

## *Dehalogenimonas*

**Karl Protil**

**Monday Class**

### **Introduction**

*Dehalogenimonas* is a genus of bacteria first proposed in 2009. These bacteria were discovered in a Superfund site, and they respire via reductive dehalogenation, pairing halogens with hydrogen ions.<sup>1</sup> At the time of writing, three species have been identified: *D. lykanthroporepellens*, *D. alkenigignens*, and *D. formicexedens*.<sup>2</sup> Given their ability to alter potentially toxic substances in the environment, these bacteria may be useful in bioremediation.<sup>3</sup>

### **Discovery**

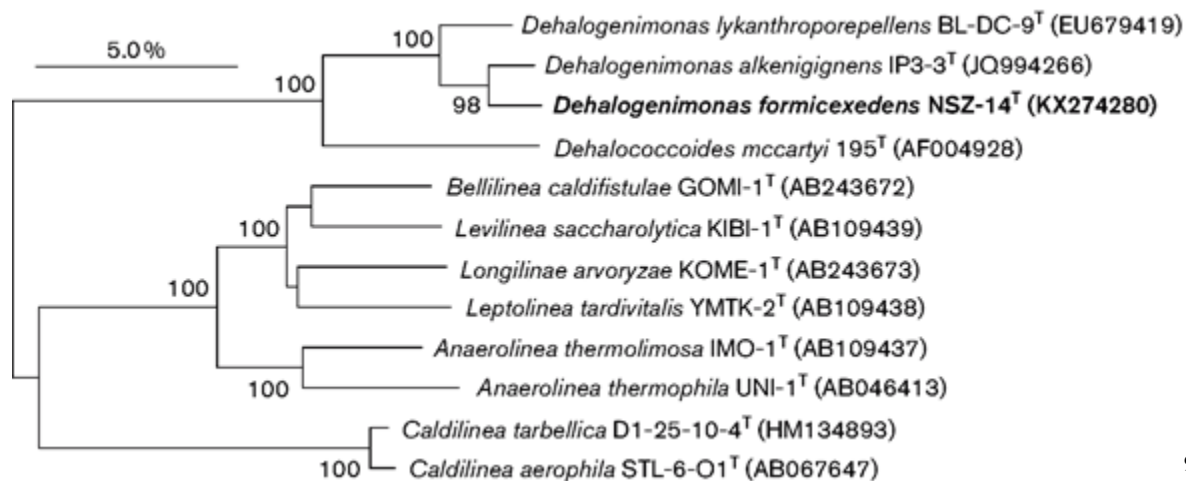
*Dehalogenimonas* was first classified in 2009, having been isolated from a Superfund site in Louisiana. Two strains of this bacteria were isolated, and they were initially thought to be part of the genus *Dehalococcoides*.<sup>4</sup> Further research indicated, for several reasons, that these two strains were part of a new genus named *Dehalogenimonas*. First, the 16S rRNA gene sequences were only 90% similar between the two strains discovered and *Dehalococcoides*. In addition, the overall genomic guanine and cysteine concentration were significantly different: *Dehalogenimonas* had roughly 54 mol% of C+G while *Dehalococcoides* had roughly 47 mol% of C+G. The fatty acids used in *Dehalogenimonas* and *Dehalococcoides* also differed. Lastly, *Dehalogenimonas* and *Dehalococcoides* reductively dehalogenate different compounds. The two strains of *Dehalogenimonas* were found to be of the same species, *Dehalogenimonas lykanthroporepellens*.<sup>5</sup>

### **Species**

To date, three species of *Dehalogenimonas* have been discovered. *D. lykanthroporepellens*, the first species, was discovered in 2009.<sup>6</sup> *Dehalogenimonas alkenigignens* was discovered in 2013. Scientists revisited the Superfund site where *D. lykanthroporepellens* was originally discovered and took samples of groundwater following the same protocols established by that original paper. Two strains were isolated, just as in the original paper. These strains went through a variety of biochemical tests alongside *D. lykanthroporepellens* to determine if they represented a new species. Some minor differences were found, mainly regarding the concentrations of different chemicals at which reductive dehalogenation can occur. In addition, 16S rRNA sequencing showed that, while the two strains were 99.9% similar (only 1 bp difference), they were only roughly 96% similar to *D. lykanthroporepellens*. Due to these two factors (reductive dehalogenation and 16S rRNA differences), the two strains were determined to be a new species, *Dehalogenimonas alkenigignens*.<sup>7</sup>

*Dehalogenimonas formicexedens* was the third species of *Dehalogenimonas* to be discovered. It was discovered in 2017. A sample was taken from the same Superfund site where

the other two species were discovered. The bacteria isolated was sequenced. The 16S rRNA sequencing showed that it was 97.63% similar to *D. alkenigignens* and 95.05% similar to *D. lykanthroporepellens*. During an array of tests, some differences were found between *D. formicexedens* and the other two species in *Dehalogenimonas*. In contrast to the other species, *D. formicexedens* cannot perform dechlorination when the NaCl concentration is above 1.1%, the temperature is below 15 degrees or above 42 degrees Celsius, or the pH is above 8. The proportions of fatty acids were also different between all three species. Due to these three factors (16S rRNA sequence, dechlorination bounds, and fatty acid differences), a new species was proposed: *Dehalogenimonas formicexedens*.<sup>8</sup>



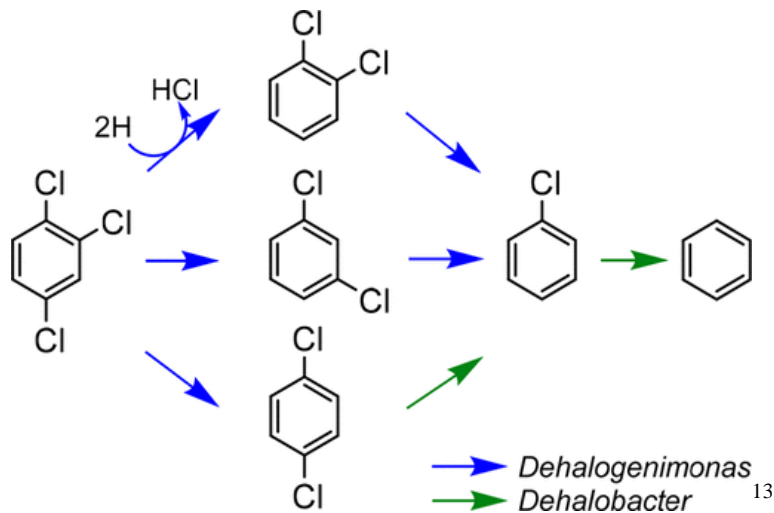
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## Description

*Dehalogenimonas* is mesophilic, which means it thrives in moderate temperatures. The cells are irregular cocci that have a 0.3-0.6 µm diameter. It does not form spores and is non-motile. *Dehalogenimonas* is a Gram-negative bacterium, and it is resistant to both ampicillin and vancomycin. It is strictly anaerobic, using hydrogen as an electron donor. It can reductively dehalogenate a variety of chlorinated carbon compounds, and these chlorinated carbon compounds are essential for its growth.<sup>10</sup>

## Reductive Dehalogenation

In a study with 1,2,4-trichlorobenzene (TCB), *Dehalogenimonas* used TCB and hydrogen for respiration. This resulted in the expiration of HCl and a variety of dichlorobenzenes. It was able to further reduce these dichlorobenzenes into chlorobenzenes.<sup>11</sup> In another experiment, *Dehalogenimonas* reductively dehalogenated 1,2,3-trichloropropane into allyl chloride. Allyl chloride was abiotically reduced into numerous compounds, including allyl mercaptan and allyl methyl sulfide. These compounds have a garlic scent, which is why the first discovered species was named *lykanthroporepellens* (because garlic repels werewolves, also known as lykan).<sup>12</sup> The TCB reduction pathway is shown below.



### Genome

A study of the *D. lykanthroporepellens* genome (the only known species at the time of publication) showed that it has a single circular chromosome with roughly 1.7 million base pairs. It has 1,771 genes: 51 that code for RNA and 1,720 that code for proteins. The strain studied had a large prophage region which composed roughly 4% of the genome. Prophage regions are bacteriophage genomes that have been inserted into a bacterial genome. The genome was also composed of roughly 4.3% insertion sequence elements, DNA sequences that can excise themselves from the genome and move to a different location in the genome.<sup>14</sup>

### Amino Acids

*D. lykanthroporepellens* has 47 tRNA genes. These genes code for a total of 21 proteins: the 20 universal amino acids and selenocysteine. Selenocysteine synthesis is controlled by the *selCDAB* operon. *selC* codes for selenocysteine-inserting tRNA, the anticodon for the UGA codon (UGA is typically the stop codon). *selD* codes for selenophosphate synthetase, which synthesizes monoselenophosphate from ATP and selenide. *selA* codes for selenocysteine synthase, which turns serine-acylated tRNA into selenocysteine-tRNA using monoselenophosphate. *selB* encodes GTP-dependent selenocysteine-specific elongation factor, a protein that interacts with selenocysteine-tRNA and selenocysteine inserting sequence. This interaction allows selenocysteine to be added at UGA codons instead of transcription being terminated.<sup>15</sup> This *selCDAB* operon is unique to *Dehalogenimonas* and is shared across all species in the genus.<sup>16</sup> Selenocysteine is a relatively common non-universal amino acid, sometimes referred to as the 21st amino acid. Proteins with selenocysteine have been shown to catalyze reduction reactions.<sup>17</sup> Given the importance of reduction to the normal functioning of *Dehalogenimonas*, selenocysteine may play a role in the reduction reactions it carries out.

### Potential Uses

*Dehalogenimonas* alone is unlikely to be useful in eliminating industrial toxins. For example, it reduces 1,1,2-trichloroethane (TCA) into vinyl chloride. TCA is 165th on the CDC's

Priority List of Hazardous Substances, while vinyl chloride is 4th.<sup>18,19</sup> Although these are not ranked strictly on toxicity, as frequency and likelihood of exposure are factored in, vinyl chloride is clearly not an acceptable end product. Other reductions are not any more favorable. Trichlorobenzene can be converted into dichlorobenzene, chlorobenzene, or benzene (with the assistance of *Dehalobacter* bacteria).<sup>20</sup> All of these chemicals are on the Substance Priority List.<sup>21</sup> However, *Dehalogenimonas* may be useful in environmental cleanup when used with other chemicals or bacteria. For instance, a bacteria or chemical that could convert dichlorobenzene into less harmful products could be used alongside *Dehalogenimonas*. At the time of writing, however, there has been no published research on this.

*Dehalogenimonas* could be useful in industrial applications. Vinyl chloride is an essential component of polyvinyl chloride (PVC), a very common construction product. At this point, *Dehalogenimonas* has not been used in PVC production. Although it is certainly theoretically possible, there is no indication at this point that it would be advantageous to use *Dehalogenimonas* for PVC production. In addition, highly efficient processes and advanced production infrastructures for the production of PVC already exist given its widespread use in construction.<sup>22</sup>

## See Also

- [Dehalococcoides](#)
- [Reductive Dehalogenation](#)
- [Reductive Dehalogenases](#)
- [Halorespiration](#)
- [Superfund Sites](#)
- [Selenocysteine](#)
- [Bioremediation](#)

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<sup>1</sup> Moe WM, Yan J, Nobre MF, da Costa MS, Rainey FA (November 2009). “*Dehalogenimonas lykanthroporepellens* gen. Nov., sp. Nov., a reductively dehalogenating bacterium isolated from chlorinated solvent-contaminated groundwater.” *International Journal of Systematic and Evolutionary Microbiology*. **59**(11): 2692-2697. doi: 10.1099/ijms.0.011502-0

<sup>2</sup> Key TA, Bowman KS, Lee I, Chun J, Albuquerque L, da Costa MS, Rainey FA, Moe WM (May 2017). “*Dehalogenimonas formixecedens* sp. Nov., a chlorinated alkane-respiring bacterium isolated from contaminated groundwater.” *International Journal of Systematic and Evolutionary Microbiology*. **67**(5): 1366-1373. doi: 10.1099/ijsem.0.001819

<sup>3</sup> Rosell M, Palau J, Morton SH, Caminal G, Soler A, Shouakar-Stash O, Marco-Urrea E (January 2019). “Dual carbon - chlorine isotope fractionation during dichloroelimination of 1,1,2-trichloroethane by an enrichment culture containing *Dehalogenimonas* sp.” *Science of The Total Environment*. **648**: 422-429. doi: 10.1016/j.scitotenv.2018.08.071

<sup>4</sup> Yan J, Rash BA, Rainey FA, Moe WM (April 2009). “Isolation of novel bacteria within the *Chloroflexi* capable of reductive dechlorination of 1,2,3-trichloropropane.” *Environmental Microbiology*. **11**(4): 833-843. doi: 10.1111/j.1462-2920.2008.01804.x

<sup>5</sup> Moe WM, Yan J, Nobre MF, da Costa MS, Rainey FA (November 2009). “*Dehalogenimonas lykanthroporepellens* gen. Nov., sp. Nov., a reductively dehalogenating bacterium isolated from chlorinated solvent-contaminated groundwater.” *International Journal of Systematic and Evolutionary Microbiology*. **59**(11): 2692-2697. doi: 10.1099/ijms.0.011502-0

<sup>6</sup> Ibid.

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- <sup>7</sup> Bowman KS, Nobre MF, da Costa MS, Rainey FA, Moe WM (April 2013). “*Dehalogenimonas alkenigignens* sp. Nov., a chlorinated-alkane-dehalogenating bacterium isolated from groundwater.” *International Journal of Systematic and Evolutionary Microbiology*. **63**(4): 1492-1498. doi: 10.1099/ijs.0.045054-0
- <sup>8</sup> Key TA, Bowman KS, Lee I, Chun J, Albuquerque L, da Costa MS, Rainey FA, Moe WM (May 2017). “*Dehalogenimonas formixecedens* sp. Nov., a chlorinated alkane-respiring bacterium isolated from contaminated groundwater.” *International Journal of Systematic and Evolutionary Microbiology*. **67**(5): 1366-1373. doi: 10.1099/ijssem.0.001819
- <sup>9</sup> Ibid.
- <sup>10</sup> Moe WM, Yan J, Nobre MF, da Costa MS, Rainey FA (November 2009). “*Dehalogenimonas lykanthroporepellens* gen. Nov., sp. Nov., a reductively dehalogenating bacterium isolated from chlorinated solvent-contaminated groundwater.” *International Journal of Systematic and Evolutionary Microbiology*. **59**(11): 2692-2697. doi: 10.1099/ijs.0.011502-0
- <sup>11</sup> Qiao W, Luo F, Lomheim L, Mack EE, Ye S, Wu J, Edwards EA (October 2018). “A *Dehalogenimonas* Population Respires 1,2,4-Trichlorobenzene and Dichlorobenzenes.” *Environmental Science & Technology*. **52**: 13391-13398. doi: 10.1021/acs.est.8b04239
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- <sup>15</sup> Ibid.
- <sup>16</sup> Key TA, Bowman KS, Lee I, Chun J, Albuquerque L, da Costa MS, Rainey FA, Moe WM (May 2017). “*Dehalogenimonas formixecedens* sp. Nov., a chlorinated alkane-respiring bacterium isolated from contaminated groundwater.” *International Journal of Systematic and Evolutionary Microbiology*. **67**(5): 1366-1373. doi: 10.1099/ijssem.0.001819
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- <sup>19</sup> “Substance Priority List.” atsd.cdc.gov. N.p., N.d. Web. 17 January 2020.  
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