

**CULTUROMICS OF STRICT
ANAEROBIC GUT BACTERIA
REVEALS FAMILY FINGERPRINTS**

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Family	Mother 1	Father 1	Child 1	Child 2	Mother 4	Father 4	Child 8	Child 9	Child 10
<i>Lachnospiraceae</i>	17	12	31	0	0	0	0	0	2
<i>Peptostreptococcaceae</i>	20	3	6	3	0	0	0	0	0
<i>Eubacteriaceae</i>	7	1	0	0	0	0	0	0	0
<i>Streptococcaceae</i>	1	3	8	3	1	0	1	3	0
<i>Clostridiaceae</i>	2	0	3	0	1	1	1	7	0
<i>Veillonellaceae</i>	0	0	0	2	0	1	0	2	0
<i>Enterococcaceae</i>	0	0	0	3	0	0	6	8	5
<i>Bacteroidaceae</i>	23	6	12	0	8	10	7	14	5
<i>Bifidobacteriaceae</i>	6	11	7	36	34	33	48	83	38
<i>Coriobacteriaceae</i>	0	0	6	0	1	8	0	0	0
<i>Enterobacteriaceae</i>	0	17	0	24	3	10	8	14	0

Figure 1: Number of isolates belonging to each bacterial family identified in the members of family 1 and 4. *Lachnospiraceae* is the most abundant in family 1 whereas *Bifidobacteriaceae* is the most abundant in family 4.

MSP Dendrogram

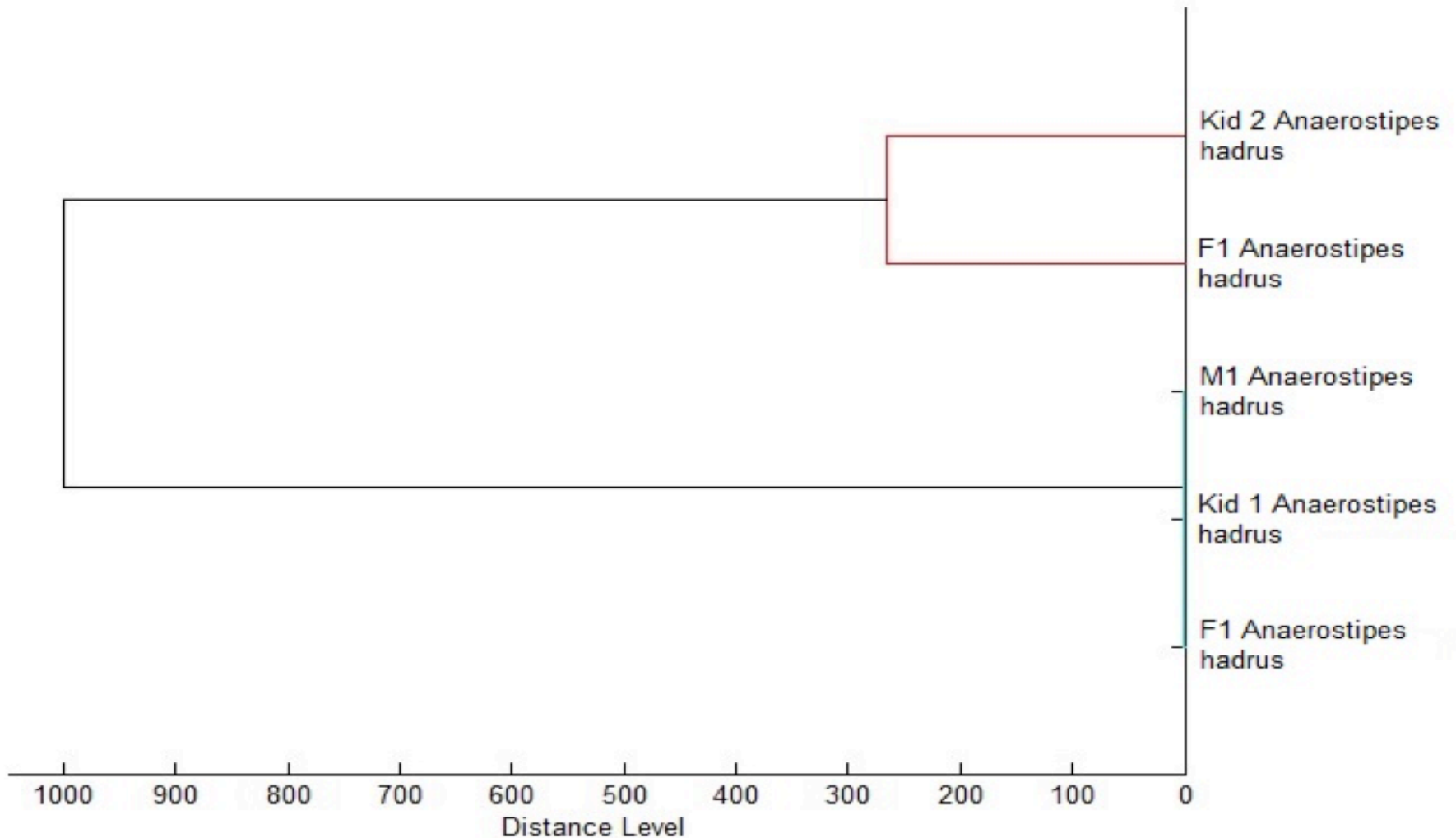


Figure 2: Phyloproteomic dendrogram showing the relationship between the *A. hadrus* strains isolated from different members of family 1. Note that mother, father and kid 1 share the same strain.