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Commentary

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Genotypic analysis of *Bacillus cereus* and its approaches of several groups of species

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Description

The *Bacillus cereus* group of microbes are spore-forming, environment-wide organisms. Therefore, it is feasible for *B. cereus* to infect a variety of consumer goods, including cosmetics either as raw materials or during manufacturing. Eye infections can arise from B. cereus contamination of cosmetics applied close to the eyes especially in persons who already have trauma or injury to this region. Some of those infections might be so severe that they can impair vision. Any pathogen that can be cultivated from cosmetic goods is likely to have the genetic make-up necessary to survive in the cosmetics matrices and to withstand the preservatives used to keep germs from growing during regular consumer usage of the product [1]. Therefore, by profiling isolates discovered as contaminants in the products we can find elements that might contribute to pathogenicity and persistence as well as isolates that might end up as helpful reference strains.

Genomic analysis can reveal the toxin-producing capacities a specific isolate possesses and aid in determining whether additional virulence genes were acquired. The *B. cereus* group consists of at least twelve closely related species, including *B. anthracis*, *B. cereus*, *B. thuringiensis*, *B. mycoides*, *B. pseudomycoides*, *B. weihenstephanensis*, *B. cytotoxicus*, *B. wiedmanni*, and *B. toyonensis*, as well as the recently discovered *B. paranthracis*, *B. pacificus*. Some of them carry strong toxins such as the two large plasmids known as pXO1 and pXO2 that create the tripartite anthrax toxin and cause the lethal effects of B. anthracis, the pathogen that causes anthrax. The insect pathogen *B. thuringiensis* can create immune inhibitor metalloproteases that can seriously harm the eyes, but it also makes crystal poisons that make it useful as a commercial biopesticide [2]. *B. cereus can* create toxins that cause eye infections, systemic infections and gastrointestinal illnesses.

Some strains of *B. cereus* may also possess particular genes that provide resistance to antimicrobials or preservatives. However the durability of their spores, which can endure severe environments may account for some of *B. cereus* persistence in cosmetic matrices. Preservatives are used in cosmetics to reduce the overall concentration of aerobic bacteria per gram and prevent the persistence of high-virulence microbial diseases. *B. cereus* strains that endure in spite of preservatives present hygienic problems and may be suitable microbiological candidates for studies on the safety of cosmetics. When using eye cream preserved with parabens, we previously noticed that the *B. cereus* reference strain ATCC14579 was not adequately suited for long-term survival. Here, as part of a microbiological examination of eye area cosmetics created with non-traditional preservatives, we genetically identify a strain of *B. cereus* known as "3A-ES" that was originally characterised as *B. cereus* 3A and isolated from eye shadow [3]. The cosmetics under investigation were obtained from regular retail stock and had been made with plant extracts some of which may have been intended to work as antibacterial agents, as well as minerals, mica, and iron oxides, organic seed oils, tapioca, corn and mica powders. These cosmetics lacked the conventional preservatives that are more frequently found in cosmetic products, such as organic acids, alcohols, phenols, aldehydes and formaldehyde releas-

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ers, isothiazolinines, biguanides or compounds containing quaternary ammonium.

The Pleiotropic Transcriptional Regulator activates a number of the virulence factors released by members of the *B. cereus* group, including enterotoxins, haemolysins, Phospholipases, and Proteases (PlcR). The presence of PapR, a short signalling peptide that functions as a quorum-sensing effector is necessary for PlcR activity to reach its peak at the start of the stationary growth phase. In particular, PapR is exported processed and then imported back into the bacterial cell as a heptapeptide. This processed heptapeptide then interacts with PlcR to help it attach to the nucleotidic sequence PlcR box which is situated upstream of its target genes [4]. The genome of *B. cereus* 3A-ES had this pair of PlcR/PapR transcription regulators, and the presence of PlcR has previously been linked to the swift destruction of retinal function in cases of Bacillus endophalmitis. *B. cereus* also possessed the same transcription regulators, toxin and enzyme genes as other *B. cereus* group members.

These genes included the gastrointestinal infection-causing Cytotoxin K (cytK), the Haemolytic Enterotoxin Genes (hblCDA) and three Nonhemolytic Enterotoxin Genes (NheABC). Additionally, pore-forming toxins including thiol-activated cytolysins, hemolysin A and hemolysin III, which are involved in non-gastrointestinal infections were found. Genes for enzymes like phospholipase C and collagenases are also present in *B. cereus* 3A-ES. Collagenase phosphatidylcholine-phosphatolipase C, and tipartite hemolysin BL may increase the severity of *B. cereus* endophthalmitis. Metalloproteases of the Immune Inhibitor A (InhA) subclass were another noteworthy toxin subclass identified in 3A-ES. More recently Inh-A metalloproteases have been demonstrated to be independently related with both retinal injury and degeneration of the vitreous region of eyes infected with Bacillus species. These have been demonstrated to help *B. cereus* spores endure and avoid assaults from macrophages. Although these toxins are strongly linked to the synthesis of tissue-destructive or reactive exoenzymes, damage to ocular tissues may not be entirely attributable to specific toxins alone, according to research on strains with various gene combinations. Virulence may be caused by toxin combinations or toxin interactions with other factors [5].

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