Whole genome analysis of Bizionia argentinensis: the white genome project

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Background

The psicrotolerant bacteria Bizionia argentinesis (BA) was isolated from the National Antarctic Territory [1] as part of the "White Genome" Project in collaboration with Bio Sidus and the Argentine Antarctic Institute. We present here the annotation of the whole genome shotgun and a through analysis of the protein profiles and the biochemical pathways.

Results

We analyzed the general metabolic behavior of the bacteria and found systems that explain the adaptation of the organism to low temperatures, as well as the presence of at least four 'cold-shock protein' coding sequences (KEGG ORTHOLOGY: K03704) that works at transcription level. Also, were found an important number of genes in common with other well known psicrofilic organisms like Flavobacterium psychrophilum [2] and the psicrotolerant Gramella forsetii[3], which share with BA an extensive hydrolytic capability to transform sedimentary organic nitrogen in NH4+ and N2, to collaborate in the geochemical cycle of nitrogen.

Conclusions

This bacteria can tolerate temperatures around the 0°C, due to the presence of mechanisms that allow biological systems to adapt themselves to this particular life conditions and the capacity to hydrolyze sedimentary organic nitrogen.

References

1. Bercovich A, Vazquez SC, Yankilevich P, Coria SH, Foti M, Hernández E, Vidal A, Ruberto L, Melo C, Marenssi S, Criscuolo M, Memoli M, Arguelles M, Mac Cormack WP. Bizionia argentinensis sp. nov., isolated from surface marine water in Antarctica. Int J Syst Evol Microbiol. 2008 Oct.

2. Nematollahi A, Decostere A, Pasmans F, Haesebrouck F. Flavobacterium psychrophilum infections in salmonid fish. J Fish Dis. 2003 Oct.

3. Bauer M, Kube M, Teeling H, Richter M, Lombardot T, Allers E, Würdemann CA, Quast C, Kuhl H, Knaust F, Woebken D, Bischof K, Mussmann M, Choudhuri JV, Meyer F, Reinhardt R, Amann RI, Glöckner FO. Whole genome analysis of the marine Bacteroidetes'Gramella forsetii' reveals adaptations to degradation of polymeric organic matter. Environ Microbiol. 2006 Dec.

