essence of the phenomena depicted above and correlations hidden behind them, it seems justified to refer to the Conceptual Blending Theory (henceforth: CBT) founded jointly by Gilles Fauconnier and Mark Turner[10] and developed by other linguists[11]. CBT highlights the emergent character of the formation of meaning. Thus, it seems to be an all the more appropriate theoretical framework for the analysis of formally complex neosemantic expressions such as SARS-CoV-2. The theory is based upon the concept of mental spaces, which have been defined as "small conceptual packets construed as we think and talk, for local understanding and action"[12].

In the ensuing analysis a slightly modified six-space-model will be proposed, anchored not only in the original four-space-integration network envisaged by G. Fauconnier and M. Turner but also in the contextual approach to conceptual blending, developed by P.A. Brandt[13] and L. Brandt[14] and T. Oakley and S. Coulson[15] as well as in the anthropocentric paradigm of human (language) knowledge as proposed by S. Grucza[16] and V. Yngve[17]. The revised approach shall consider the specificity of LSP and (specialized) human knowledge along with ontological conditions of human mental processes in general and conceptual integration in particular.

As opposed to the model presented by P.A. Brandt and L. Brandt, T. Oakley and S. Coulson and R. Augustyn and E. Prażmo[18], the entire conceptual integration process is physically initiated not in the Discourse Space but in the Relevance Space. All of the authors mentioned above locate discourse participants in the Discourse Space, whereas (specialised) knowledge, purpose, situational relevance should be located in

[10] Ibid.

[11] Brandt, P. A., *Mental spaces and cognitive semantics: a critical comment*, "Journal of Pragmatics", 2005, 37, p. 1578–1594. Brandt, L., *The Communicative Mind: A Linguistic Exploration of Conceptual Integration and Meaning Construction*, Newcastle upon Tyne, Cambridge Scholars Publishing, 2013. Oakley, T., Coulson, S., *Connecting the dots: Mental spaces and metaphoric language in discourse*, [In:] T. Oakley, A. Hougaard (Eds.), *Mental Spaces in Discourse and Interaction*, Amsterdam/Philadelphia, John Benjamins, 2008, p. 27–50.

[12] Fauconnier G., Turner, M., *The Way We Think: Conceptual Blending and the Mind's Hidden Complexities*, New York, Basic Books, 2002.

[13] Brandt, P.A., op. cit.

[14] Brandt L., op. cit.

[15] Oakley T., Coulson S., op. cit.

[16] Grucza S., *Lingwistyka języków specjalistycznych*, Warszawa, Euro-Edukacja, 2008.

[17] Yngve V. H., *Linguistics as a Science*, "The Library Quarterly: Information, Community, Policy", 1986, 58(4), p. 400–402.

[18] Augustyn R., Prażmo E., *The Spread of 'Chinese Virus' in the Internet Discourse: A Cognitive Semantic Analysis*, "GEMA Online Journal of Language Studies", [online], 2020, 20(4), p. 209–227, retrieved September 23, 2021, from https://ejournal.ukm.my/gema/article/view/41755/11433.

the Relevance Space. It should, however, be noted that in the light of the ontology of human knowledge and languages[19] each type of human knowledge (be it declarative, procedural or language knowledge etc.) is an intrinsic attribute of specific individuals' brains. More specifically, the processes of synaptic transmission involved in conceptual blending at biological level begin in brains of particular individuals, not in an unspecified space between them. In the light of the anthropocentric linguistics, discourse is defined as making use of texts by particular participants of a particular communicative interaction in order to attain a specific (communicative) goal[20]. To perform discourse acts, individuals acquire specific abilities referred to as discoursive competence. I, therefore, propose to consider the latter as a capacity of each individual to put a set of specific goal-directed constraints on each act of using (specialised) texts. Consequently, acts of creating texts and acts of using them in a discoursively determined way should be conceptually separated. What is more, discoursive competence internalized by individuals must be conceptually distinguished from specific discourse acts. Furthermore, (specialized) language as well as communicative competence seems to be a component of the (specialised) discoursive competence[21]. Hence, I suggest to place (specialised) discourse participants, their specialised (background, language etc.) knowledge and their specialised discoursive competence in the Relevance Space, whereas the Discourse Space should comprise specific discourse acts performed by discourse participants. This kind of conceptual differentiation between the Discourse Space and the Relevance Space seems necessary, as potential relevance of inferences emerging in the blend must be examined by particular discourse participants before the inferences are fed back (conceptual integration is a recursive process) to the subject of discourse.

Two Input Spaces (henceforth: Inputs) reflect salient elements of two distinct events, things or phenomena. In conceptual integration, respective counterparts in both Inputs are interlinked on the basis of cross-space mapping and selectively projected into a new Blended Space. Mechanisms of cross-space mapping and selective projection connect the topologies of the Inputs. Such topological interblend appears in the blend and generates emerging structure.

Roles or other elements shared by the Inputs constitute a more schematic frame or a Generic Space. The Generic Space contains characteristics that Inputs have in common. It connects the Inputs, giving an appropriate structural foundation for the blend. It should be underlined that "generic spaces (…) are anchored in existing conceptual structure"[22], providing a strong conceptual link to the actual knowledge of the conceptualizer and a template for future blends.

[19] Grucza S., op. cit. Yngve V.H., op. cit.

[20] Grucza S., op. cit. p. 132.

[21] Ibid.

[22] Fauconnier G., Turner M., *Conceptual Blending, Form and Meaning*, "Sémiotique cognitive – Cognitive Semiotics", [online], 2003, 19, p. 57–86, retrieved July 12, 2021, from https://pdfs.semanticscholar.org/8e66/909dca584a45bb38dc25ce86701947f135e4.pdf.

The spaces mentioned above are linked with the Blended Space (henceforth: the blend), where selected elements from the Inputs are integrated into a novel structure and mentally simulated in order to experiment with various framings[23]. The blend demands particular attention, as it generates meaning aspects, which are non-derivable from the meaning of respective elements inherited from the Inputs[24] In general, the blend does not 'contain' any emergent meaning. It comprises dynamic online simulation processes, which lead to the emergence of a relatively fixed meaning in the Elaboration Space. The latter draws on a mentally available blend with a proper, firmly fixed frame. This frame activates the blend's novel meaning only in relation to contextual demands specified in the Relevance Space[25], which seems particularly relevant to the specificity of specialised discourse.

The topology of each mental space in a given conceptual integration network is determined by a set of conceptual relationships called vital relations, such as cause-effect, identity, change, part-whole, analogy, uniqueness, property etc.[26]. Inter-spatial relations of this type connect corresponding elements form the Inputs, providing a foundation for selective projection into the blend. The conceptual integration process allows us to achieve compressions of vital relations, which determine the creativity of the blend and the ultimate structure of the Elaboration Space. Compression patterns typical for a given blend allow us to capture its' character and the way it functions in different contextual conditions.

According to this revised CBT model, the recursive process of blending allows the conceptualizer to refer the inferences generated in the blend to the subject of the current specialised discourse. In accordance with the anthropocentric paradigm, such an act of reference can be performed only in the Relevance Space – in relation to the specialised knowledge of discourse participants - subsequently reaching the Discourse Space. Selected practical aspects of the revised CBT model will be outlined in the ensuing analytical part.

CORPUS DATA AND SEMANTIC COGNITIVE ANALYSIS OF THE NAME "SARS-CoV-2"

Below, a semantic cognitive model will be presented, which reflects the interplay of selected vital relations and other significant elements of the relevant input spaces involved into the emergence of the compound "SARS-CoV-2" as a novel blend (or neo-concept). The model is based on a semantic cognitive analysis of selected excerpts taken from papers on phenotypic characteristics of SARS-CoV and SARS-CoV-2 published in Nature magazine.

[23] Brandt P.A., op. cit. Brandt L., op. cit.

[24] Fauconnier G., Turner M., *The Way We Think…*

[25] Augustyn R., Prażmo E., op. cit., p. 214.

[26] Fauconnier G., Turner M., *Jak myślimy …*, p. 140–151.

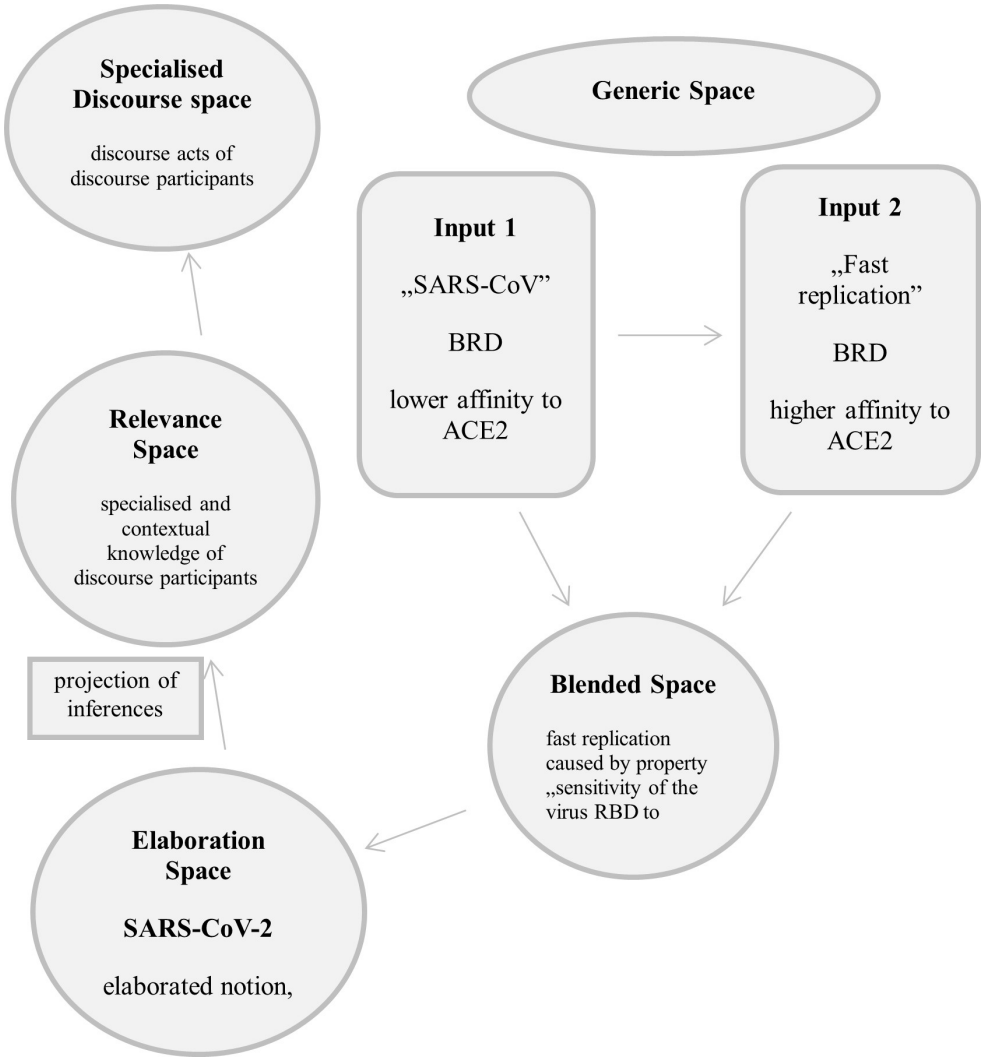

Fig. 1. CBT model of the compound "SARS-CoV-2". Source: author's own elaboration based on T. Oakley and S. Coulson[27]

As mentioned above, the Specialised Discourse Space includes specialised discourse acts performed by discourse participants, leading to the emergence of the name "SARS-CoV-2" and the underlying conceptual blend. Discourse participants (especially experts, e.g. virologists, doctors, terminologists), their specialised knowledge, linguistic and background knowledge, contextual and situational relevance, considered as intrinsic properties of their minds, are schematically captured as the Relevance Space.

[27] Oakley T., Coulson S., op. cit.

The frame containing elements shared by the Inputs – the Generic Space – pertains to already existing knowledge concerning the family of Coronaviridae. It should be underlined that the taxonomical level of family was considered relevant because salient properties of the spike (S) protein common to the "SARS-CoV" Input and the "Fast replication" Input manifest themselves at this level[28]. The common protein properties are the actual conceptual elements contained in both Inputs. They provide a link between the Inputs, constituting a structural foundation for the blend called "SARS-CoV-2" as will be shown below. Moreover, the piece of knowledge represented by the Generic Space is a basic point of reference in "running" the blend i.e. trying out different framing possibilities in the Blended Space.

The actual interplay of knowledge elements, which determine the emergence of the name and the way it is used in specialised discourse, can be analyzed in terms of relations linking the Inputs and the blend. The frame of Input 1, called "SARS-CoV"[29], contains semantic elements concerning exclusively the SARS-CoV virus. It must be noted that "SARS-CoV" is a blend deriving from a combination of two inputs: "SARS" and "coronavirus". This indicates that the compound "SARS-CoV-2" is a multi-blend resulting from multi-scope blending processes[30]. Input 2 is framed by the aspect of efficient viral replication, which distinguishes it from Input 1.

Vital relations and fundamental compression patterns identified in the blend result from basic similarities and differences between the frames of the Inputs, which fundamentally manifest themselves in two domains: within structural and functional convergence between the SARS-CoV-2 and SARS-CoV RBD (receptor-binding domain in the S1 subunit of the spike (S) protein) and within the binding affinity for the ACE2 receptor of the S protein[31].

(1) "The affinity of the SARS-CoV-2 RBD to ACE2 has been shown to be similar or stronger than that of the SARS-CoV RBD"[32]. In this excerpt, the affinity of the SARS-CoV-2 RBD (receptor-binding domain in the S1 subunit[33]) to the ACE2 receptor is specified as similar or stronger than the affinity of the SARS-CoV RBD to ACE2. Accordingly, the affinity of the SARS-CoV RBD to ACE2 is similar or weaker than the

[28] Gorbalenya A.E. et al., op. cit.

[29] As noted in the introduction, the name "SARS-CoV-2" was not derived from the SARS disease but from the compound "SARS-CoV". Consequently, Input 1 has not been called "SARS" but "SARS-CoV".

[30] Fauconnier G., Turner M., *Jak myślimy* …, p. 417–461.

[31] Coronaviridae Study Group of the International Committee on Taxonomy of Viruses, op. cit. Wanbo T. et al., op. cit. V'kovski P. et al., op. cit.

[32] V'kovski P. et al., op. cit.

[33] cf. Gorbalenya A.E. et al., op. cit.: "The S protein mediates viral entry into host cells by first binding to a host receptor through the receptor-binding domain (RBD) in the S1 subunit and then fusing the viral and host membranes through the S2 subunit. SARS-CoV and MERS-CoV RBDs recognize different receptors. SARS-CoV recognizes angiotensin-converting enzyme 2 (ACE2) as its receptor (…)".

affinity of the SARS-CoV-2 RBD to ACE2. Thus, the affinity of the SARS-CoV-2 RBD to the ACE2 receptor and the affinity of the SARS-CoV RBD to the ACE2 are counterparts in the inputs. As such, they are connected on the basis of (functional) similarity. In terms of the CBT approach the relationship between the RBD-elements in both Inputs constitutes the main source of similarity, providing a conceptual foundation for compressing this relation into uniqueness in the emerging blend.

(2) "The RBD region is a critical target for neutralizing antibodies (nAbs), and SARS-CoV-2 and SARS-CoV RBD are ~73%–76% similar in sequence"[34].

(2a) "Mutations of key residues play an important role in enhancing the interaction with ACE2. F486 in SARS-CoV-2, instead of I472 in SARS RBD, forms strong aromatic–aromatic interactions with ACE2 Y83, and E484 in SARS-CoV-2-CTD, instead of P470 in SARS RBD, forms ionic interactions with K31, which leads to higher affinity for receptor binding than RBD of SARS-CoV"[35].

In excerpt (2), the (structural[36]) similarity between the SARS-CoV-2 and SARS-CoV RBD manifests itself as an effect of blending of higher complexity than in excerpt (1). Despite a relatively high mutual similarity in sequence (up to 76%), the SARS-CoV-2 RBD shows a slightly higher affinity for the ACE2 receptor than the SARS-CoV RBD (excerpt [2a], cf. excerpt [1]). Lacking contradiction between those two excerpts indicates that the difference in the affinity of the BRDs to ACE2 between the Inputs has been regarded as sufficiently low to be compressed to similarity in the blend. It should be noted that difference is an outer-spatial vital relation, which cannot be scaled down[37]. After compression to similarity scaling down, i.e. assessing and juxtaposing the strength of interaction between the BRDs and ACE2, becomes possible. Relations emerging between the affinity of SARS-CoV-2 and SARS-CoV RBD to ACE2 show that more explicit reference to the relevant specialised knowledge reveals deeper levels of conceptual blending. This can be accounted for by the activation of more detailed framing in the Relevance Space, concerning mutations of key residues and RBD interactions with receptors. It should, therefore, be noted that a precise reconstruction of each conceptual integration network is closely linked to the activation of the Relevance Space.

(3) "The amino acid sequence of the SARS-CoV and SARS-CoV-2 RdRPs show a >95% similarity with most changes located in the nidovirus RdRP-associated nucleotidyltransferase domain, which, despite being a genetic marker of Nidovirales, has yet to be functionally elucidated"[38]. On the basis of this excerpt an interesting

[34] Huang Y., *Structural and functional properties of SARS-CoV-2 spike protein: potential antivirus drug development for COVID-19*, "Acta Pharmacologica Sinica", [online], 2020, 41, p. 1141–1149, retrieved February 17, 2021, from https://www.nature.com/articles/s41401-020-0485-4.

[35] Ibid.

[36] As opposed to the functional aspect highlighted in excerpt (1).

[37] Fauconnier G., Turner M., *Jak myślimy* …, p. 487.

[38] V'kovski P. et al., op. cit.

blend can be reconstructed. The amino acid sequence of the SARS-CoV RdRP (RNA dependent RNA polymerase) has been identified with the analogical part of SARS-CoV-2. Thus, similarity has been compressed to uniqueness. Such a strong compression is possible because the relation of uniqueness allows the blend to satisfy the principle of relevance with respect to a very narrow scope of specialised knowledge (the amino acid sequence only) in the Relevance Space, excluding other differentiating aspects of their structure. In other words, the Relevance Space determines compression patterns by means of contextual constraints. Not only phenotypical similarities, but also significant differences between SARS-CoV and SARS-CoV-2 also exert an immense influence on the topology of the blend "SARS-CoV-2":

(4) "Given these similarities in receptor usage and cleavage requirements, it is surprising that SARS-CoV and SARS-CoV-2 display marked differences in virus replication efficiency and spread. "SARS-CoV primarily targets pneumocytes and lung macrophages in lower respiratory tract tissues, where ACE2 is predominantly expressed, consistent with the lower respiratory tract disease resulting from SARS-CoV infection and the limited viral spread. By contrast, SARS-CoV-2 replicates abundantly in upper respiratory epithelia, where ACE2 is also expressed, and is efficiently transmitted"[39]. Despite undeniable similarities within the affinity of the virus RBDs to ACE2 there is a strong contrast between SARS-CoV and SARS-CoV-2. This excerpt shows differences in virus replication efficiency and spread. Both viruses target zones of respiratory tract, where the ACE2 receptor is expressed, but they replicate at different paces. The characteristics of fast replication has no counterpart in Input 1 "SARS-CoV" and is therefore inherited by the blend from Input 2 "Fast replication".

It has been proven that both viruses bind to human ACE2 with different dissociation constants: (5) "SARS-CoV-2 S binds to human ACE2 with a dissociation constant (K_D) of 14.7 nM, though that of SARS-CoV S is 325.8 nM, indicating that SARS-CoV-2 S is more sensitive to ACE2 than is SARS-CoV S."[40] Therefore, the outer-spatial relation of difference, which cannot be scaled down as mentioned above, has been compressed to property "sensitivity of the virus RBD to ACE2" in the blend, which, in turn, can be scaled down and gives us human-scale understanding or insight into this scientific problem.

The "Fast replication" frame resulting from Input 2 is another semantic structure which determines not only the topology, but also the potential dynamics of the blend, reflected by the Elaboration Space: (6) "This conclusion is consistent with the wide spread of SARS-CoV-2 within a short period of time and was also echoed by the finding that SARS-CoV-2 Spike (S) protein had 10- to 20-fold higher affinity to human angiotensin-converting enzyme 2 (ACE2) receptor than that of SARS-CoV based on the Cryo-EM structure analysis of S proteins"[41].

[39] Ibid.

[40] Huang Y. et al., op. cit.

[41] Zheng J., op. cit.

Expressions such as "the wide spread of SARS-CoV-2", "within a short period of time", "SARS-CoV-2 Spike (S) protein", "higher affinity to (…)" constitute the "Fast replication" frame. The frame elements mentioned above "run" the entire blend. As a consequence, the inferences resulting from the blend are fed back to Input 2 and therefore referred to a real-world problem, i.e., a specific property of the Spike (S) protein (its' affinity to ACE2). Below, another exemplification of the recursive projection of inferences from the blend onto one of the inputs will be presented: (7) "As we currently understand, SARS and COVID-19 are a consequence of virus-encoded functions and delayed interferon responses and, in severe cases, they are associated with dysregulated immune responses and immunopathologies. Indeed, rapid and uncontrolled viral replication of SARS-CoV has been demonstrated to evade the host innate immune activation during its initial steps. As a consequence, the increase in aberrant pro-inflammatory responses and immune cell infiltration in the lungs provoke tissue damage and contribute to the clinical manifestation of SARS"[42].

Knowledge of compression patterns typical for the species prototype SARS-CoV, represented by the expression "uncontrolled viral replication of SARS-CoV", is selectively projected on the SARS-CoV"-derived blend "SARS-CoV-2". The recursive projection of inferences ("the increase in aberrant pro-inflammatory responses" and "immune cell infiltration in the lungs") emerging in the blend "SARS-CoV-2" onto the input containing the "Fast replication" frame allows to conclude on real-world phenomena/ processes, in this case on the clinical progression of the severe acute respiratory syndrome (SARS) or rather COVID-19.

SUMMARY OF ANALYSIS RESULTS

In this section main conclusions from the data analysis will be summarized and presented in a more compact form, without direct reference to excerpts taken from highly specialized texts. Specific compression patterns present in the blend "SARS-CoV-2" are structured by similarities and differences between the frames of the Inputs. These manifest themselves within two phenomena: the SARS-CoV and SARS-CoV-2 binding affinity for the ACE2 receptor of the S protein as well as structural and functional convergence between the SARS-CoV RBD (receptor-binding domain in the S1 subunit of the spike (S) protein) and SARS-CoV-2. Having been identified as counterparts in the inputs, the properties "affinity of the SARS-CoV RBD to the ACE2 receptor" and "affinity of the SARS-CoV-2 RBD to the ACE2 receptor" are conceptually linked on the basis of (functional) similarity. The relation of similarity originates from the interdependency between the RBD-elements in the Inputs, which in turn allows to compress similarity into uniqueness in the blend.

However, due to the activation of a more detailed frame it becomes visible that the structural similarity between the SARS-CoV and SARS-CoV-2 RBD results from

[42] V'kovski P. et al., op. cit.

more complex blending processes than indicated above. It appears that there is no contradiction between a relatively high mutual similarity in sequence (up to 76%) and the fact that the SARS-CoV-2 RBD exhibits a slightly higher affinity for the ACE2 receptor than the SARS-CoV RBD. This shows that the relation of difference (in the affinity to ACE2) identified between the Inputs has been compressed to similarity in the blend, as its' significance was sufficiently low. The strength of interaction between ACE2 and the virus BRDs can thereby be juxtaposed and assessed because similarity, unlike difference, is a vital relation which can be scaled down.

Reflecting on the above analysis results it should be emphasized that relations emerging as an effect of more detailed framing (i.e. involving direct reference to specialised knowledge) reveal more complex dimensions of conceptual blending.

Furthermore, it has been shown that Relevance Space determines compression patterns by means of specific contextual constraints. The amino acid sequence of the SARS-CoV RdRP (RNA dependent RNA polymerase) shows high similarity to the analogical part of SARS-CoV-2. Such a high level of similarity (>95%) makes it possible to compress similarity to uniqueness, which constitutes a very strong compression. The relation of uniqueness enables the blend to satisfy the principle of relevance by reference to a relatively narrow scope of specialised knowledge (ie. to the amino acid sequence alone) in the Relevance Space, without involving other distinctive elements of their structure. For this reason such a strong compression becomes possible.

Furthermore it has been proven that not only phenotypical similarities but also differences between SARS-CoV-2 and SARS-CoV determine the structure of the blend "SARS-CoV-2". In this respect, the fact that both viruses bind to human ACE2 with different dissociation constants has turned out to be crucial. On this basis, the outer-spatial[43] relation of difference has been compressed to property "sensitivity of the virus RBD to ACE2" in the blend. As indicated above, the relation of difference cannot be scaled down, whereas the aforementioned property can undergo the process of scaling down and therefore give us human-scale insight into the relevant scientific problem.

Phrases such as "the wide spread of SARS-CoV-2", "higher affinity to (…)", "within a short period of time" constitute another semantic construction which not only determines the topology but also rules the dynamics of the blend. This construction has been conceptually depicted as the "Fast replication" frame represented in Input 2. The primary function of the frame elements (i.e. phrases) indicated above is to "run" the blend. As a result, the inferences from the blend are fed back to Input 2, and thus, referred to a real-world problem, i.e., to a particular property of a virus, such as the affinity of the Spike (S) protein to ACE2.

The main conclusion of the study is based on the recognition that knowledge of compression patterns typical for the species prototype SARS-CoV, manifesting

[43] A relation established not between elements within one of the inputs but between elements localized in different inputs.

itself i.a. within the phrase "uncontrolled viral replication of SARS-CoV", is selectively projected on the blend "SARS-CoV-2" derived from the blend "SARS-CoV". The inferences which emerged in the blend "SARS-CoV-2" ("the increase in aberrant pro-inflammatory responses" and "immune cell infiltration in the lungs") are selectively projected onto the input representing the "Fast replication" frame, which makes it possible to conclude on real-world phenomena, i.e. on the clinical progression of COVID-19.

CONCLUSIONS AND SCOPE FOR FURTHER RESEARCH

As shown above, the organizing frame of the blend inherits conceptual elements derived from both Input frames. As such, it constitutes an effect of double-scope blending – the main source of human creativity. The RBD-elements in both Inputs are linked on the basis of similarity, which is compressed into uniqueness in the blend. The property of "fast replication", which allows the conceptualizer to 'run' the entire blend, does not have any counterpart in Input 1 and is, therefore, directly inherited from Input 2. This indicates that the topologies of both inputs are inconsistent at the level of properties and cause-effect. The compression of difference (within dissociation constants with which both viruses bind to human ACE2) to property "sensitivity of the virus RBD to ACE2" in the blend, gives us human-scale insight into the crucial property of the blend (SARS-CoV-2). The emergent structure in the blend is based on a novel relation of cause-effect, which did not appear in any of the inputs: fast replication is caused by the property "sensitivity of the virus RBD to ACE2". The captured compression patterns and structural specificity of the emerging blend make the compound "SARS-CoV-2" an efficient formal template for double-scope blending in future SARS-CoV-2 research concerning new mutations.

In order to optimize the outlined SARS-CoV-2 model as a future template for exploring linguistically expressed forms concerning SARS-CoV-2 mutations, more excerpts from highly specialized texts published in highest-ranking scientific journals should be analyzed to gain a more detailed insight into two subcategories of semantic entities crucial for the emergence of mutations: salient properties and functional specificity of the spike (S) protein as well as the viral transmissibility[44]. The optimization of these two subcategories within the presented SARS-CoV-2 model is crucial because new SARS-CoV-2 variants have been shown to arise from mutations of the SARS-CoV-2 spike protein, which in turn mediates the attachment of the virus to cell-surface receptors of the host leading to a fusion between cell membranes and virus[45]. As such, a thorough reconstruction of compression patterns within salient

[44] Harvey W.T. et al., *SARS-CoV-2 variants, spike mutations and immune escape*, "Nature Reviews Microbiology" 1, 2021, 9, p. 409–424. V'kovski P., op. cit. Wanbo T., op. cit. Huang Y., op. cit.

[45] Resende P. C. et al., *Spike E484K Mutation in the First SARS-CoV-2 Reinfection Case Confirmed in Brazil, 2020*, 2021, retrieved November 12, 2021, from https://virological.org/t/spike-e484k-mutation-in-the-first-sars-cov-2- reinfection-case-confirmed-in-brazil-2020/584.

properties of the SARS-CoV-2 spike protein as well as interplay of mutations within the spike protein and increased transmissibility as an essential property of emerging variants will become a structural template for tracking linguistic ways to refer to phenotypic changes within different variants of the coronavirus. In order to enhance the usefulness of the „SARS-CoV-2" Input in the multiple blend „SARS-CoV-2 mutations" it is necessary to concentrate on antigenicity as an essential property, which determines the emergence of mutations. Therefore, to examine salient properties of the SARS-CoV-2 spike protein responsible for the viral antigenic reactivity it is necessary to conduct a more detailed analysis of the property "sensitivity of the virus RBD to ACE2", which emerged in the "SARS-CoV-2" blend. Semantically relevant excerpts from highly specialized texts concerning ACE-2 blocking antibodies that bind the spike protein[46] will be identified, which will allow researchers to establish the topology of the „SARS-CoV-2 mutations" blend (or potential multiple-blend input) by reconstructing essential vital relations and compression patterns.

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Decoding the Virus: Blending Patterns behind the Name "SARS-CoV-2"

Abstract: The disruptive impact of the SARS-CoV-2 pandemic raised awareness of the need for elucidation of its' conceptual framework among contemporary linguists. This paper attempts to reconstruct the most fundamental conceptual relations within the compound "SARS-CoV-2" in terms of the Conceptual Blending. The main hypothesis for this research states that certain compression patterns and the structural specificity of the emerging blend make the compound "SARS-CoV-2" an efficient conceptual and formal template for multi-scope blending in future linguistic research concerning mutations of the coronavirus. The topology of mental spaces, the emergent structure within the blend, main compression patterns emerging from specific contextual constraints, the interplay of various vital relations, the dynamics of change and the potential to scale down vital relations (transmissibility and transmission dynamics of the SARS-CoV-2 virus) will be outlined. A seven-space-model of the SARS-CoV-2 conceptual integration network will be proposed. The results of analysis of intra- and outer-spatial vital relations connecting the input spaces and respective compression patterns will be demonstrated with reference to similarities and differences between SARS-CoV and SARS-CoV-2.

Keywords: conceptual blending, mental space, anthropocentric linguistics, SARS-CoV-2, SARS-CoV

DOI: https://doi.org/10.34864/heteroglossia.issn.2084-1302.nr13.art6