

# Trends in microbiome research

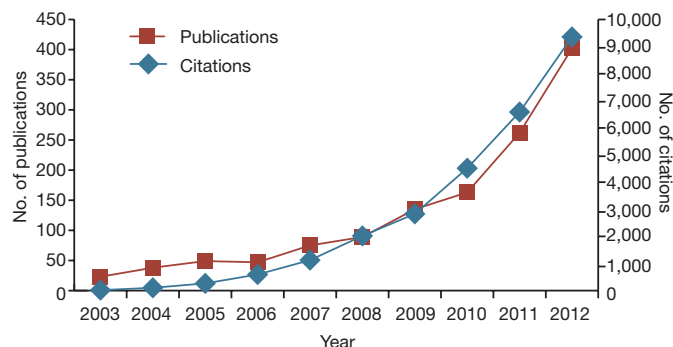
Susan Jones

More than a decade after the first paper detailing the immense diversity of human microflora (*Proc. Natl. Acad. Sci. USA* **96**, 14547–14552, 1999), the microbiome research literature has expanded enormously. This reflects an influx of funding from such agencies as the US National

Institutes of Health and the European Union's MetaHIT project. In contrast to publications, microbiome-related patents have increased less markedly. Recently published trials underscore the clinical promise of this research.

## Publications over time

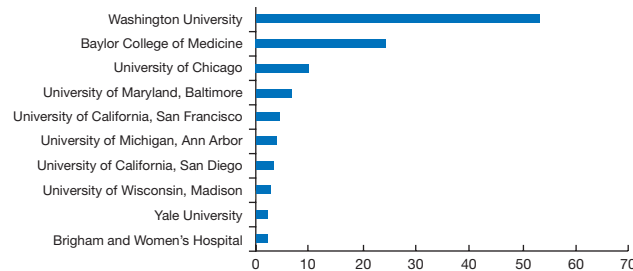
Since 2003, microbiome research publications have undergone explosive growth.



Source: Thomson Reuters Web of Science, accessed 6/3/2013, using title search terms (human microbiota, human microbiome, microbiome, human microbial, human microbes or gut ecology) for the period 2003–2013. Citations are to source items indexed within Web of Science. All article types are included.

## Top ten institutions receiving microbiome funding

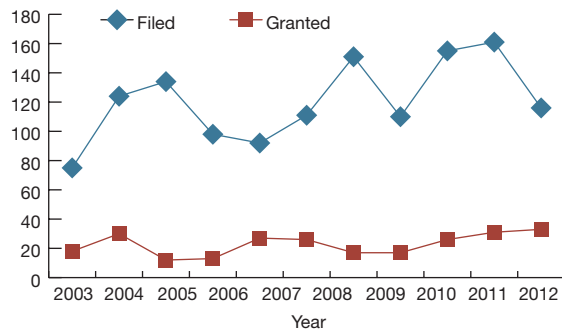
Washington University has received by far the greatest amount of microbiome-related funding.



Source: Bernat Olle, Pure Tech Ventures and Vedanta Biosciences.

## Patenting related to the microbiome

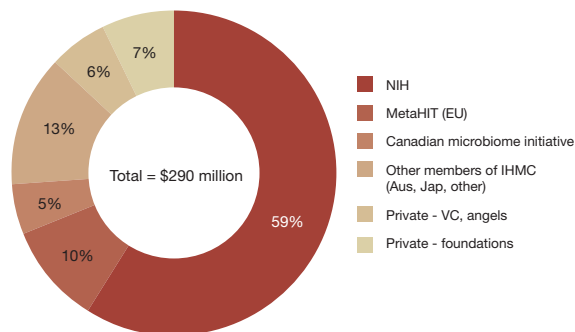
The number of patent filings reached a peak in 2011.



Source: IP Checkups, a patent analytics firm (<http://www.ipcheckups.com/>). United States Patent and Trademark Office and European Patent Office published applications and grants. Search terms: enterotype, microflora, microbiota, fecal transplantation, microbiome, probiotic, bacteriotherapy and bacterial therapy.

## Funding for microbiome research

US National Institutes of Health (NIH) has provided nearly two-thirds of funding.



Source: Bernat Olle, Pure Tech Ventures and Vedanta Biosciences. IHMC, International Human Microbiome Consortium. VC, venture capitalists.

## Notable recent trial and clinical study results

Publication	Indication	Result summary
van Nood, E. <i>et al.</i> <i>N. Engl. J. Med.</i> <b>368</b> , 407–415 (2013)	<i>Clostridium difficile</i> associated long-standing diarrhea	Three-arm randomized FECAL (fecal therapy to eliminate <i>C. difficile</i> -associated long-standing diarrhea) trial showed that infusion of donor feces was significantly more effective for the treatment of recurrent <i>C. difficile</i> infection than the use of vancomycin.
Vrieze, A. <i>et al.</i> <i>Gastroenterology</i> <b>143</b> , 913–916 (2012)	Metabolic syndrome	Two-arm randomized FATLOSE (fecal administration to lose weight) trial showed that transfer of intestinal microbiota from lean individuals increased insulin sensitivity in individuals with metabolic syndrome.
Graessler, J. <i>et al.</i> <i>Pharmacogenomics J.</i> doi:10.1038/tpj.2012.43 (2 October 2012)	Morbid obesity and type II diabetes	Pilot study of six patients in which metagenomic sequencing revealed extensive changes in the gut microbiome before and 3 months after bariatric surgery that correlated with post-operative improvements including weight loss, and improved glucose and lipid metabolism.

Susan Jones is Senior Editor at Nature Biotechnology.

## Top ten cited research articles in human microbiome research (2003–2013)

Article	Times cited
Eckburg, P.B. <i>et al.</i> Diversity of the human intestinal microbial flora. <i>Science</i> <b>308</b> , 1635–1638 (2005).	1,433
Turnbaugh, P.J. <i>et al.</i> An obesity-associated gut microbiome with increased capacity for energy harvest. <i>Nature</i> <b>444</b> , 1027–1031 (2006).	1,064
Gill, S.R. <i>et al.</i> Metagenomic analysis of the human distal gut microbiome. <i>Science</i> <b>312</b> , 1355–1359 (2006).	902
Turnbaugh, P.J. <i>et al.</i> A core gut microbiome in obese and lean twins. <i>Nature</i> <b>457</b> , 480–484 (2009).	786
Qin, J. <i>et al.</i> A human gut microbial gene catalogue established by metagenomic sequencing. <i>Nature</i> <b>464</b> , 59–65 (2010).	776
Ley, R.E. <i>et al.</i> Microbial ecology—human gut microbes associated with obesity. <i>Nature</i> <b>444</b> , 1022–1023 (2006).	734
Ley, R.E. <i>et al.</i> Obesity alters gut microbial ecology. <i>Proc. Natl. Acad. Sci. USA</i> <b>102</b> , 11070–11075 (2005).	668
Frank, D.N. <i>et al.</i> Molecular-phylogenetic characterization of microbial community imbalances in human inflammatory bowel diseases. <i>Proc. Natl. Acad. Sci. USA</i> <b>104</b> , 13780–13785 (2007).	536
Palmer, C. <i>et al.</i> Development of the human infant intestinal microbiota. <i>PLoS Biol.</i> <b>5</b> , e177 (2007).	428
Ley, R.E. <i>et al.</i> Evolution of mammals and their gut microbes. <i>Science</i> <b>320</b> , 1647–1651 (2008).	420

Source: Thomson Reuters Web of Science, accessed 6/03/2013, using title search terms (human microbiota, human microbiome, microbiome, human microbial, human microbes or gut ecology) for the period 2003–2013.