Bifidobacteria are early colonizers of the breast-fed infant colon and often dominate the lower gastrointestinal tract (GIT) prior to weaning. Accordingly, the infant-isolated *Bifidobacterium longum* ssp. *infantis* ATCC 15697 utilizes human milk oligosaccharides (HMO) as a sole carbon source, a trait that is not universal in the bifidobacteria. We have previously profiled the soluble oligosaccharides of the human milk glycome, thereby elucidating the extent to which these host-indigestible sugars are available to GIT microbiota. Moreover, mass-spectrometry-based glycoprofiling has revealed that *B. longum* ssp. *infantis* preferentially consumes small mass HMOs abundant early in the lactation cycle suggesting a colonization strategy. To explore this further, the ATCC 15697 genome was fully sequenced to enable systems-level investigations into the genetic basis and the molecular mechanisms contributing to this interesting phenotype. Comparative analysis of the ATCC 15697 genome has identified a bias towards COGs and loci predicted to utilize mammalian-derived carbohydrates. Many of these genomic features encode enzymes that are active on HMOs and their derivatives including a novel 40-kb region dedicated to oligosaccharide utilization. Subsequent biochemical and molecular characterization of HMO-related glycosidases and transport proteins have further resolved the mechanism by which *B. longum* ssp. *infantis* imports and catabolizes milk oligosaccharides. Two additional ssp. *infantis* genomes were sequenced and confirmed that these features are not unique to ATCC 15697 and likely constitute a competitive strategy developed by the subspecies. In addition, these genes represent markers of HMO metabolic potential to be exploited in ecological surveys of the infant microbial consortium. While most prebiotics are purported to mimic the bifidobacterial enrichment promoted by HMOs, a fundamental understanding of the evolutionarily-refined prototype has been incomplete. These studies are part of a larger collaboration to examine the molecular interactions, and ecological consequences, of HMO utilization in order to functionally annotate these complex oligosaccharides.