

Supplementary Materials

Gut Health and Cancer: Exploring the Microbiome Connection

Slides presented by **Dr. Sabine Hazan** during the webinar hosted by **Dr. Joseph Varon** on October 14, 2026.

Six slides in the order they appeared: the COVID-19 severity chart, the lifespan curve, the conference poster, the participant table, the abundance table, and the genus-level figure.

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Figure 3 Relative abundance of *Bifidobacteria* in SARS-CoV-2 positive patients compared to high-risk healthy controls, grouped by disease severity

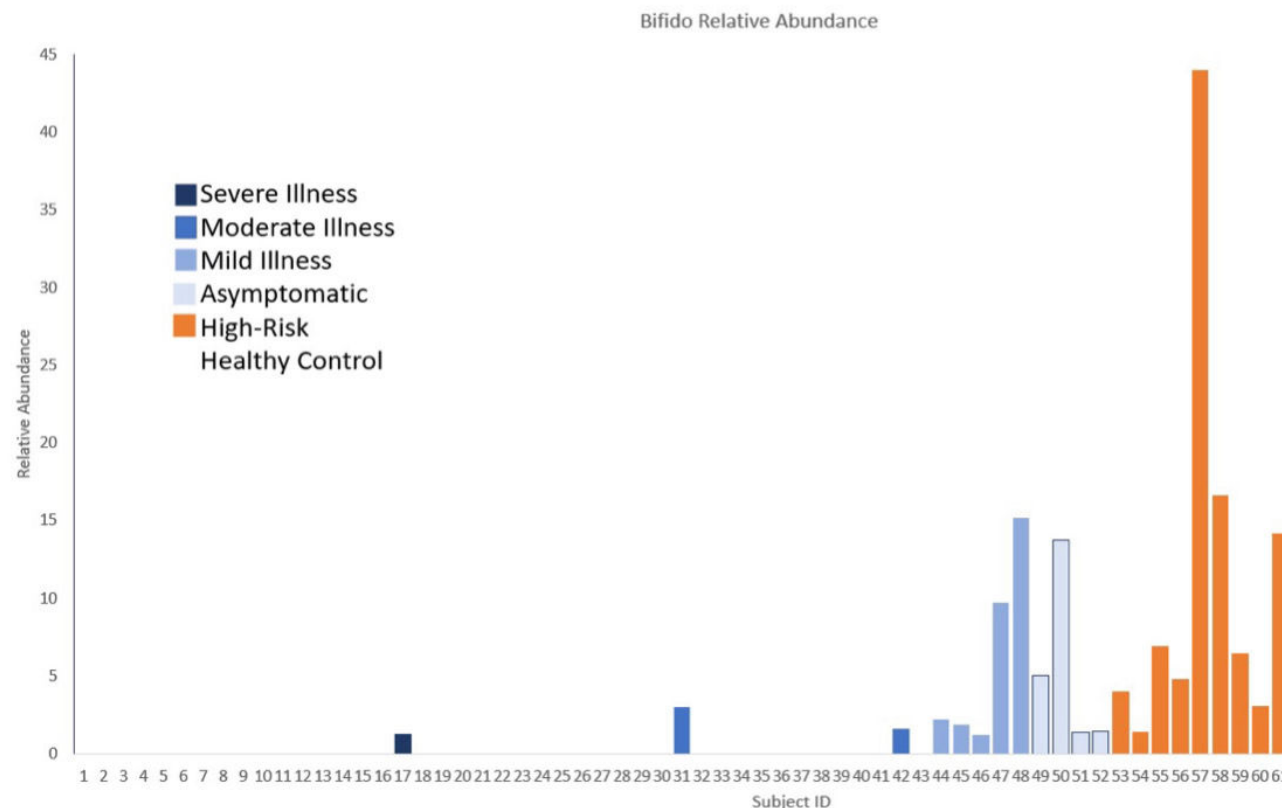
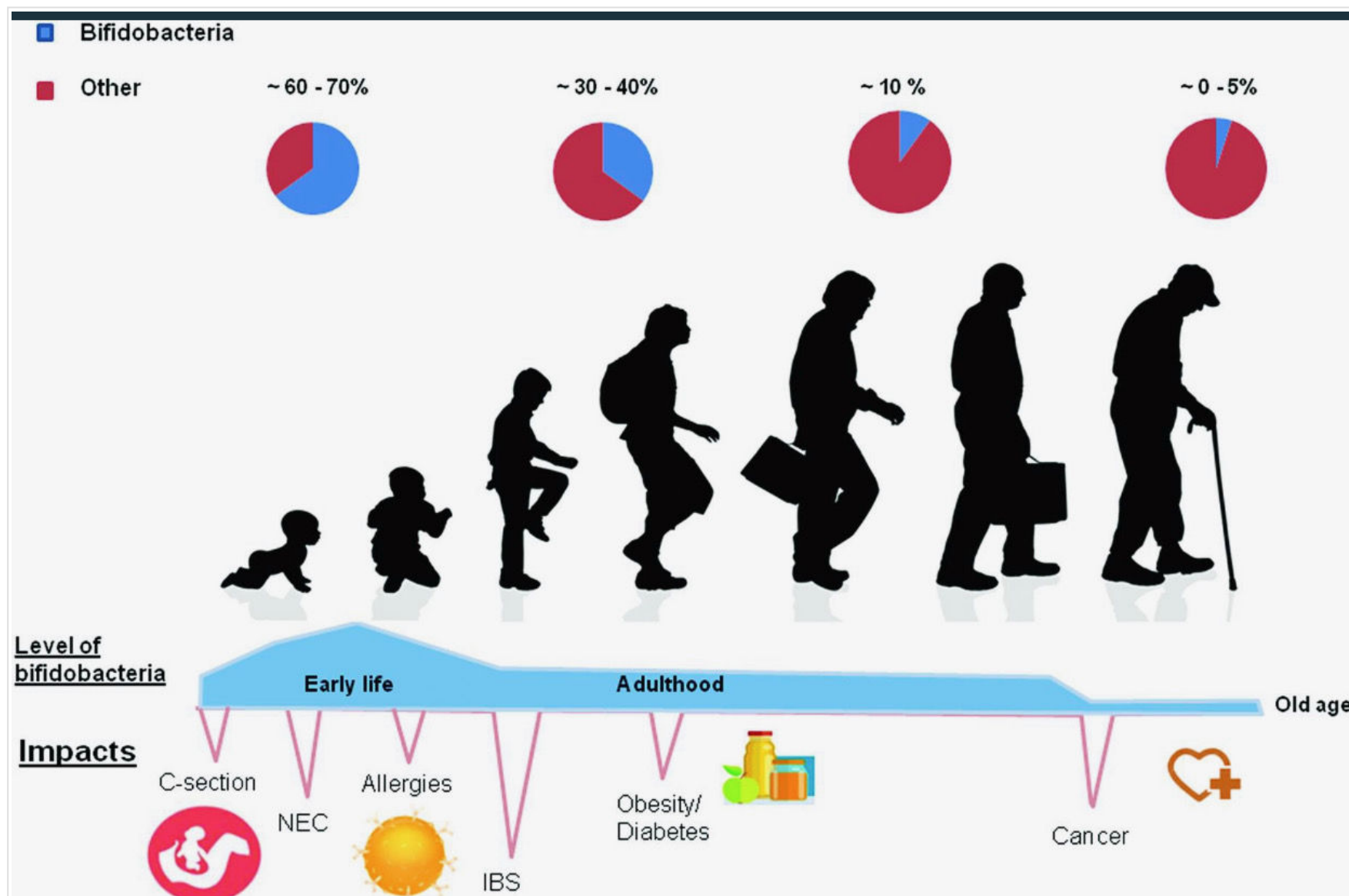


Figure 3. Relative abundance of Bifidobacteria in SARS-CoV-2 positive patients compared to high-risk healthy controls, grouped by disease severity.

The COVID study Dr. Hazan opened with: severe cases at or near zero, exposed-but-never-infected controls high.



Bifidobacteria across the lifespan.

Share of the gut community from early life (about 60 to 70 percent) to old age (about 0 to 5 percent), with the conditions Dr. Hazan associates with its loss along the way.



LOSS OF *BIFIDOBACTERIUM* IN ADULTS WITH A HISTORY OF INVASIVE CANCER

Poster #

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Introduction

Cancer is a family of diseases characterized by uncontrolled growth and spread of abnormal cells. A contributor to the pathogenesis of multiple cancers is chronic inflammation (1), and gut dysbiosis is associated with an increased inflammatory state (2). Commensal bacteria, particularly *bifidobacterium*, appear to provide antitumor protection (3) and may be a novel source of cancer therapeutics. However, associations between gut microbiome composition and cancer occurrence are poorly understood. The purpose of this study was to compare the gut microbiome in adults with and without a history of cancer.

Methods

- Participants
 - Control: adults without a history of cancer
 - Aggressive: adults with invasive cancer
 - Non-aggressive: adults with non-invasive cancer.
- Determined relative abundances of *Bacteroides*, *Faecalibacterium prausnitzii*, and *Bifidobacterium*
- Metagenomic Next Generation Sequencing performed on participant fecal samples
- DNA samples extracted and normalized for library downstream analysis using Shotgun Methodology
- Statistics: Kruskal-Wallis tests and Dunn's multiple comparison tests for overall and between-group differences in the relative abundances of each bacterial colony.

Figure 1. Patients with aggressive cancer had lower *Bifidobacterium* abundance

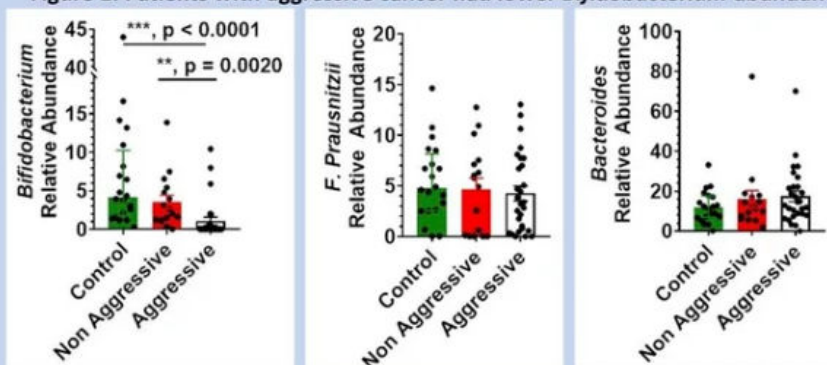


Table 1. Relative Abundance of Bacterial sp.

Study Group	Relative Abundance of <i>Bifidobacterium</i> (Median, IQR)	Relative Abundance of <i>F. prausnitzii</i> (Median, IQR)	Relative Abundance of <i>Bacteroides</i> (Median, IQR)
Control (n = 20)	4.175, 1.723-10.270	4.765, 2.548-8.158	11.780, 6.885-17.760
Aggressive (n = 28)	0.001, 0.000-10.270	3.303, 0.626-7.557	13.820, 8.219-22.250
Non-aggressive (n = 16)	2.338, 1.206-5.268	5.341, 0.026-7.433	11.860, 6.529-17.790

References

- ¹Murata M. Environ Health Prev Med. 2018 Oct 20;23(1):50.
²Zhang X, Coker OO, Chu ES, Fu K, Lau HCH, Wang YX, Chan AWH, Wei H, Yang X, Sung JJY, Yu J. Gut. 2021 Apr;70(4):761-774.
³Matson V, Fessler J, Bao R, Chongsawat T, Zha Y, Alegre ML, Luke JJ, Gajewski TF. Science. 2018; 359(6371):104-108

Results

- Sixty-four participants (20 controls, 28 with aggressive cancer, and 16 individuals with non-aggressive cancer)
- Cancer sites included: appendix, bladder, breast, colon, endometrial, lung, ovarian, prostate, testicular, thyroid, tongue, and uterus, along with lymphomas and unspecified cancer.
- Relative abundance of *Bifidobacterium* was significantly lower in individuals with aggressive cancer
 - vs. controls (p < 0.0001)
 - vs. a non-aggressive cancer (p = 0.0020).
- Relative abundance of *Bifidobacterium* was similar between controls and individuals with non-aggressive cancer (p = 0.692).
- Relative abundances of *Bacteroides* and *F. prausnitzii* were similar between study groups (p = 0.4535 and 0.6201, respectively).

Discussion

Adults with a history of invasive cancer appear to have significantly reduced levels of *Bifidobacterium* compared to adults with a history of non-invasive cancer or no history of cancer. These preliminary results suggest an association between the loss of an important anti-inflammatory and antitumor component of the gut microbiome and invasive cancer. Further research is needed to clearly elucidate how the presence or absence of specific microflora may influence cancer pathogenesis and treatment response, as well as the immunotherapeutic potential of *Bifidobacterium*.

Conference poster: Loss of *Bifidobacterium* in Adults with a History of Invasive Cancer (Hazan and Evans).

The study as first presented. Participant counts on this poster (28 aggressive, 16 non-aggressive, 20 controls) differ from the published tables that follow (25, 15, and 20).

Table 1. Study Participants Characteristics

	Aggressive cancer patients N=25	Non-aggressive cancer patients N=15	Healthy controls (n=20)
Age (mean, SEM, range)	70.95, 13.13, 46-95	63.91, 11.52, 41-79	45.72, 18.40, 20-86
Male (n, %)	9 (36%)	5 (33.33%)	10 (50%)
Female (n, %)	16 (64%)	10 (66.66%)	10 (50%)
Race (n, %)	# Of subjects (%)	# Of subjects (%)	# Of subjects (%)
White	24 (96%)	13 (86.66%)	17 (85%)
Asian	0 (0%)	0 (0%)	3 (15%)
Hispanic	0 (0%)	1 (6.66%)	0 (0%)
Unknown	1 (4%)	1 (6.66%)	0 (0%)
# Of comorbidities	# Of subjects (%)	# Of subjects (%)	# Of subjects (%)
0	21 (84%)	14 (93.33%)	19 (95%)
1	4 (16%)	1 (6.66%)	1 (5%)
Cancer site			
Breast Cancer	7	5	N/A
Lymphoma	5	-	N/A
Colon	4	-	N/A
Bladder	1	-	N/A
Ovarian	3	-	N/A
Lung Cancer	1	-	N/A
Tongue Cancer	2	-	N/A
Thyroid Cancer	1	3	N/A
Testicular Cancer	1	-	N/A
Prostate Cancer	-	3	N/A
Endometrial Cancer	-	1	N/A
Oral Cancer	-	1	N/A
Leukemia	-	1	N/A
T-cell lymphoma	-	1	N/A

Table 1. Study participant characteristics.

Age, sex, race, comorbidities, and cancer site by group. Mean age: 70.95 (aggressive), 63.91 (non-aggressive), 45.72 (controls).

Table 2. Gut Bacteria Relative Abundance in Cancer Patients Versus Controls

	Aggressive cancer patients N=25	Controls N=20	p-value
<i>Bacteroides</i> Mean % (SD)	18.12 (0.1444)	9.62 (0.0627)	0.014990
<i>Bifidobacterium</i> Mean % (SD)	1.20 (0.0274)	6.53 (0.0432)	0.000002
<i>Faecalibacterium</i> Mean % (SD)	4.38 (0.0372)	6.85 (0.0357)	0.014986
<i>Collinsella</i> Mean % (SD)	0.48 (0.0085)	1.84 (0.0203)	0.000634
<i>Roseburia</i> Mean % (SD)	3.08 (0.0597)	3.72 (0.0325)	0.059506
	Non-aggressive cancer patients N=15	Controls N=20	p-value
<i>Bacteroides</i> Mean % (SD)	16.07 (0.1748)	9.62 (0.0627)	0.197277
<i>Bifidobacterium</i> Mean % (SD)	4.24 (0.0454)	6.53 (0.0432)	0.054096
<i>Faecalibacterium</i> Mean % (SD)	5.29 (0.0443)	6.85 (0.0357)	0.271750
<i>Collinsella</i> Mean % (SD)	1.49 (0.0204)	1.84 (0.0203)	0.241565
<i>Roseburia</i> Mean % (SD)	3.60 (0.0305)	3.72 (0.0325)	0.911279

Table 2. Gut bacteria relative abundance in cancer patients versus controls.

Bifidobacterium 1.20 percent in aggressive cancer versus 6.53 percent in controls ($p = 0.000002$); *Collinsella*, *Faecalibacterium*, *Bacteroides*, and *Roseburia* shown for both cancer groups.

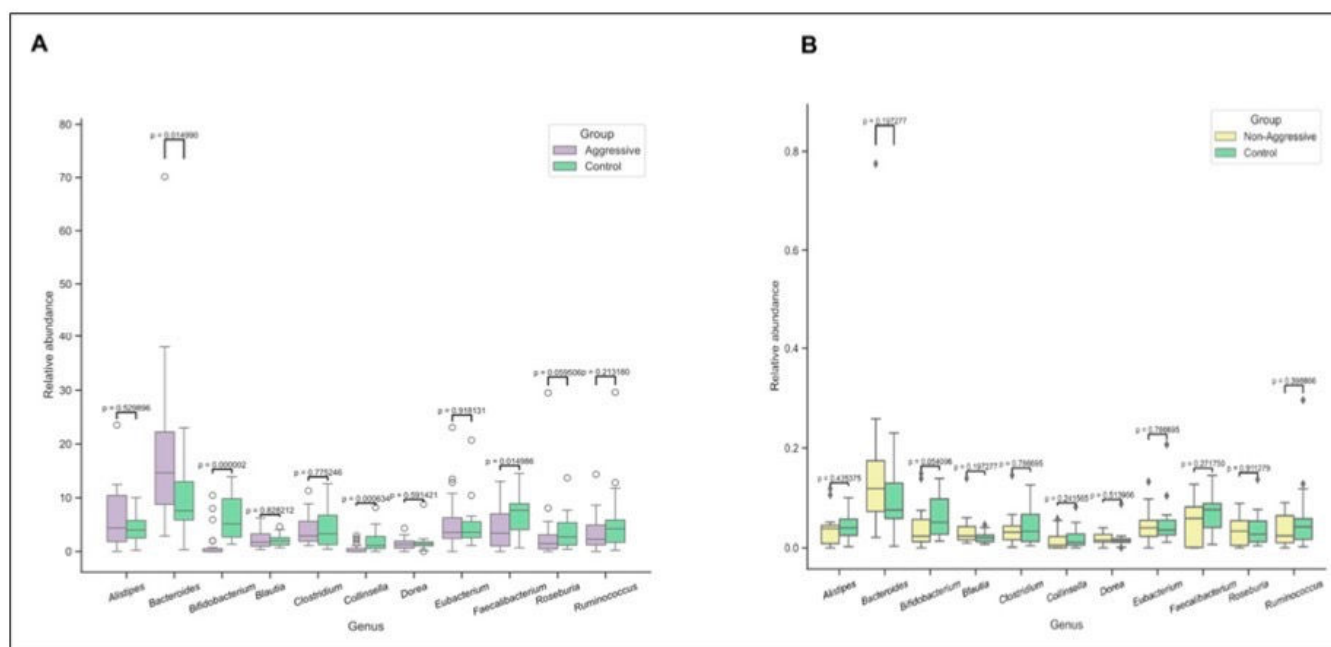


Figure 1. Relative Abundance of Gut Microbiome bacteria at the Genus Level in Adults with Histories of Aggressive Cancer compared to Controls, (A). Relative Abundance of Gut Microbiome bacteria at the Genus Level in Adults with Histories of Non-Aggressive Cancer compared to Controls, (B).

Figure 1. Relative abundance of gut microbiome bacteria at the genus level.

(A) Adults with histories of aggressive cancer compared to controls. (B) Adults with histories of non-aggressive cancer compared to controls.