Symptomic Mimicry Between SARS-CoV-2 and the Common Cold Complex

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Abstract
The recent changes in COVID-19 symptoms suggest convergent evolution of respiratory diseases. This process is analogous to the emergence of animal mimetic complexes and complements previously identified types of mimicry. A novel pathogen might go unnoticed or insufficiently counteracted if it resembles a disease that the host already faced on multiple occasions, which creates a selective pressure towards a typical symptomic phonotype. In short, the reason why so many unrelated pathogens cause similar symptoms may correspond to the reasons that drove the evolution of the ‘warning’ wasp-like colouration in various insect species.

Keywords Mimicry · SARS-CoV-2 · Symptoms · Convergence · Common cold

Historically, multiple coronavirus (Human Coronavirus-229E, OC43, NL63, and HKU1) strains had spread in human populations (Liu et al., 2021). They tend to cause symptoms usually described as the common cold. Other serologically different pathogens are known for causing similar symptoms, for instance, various rhinoviruses, influenza viruses, adenoviruses, enteroviruses, and several sources of bacterial sinusitis (Basharat et al., 2019; Heikkinen & Järvinen, 2003). Characteristic symptoms of the common cold include a runny or stuffy nose, sneezing, sore throat, fever, cough, mild headache, and body aches (Eccles, 2005).

The SARS-CoV-2 had jumped to humans probably through a single episode of zoonosis but swiftly came to dominate the global scene (Wang et al., 2020). Initially, the virus caused multiple specific symptoms, such as the loss of smell and...
taste, which, despite high prevalence among COVID-19 patients, are quite atypical of other airborne infections of the upper respiratory tract (Dawson et al., 2021; Lee et al., 2020).

Since its initial detection, the SARS-CoV-2 virus produced numerous mutations and gave rise to multiple well-known variants that differ in transmissibility, disease severity, risk of reinfection, and even their symptomatic manifestation (WHO, 2021a). Currently, the World Health Organisation recognises two variants of interest and five variants of concern (WHO, 2021b). The relatively recent variant of concern, labelled ‘delta’, causes symptoms typical of the common cold (runny nose and sneezing) more frequently than the earlier variants do (Molteni et al., 2021; Roberts, 2021).

We argue that this may not be a mere coincidence but rather a causative effect of the general pattern of symptomic mimicry.

A new dangerous disease spreading through a population is more likely unnoticed and insufficiently treated if its symptomic phenotype resembles that of a familiar pathogen. If individuals tend to view the new disease as a benign infection they faced on multiple previous occasions, they are less likely to take it seriously. Humans are known for their capacity to isolate bearers of new pathogens. Strategies to reduce the contact between healthy and possibly infected individuals were recently observed in honey bees (Pusceddu et al., 2021). Even slime mould avoids conspecifics that face increased levels of (both biotic and abiotic) stress (Briard et al., 2020). Pathogen variants that seem familiar may tend to prevail over variants with atypical symptoms in many host species.

We believe that the emergence of the common cold disease panel, which includes over 200 different, phylogenetically distant pathogens with hardly distinguishable symptoms (Eccles, 2005), is due to such mimetic process. In analogy to various animal mimicry complexes, symptomic mimicry allowed the evolution of the ‘cold disease mimicry ring’.

Alternatively, such convergence in symptomaticity could be explained by optimisation of spreading velocity. Some symptoms, such as sneezing, could facilitate the spread of the virus more than others, such as dry cough. Convergence and mimetism are not, however, mutually exclusive. Moreover, though the former may help explain the emergence of features typical of the common cold, it does not offer such an elegant explanation of the loss of the specific, ‘indicative’ symptoms.

Symptomic mimicry should not be confused with molecular mimicry debated elsewhere (Casey et al., 2021), which captures how coronavirus sequences (proteins) can go unnoticed by resembling sequences (proteins) that naturally occur within the infected organism. The gradual change in the prevalence of COVID-19 symptoms is, in our opinion, due to a selection pressure on resembling other pathogenic manifestations rather than innate components of host’s body. While molecular mimicry tries to deceive the somatic immune system, symptomic mimicry aims at evading our behavioural immunity, a system comprised of a set of cognitive, psychological, and behavioural processes activated upon the perception of specific pathogenicity-connoting signs (Schaller, 2006). Perception of such signs triggers specific emotional and behavioural responses leading to increased social avoidance and exclusion. When deceived by symptomic mimicry, the infected individual can mistake
COVID-19 for the common cold and may thus feel little need to undergo appropriate testing and isolation, giving the virus an additional opportunity to spread.

The suggested evolution of resemblance between pathogen strains is a logical complement to previously identified mimicking strategies, such as Batesian, Müllerian, and Emsleyan/Mertensian mimicry (See Fig. 1 and Table 1). Equivalent observations in predator–prey dynamics that lead to a change from the phenotype of a dangerous species towards a harmless model were previously identified as aggressive mimicry. Predators or parasites can benefit from visual or acoustic resemblance of prey’s source of sustenance (Svenson et al., 2015) or sexually receptive partner (Marshall & Hill, 2009). To the best of our knowledge, though, the natural extension of the mimicry phenomenon to diseases remained so far overlooked. Similarly to the ‘aggressive’ or ‘Mertensian mimicry’, COVID-19 symptoms are changing from COVID-19 specific to those of the common cold (i.e., COVID-19 non-specific). As a result, the delta variant of SARS-CoV-2 is a kind of virotic ‘wolf in sheep’s clothing’.

The resemblance does not necessarily evolve along the higher/lower dangerousness vector, as depicted in Fig. 1. Frequency of the mimic and model species plays a vital role in the evolution of mimicry (Brejcha et al., 2021). The evolution of similarity between species that are to some extent harmful to a prominent selective agent (see Table 1) should be, in both outlined cases of Müllerian and symptomic mimicry, directed towards a typical phenotype.

In line with the Error Management Theory, we assume that host organisms counteract rare or strange sources of discomfort more vigorously because it is better to be safe than sorry (Haselton & Buss, 2000). Novel, even relatively harmless, pathogens should thus gravitate towards symptoms typical of more common diseases. Once the mimicry complex is firmly established, newcomers have no choice but to conform to the majority. They need to communicate that they are nothing special, nothing to be worried about. Suppose the immune systems (or in a defence system in a broad sense) responds to conditioning as recently suggested (Nowlin 2021). In that case, mimicry rings might frequently emerge in both animal and plant pathogens. The notion: “Better the devil you know, than the devil you don’t” might be acknowledged across the biosphere, driving the evolution of pathogens towards symptomatic groups with relatively large between-group and small within-group variance.

To conclude, we expect later variants of SARS-CoV-2 (such as the newly discovered Omicron) to conform even more to the common cold phenotype, and we

Fig. 1  Identified mimicry types with respect to species dangerousness
| Type                     | Mimic                  | Model                  | Prominent selective agent                      | When it evolves                                                                 | Example                                                                 |
|-------------------------|------------------------|------------------------|------------------------------------------------|---------------------------------------------------------------------------------|------------------------------------------------------------------------|
| Batesian                | harmless               | dangerous              | predator avoiding the model species           | When aposematic prey is dangerous and frequent enough to accommodate an edible free-rider | Hoverflies resembling members of the wasp-like Müllerian complex     |
| Müllarian               | dangerous (likely less frequent) | dangerous (likely more frequent) | predator avoiding both species                | When two or more dangerous species can mutually benefit from similarity by raising the effective size of the pool of aposematic prey with the same warning signal | The Palearctic black-and-red mimic complex of various *Heteroptera, Auchenorrhyncha, Coleoptera, and others* |
| Emsleyan/Mertensian     | deadly                 | dangerous              | predator avoiding both species                | When the extreme cost of interaction with a mimic prevents effective learning and information transmission between members of the predator species | Texas coral snakes resembling less venomous species                  |
| The newly proposed type | dangerous (likely more dangerous or initially rarer) | dangerous (likely less dangerous or initially more common) | host avoiding both species                    | When the more dangerous or less typical species provokes a stronger action than a less dangerous or better-known species | Symptomatic mimicry of the common cold complex                         |
| Aggressive              | dangerous              | harmless               | prey or host avoiding the dangerous species   | When predators or parasites that employ a sit-and-wait strategy get at least rarely confused with neutral or beneficial stimuli for the prey | Flatworm disguised as a tasty caterpillar in a swollen eyestalk of a snail |

The focus (and the main contribution) of this article in bold
expect that the incidence of symptoms with hither specificity to COVID-19 will further decline. It seems likely that the symptoms of COVID-19, which precipitated the current global health crisis, will eventually blend with those of the common cold mimetic complex, producing a seemingly typical disease without any prominent distinguishing features.

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Declarations

Competing Interests The authors declare that they have no competing interests.

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