Intestinimonas aquisgranensis sp. nov.

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Table 1: Complete list of names proposed in the current register list.

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species *Intestinimonas aquisgranensis*	**a.quis.gra.nen'sis. m. l. fem. adj.** *aquisgranensis*, pertaining to the city of Aachen in Germany, where the bacterium was isolated	Shared the highest 16S rRNA gene sequence similarity to *Intestinimonas butyriciproducens* (96.84%) and *Lawsonibacter asaccharolyticus* (96.13%). The highest ANI values was to *Pseudoflavonifractor capillosus* with 83.7%, confirming the novel status of the isolate. The highest POCP value (59.9%) was to *Intestinimonas butyriproducens*, the type species of this genus, followed by *Pseudoflavonifractor capillosus* (59.7%). However, the genomic tree analysis placed the strain closer to *I. butyriproducens* than to *P. capillosus*. GTDB-TK also assigned the genome to the genus *Intestinimonas*, confirming the isolate as a novel species within this genus. The isolate was found to be the same species as 'Intenstinimonas timonensis' (Durand et al., 2017a), with ANI value of 96.23%. However, this species name has never been validated. Genome analysis predicted the ability to utilise starch, sulfide, and L-serine, and to produce acetate, butyrate, propionate, L-cysteine, and riboflavin (vitamin B2). The detection of tetracycline-resistant ribosomal protection protein (ARO:0000002) may indicate the antibiotic resistance potential of this strain. It grows under anaerobic conditions on BHI media and forms cells that are rod-shaped with slightly pointed ends. The G+C content is 59.8 mol%. The type strain, CLA-AA-H199T (=DSM 112680T), was most prevalent in mouse gut microbiota (27.1% of 1,000 samples positive), followed by chicken gut microbiota (24.5%), and human gut microbiota (23.4%). It was isolated from the faeces of a healthy 28-year-old man.	*Intestinimonas*	Strain: CLA AA-H199 = DSM 112680 = JCM 35876 Ts	seqco.de/i:23423