

Intestinal anaerobic bacteria in early rheumatoid arthritis

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FINLAND

Reactive arthritis

- due to mucosal infections
(Salmonella, Shigella,
Yersinia, Chlamydia)**
- degradation products of
causative microbes in
synovium**

Human intestinal flora

- over 400 bacterial species,
most anaerobic
- 1.5 kg bacterial mass/300 m²
- degradation products (muramic acid)
within circulating blood cells
(Lehtonen et al, J Infect Dis 1995,
Eur J Clin Invest 1997)

Human intestinal flora

- **composition influenced by host's genetics** (Toivanen et al, Infect Immun 2001; Vaahтовuo et al, Anton Leeuw 2001)
- **contains species with cell walls inducing experimental arthritis** (Toivanen, J Autoimmun 2001)
- **closely related bacteria, even within a species, may be arthritogenic or nonarthritogenic** (Zhang et al, Infect Immun 2001)

INTESTINAL FLORA IN EARLY RHEUMATOID ARTHRITIS

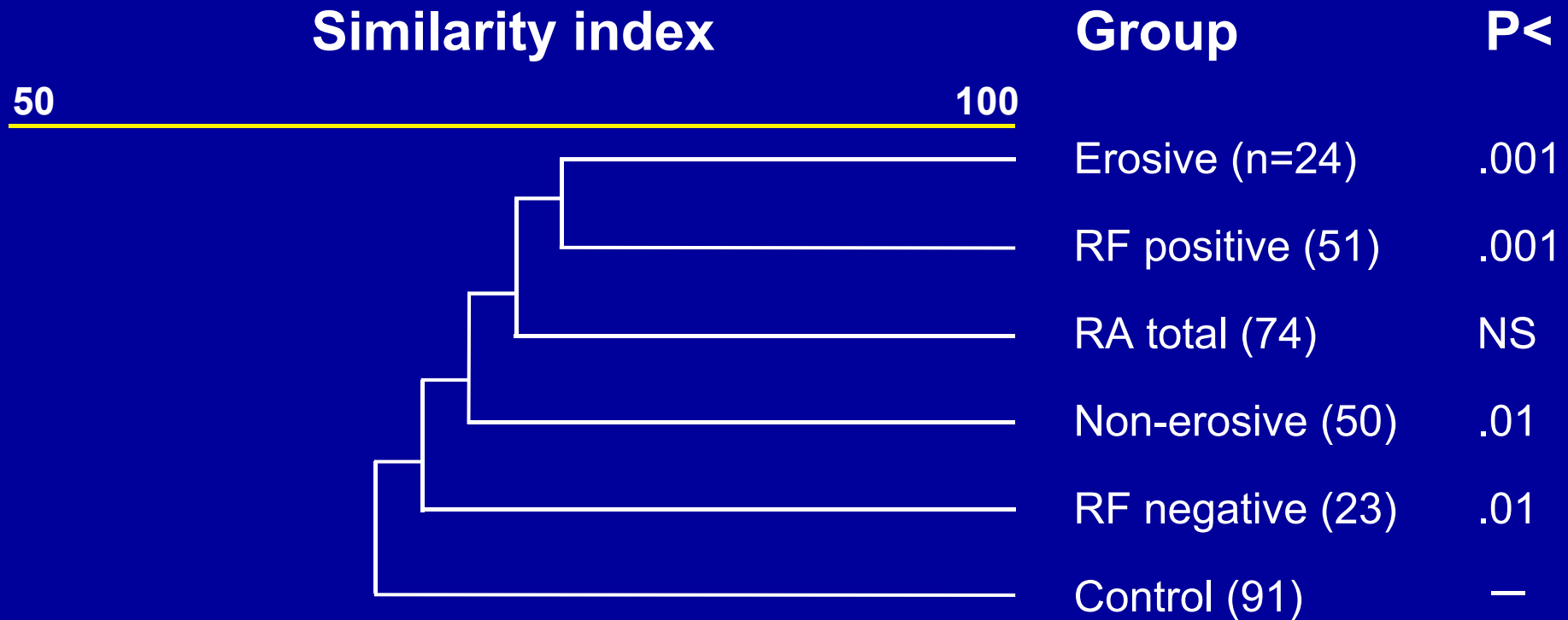
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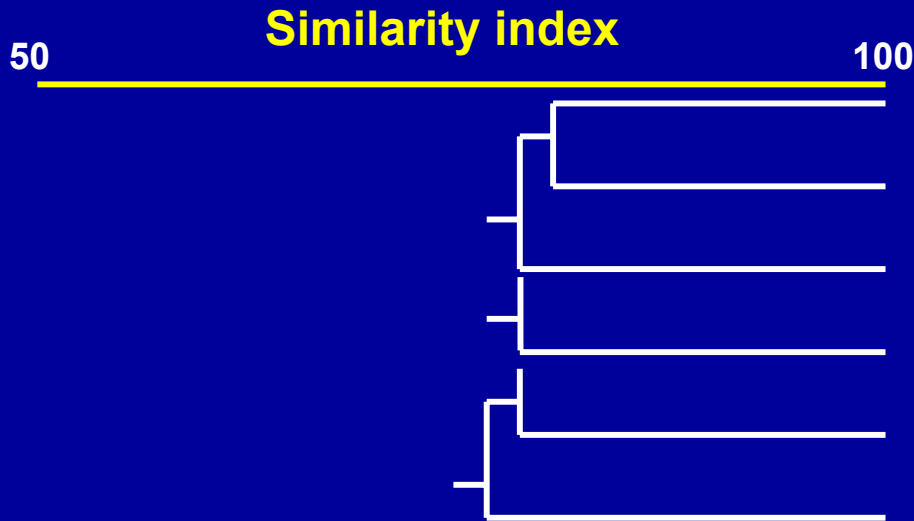
SUMMARY

To study the role of intestinal flora in the pathogenesis of RA, we have applied computerized **gas-liquid chromatography** (GLC) for **bacterial cellular fatty acids (CFAs)** present in the stool. The CFA spectra represent **the total composition of bacterial CFAs in a faecal sample**. Correlation and cluster analysis of CFA spectra gathers samples with quantitatively and...

Bacterial fatty acids (stool) in RA

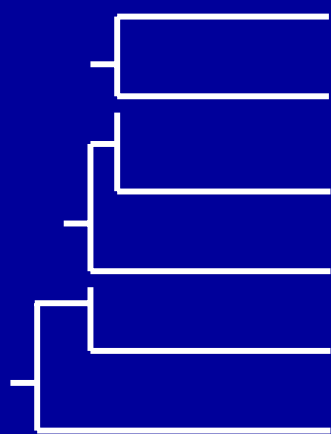


Aerobic bacteria



Staphylococcus epidermidis

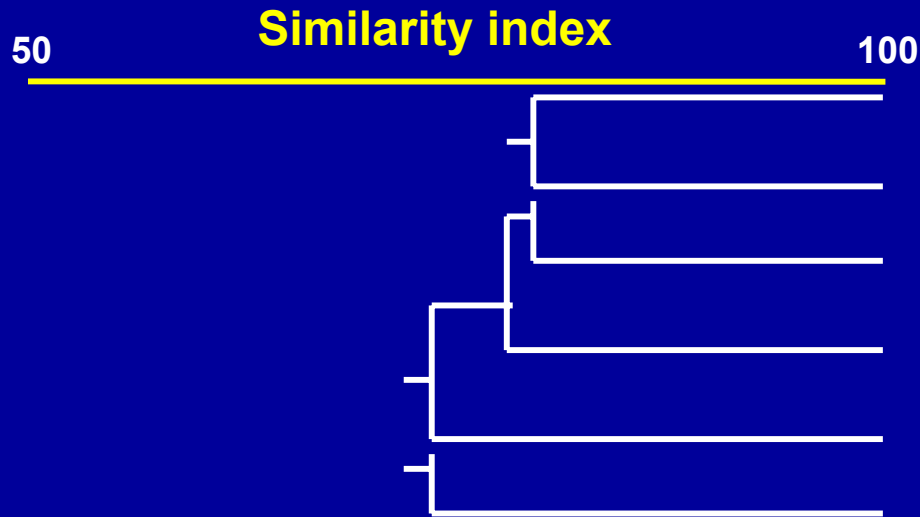
Group	P
Erosive (<i>n</i> =24)	NS
RF positive (51)	NS
RA total (74)	NS
Control (91)	-
Non-erosive (50)	NS
RF negative (23)	NS



Lactobacillus sp

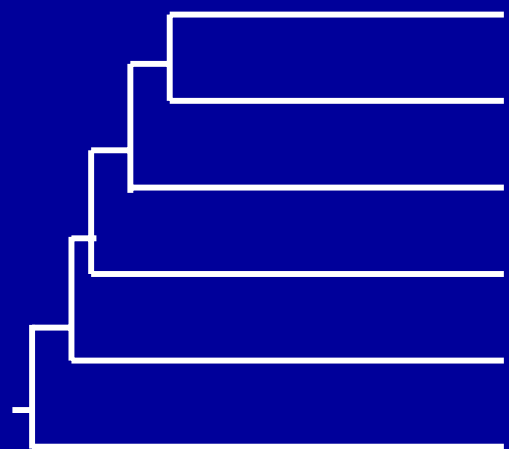
Erosive (<i>n</i> =24)	NS
RF positive (51)	NS
RA total (74)	NS
Control (91)	-
Non-erosive (50)	NS
RF negative (23)	NS

Anaerobic bacteria



Fusobacterium nucleatum

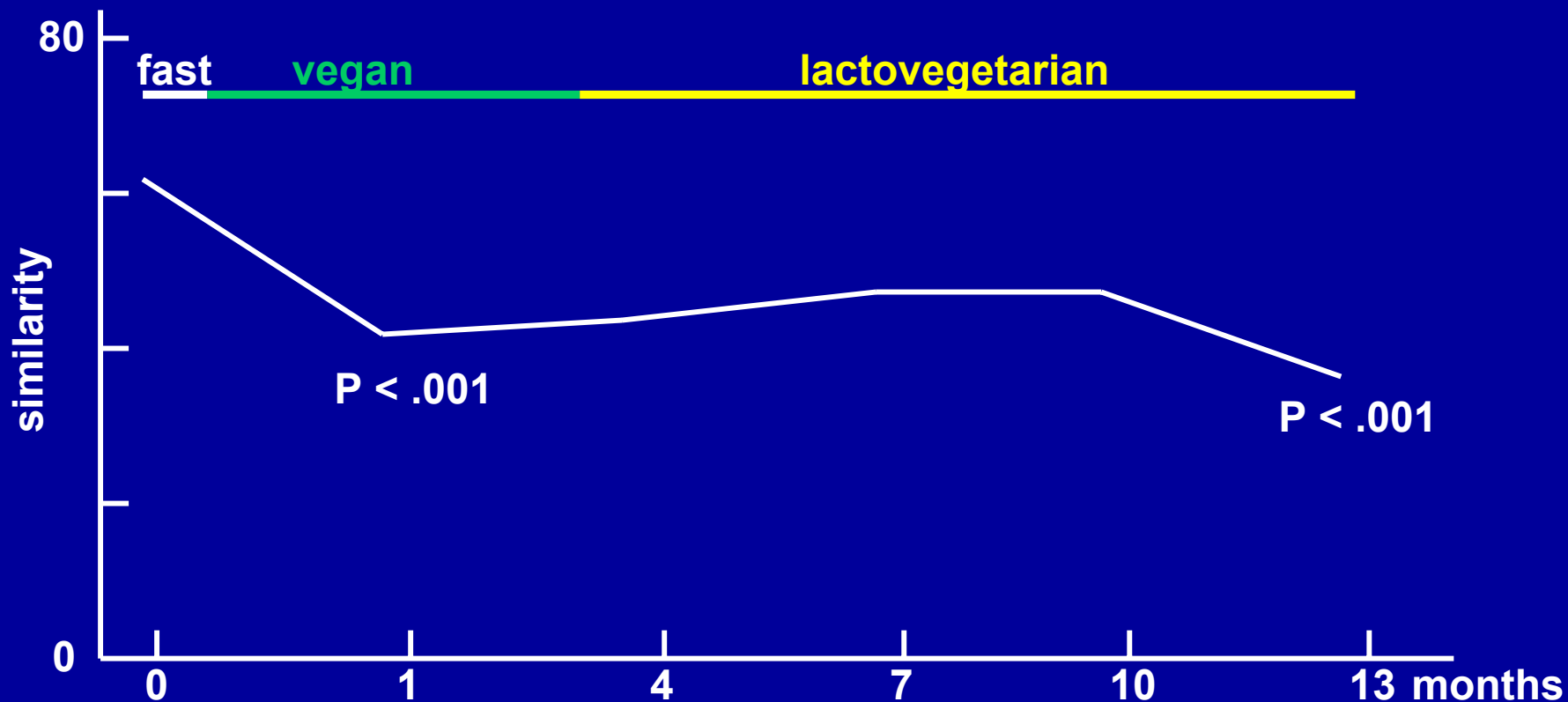
Group	P
Erosive (<i>n</i> =24)	.001
RF positive (51)	.001
RA total (74)	NS
Non-erosive (50)	.01
RF negative (23)	.01
Control (91)	-



Peptostreptococcus anaerobius

Erosive (<i>n</i> =24)	.001
RF positive (51)	.001
RA total (74)	NS
Non-erosive (50)	.01
RF negative (23)	.01
Control (91)	-

Oslo dietary trial in RA. Gut flora in patients improving vs. not improving.



Intestinal flora / 16S rRNA oligonucleotide probes

	RA	Controls
No. (m/f)	25 (10/15)	23* (4/19)
Age, yrs	63.4 ± 12.5	49.7 ± 10.6
Disease duration		
<6 months	17	5
6 months – 1 year	6	3
>1 year	2	15
RF positive / tested	15 / 23	1 / 21
ESR	37.6 ± 22.8	13.3 ± 16.4

*18 fibromyalgia, 5 degenerative joint disease

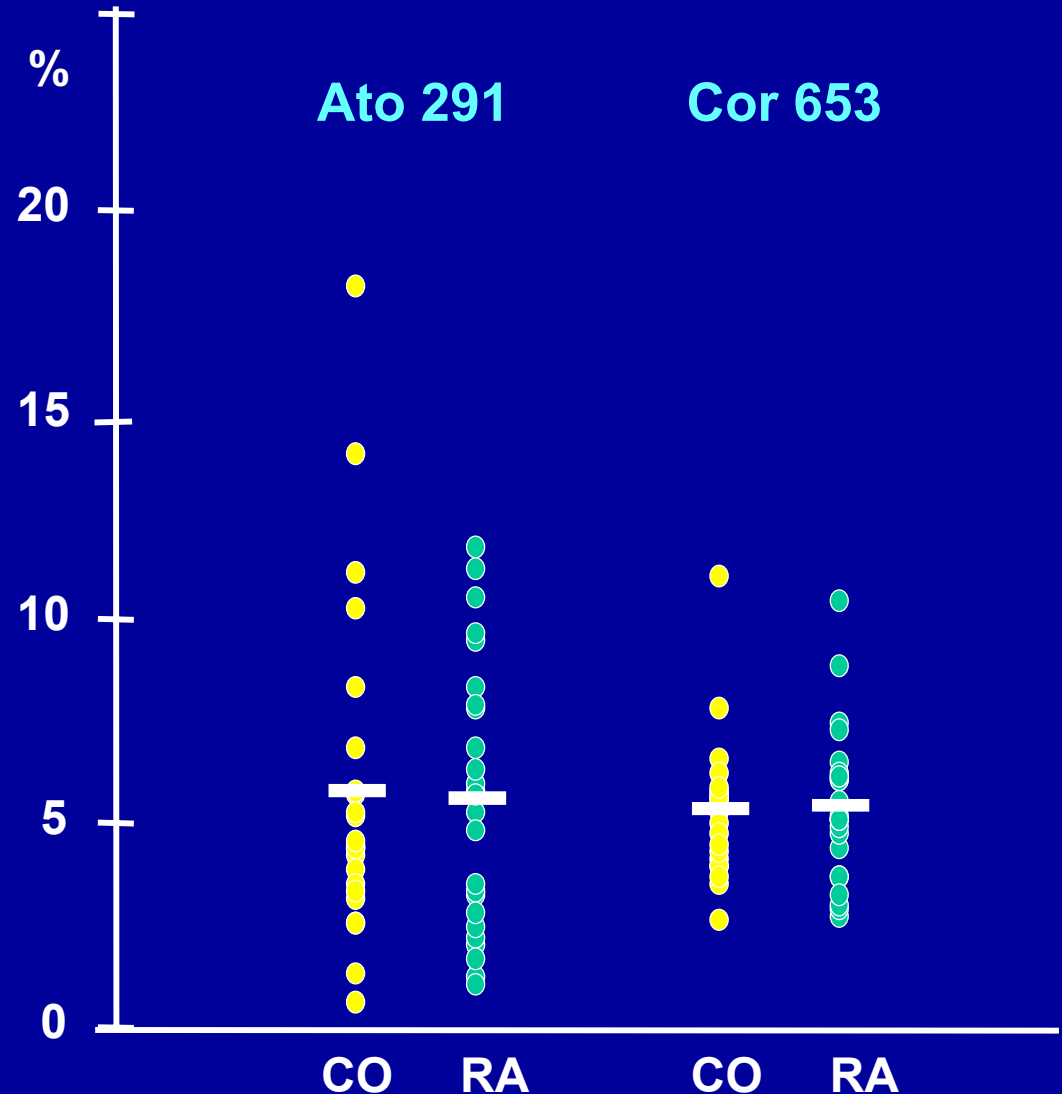
Intestinal flora / 16S rRNA oligonucleotide probes

Ato 291

Atopium
Collinsella
Coriobacterium
Cryptobacterium curtum
Eggerthella lenta
Eubacterium lentum

Cor 653

Collinsella
Coriobacterium

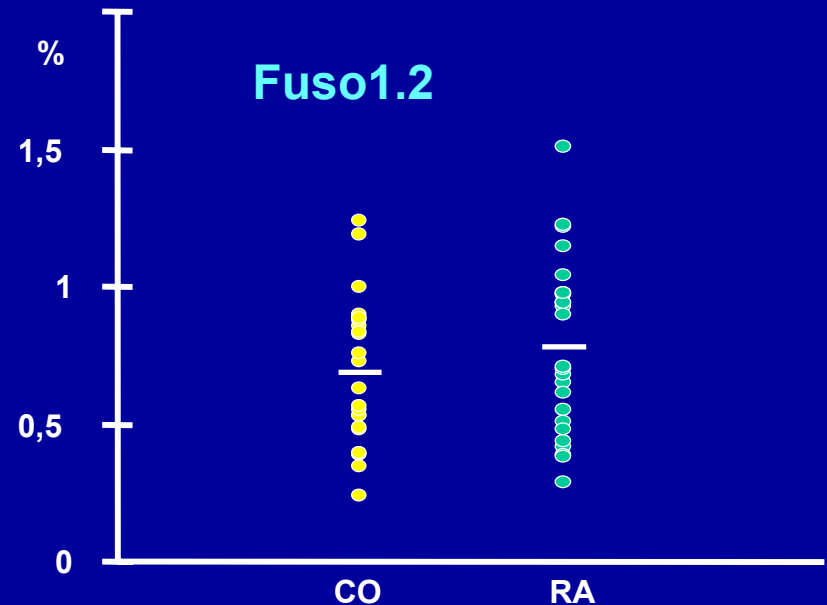
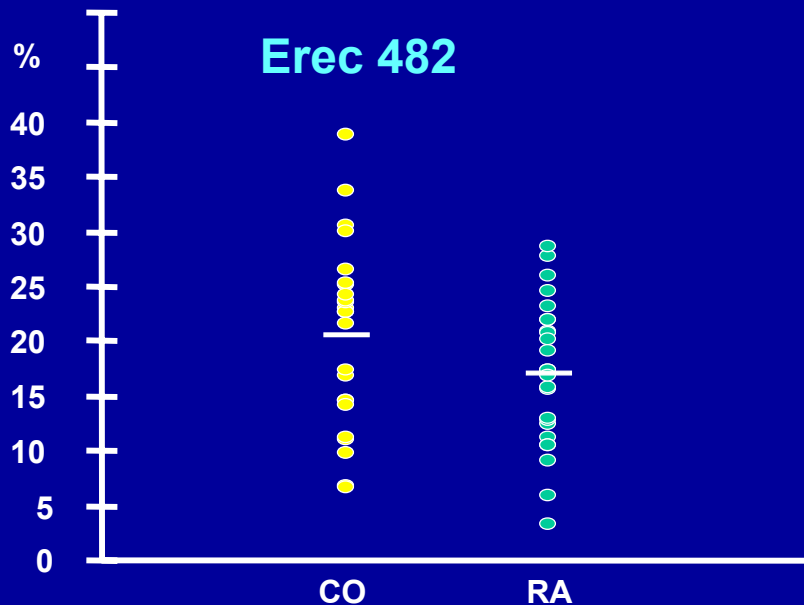
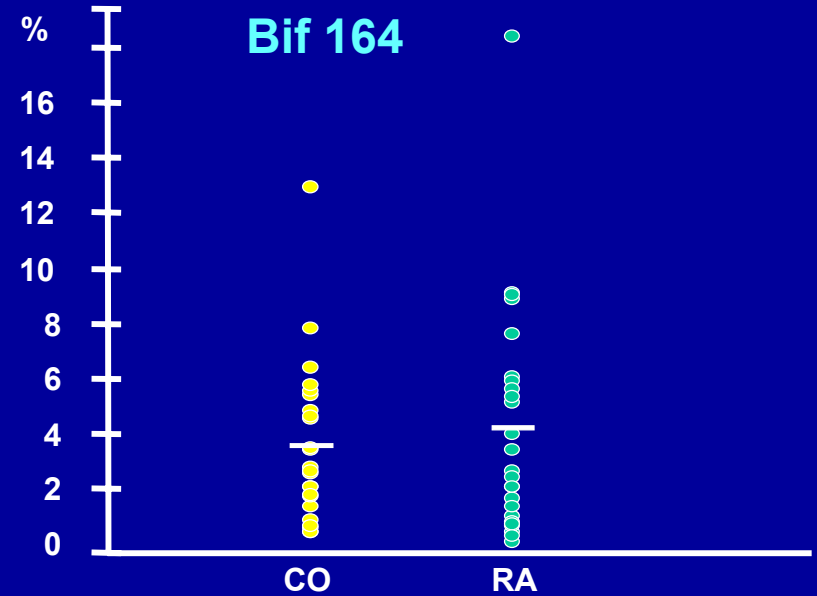


Intestinal flora / 16S rRNA oligonucleotide probes

Bif 164
Bifidobacterium

Evec 482
Eubacterium
Clostridium
Butyrivibrio
Ruminococcus

Fuso 1.2
Fusobacterium



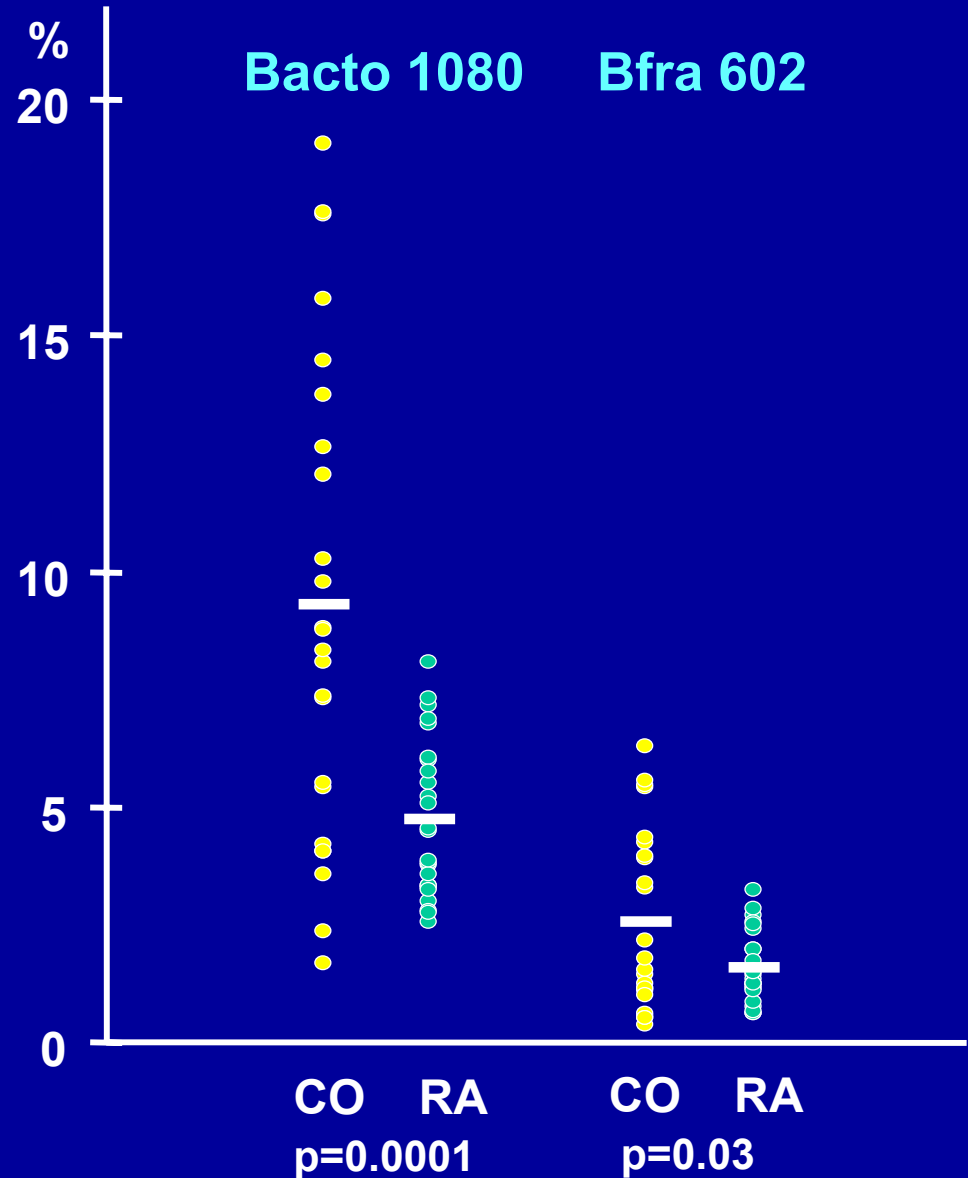
Intestinal flora / 16S rRNA oligonucleotide probes

Bacto 1080

Bacteroides
Porphyromonas
Prevotella

Bfra 602

Bacteroides fragilis group
B. thetaiotaomicron
oratus
caccae
acidofaciens
fragilis
uniformis
vulgatus
stercoris
eggerthii



Conclusions

- Anaerobic intestinal flora in RA is different from that in the controls
- Number of bacteria in Bacteroides-Prevotella- Porphyromonas group is half that of the controls

Molecular Analysis of Commensal Host-Microbial Relationships in the Intestine

**Lora V. Hooper, Melissa H. Wong, Anders
Thelin, Lennart Hansson, Per G. Falk,
Jeffrey I. Gordon**

**We colonized germ-free mice with *Bacteroides
thetaiotaomicron*. This commensal bacterium modulates
expression of mucosal barrier fortification ...**

SCIENCE VOL 291, 2 FEBRUARY, 2001

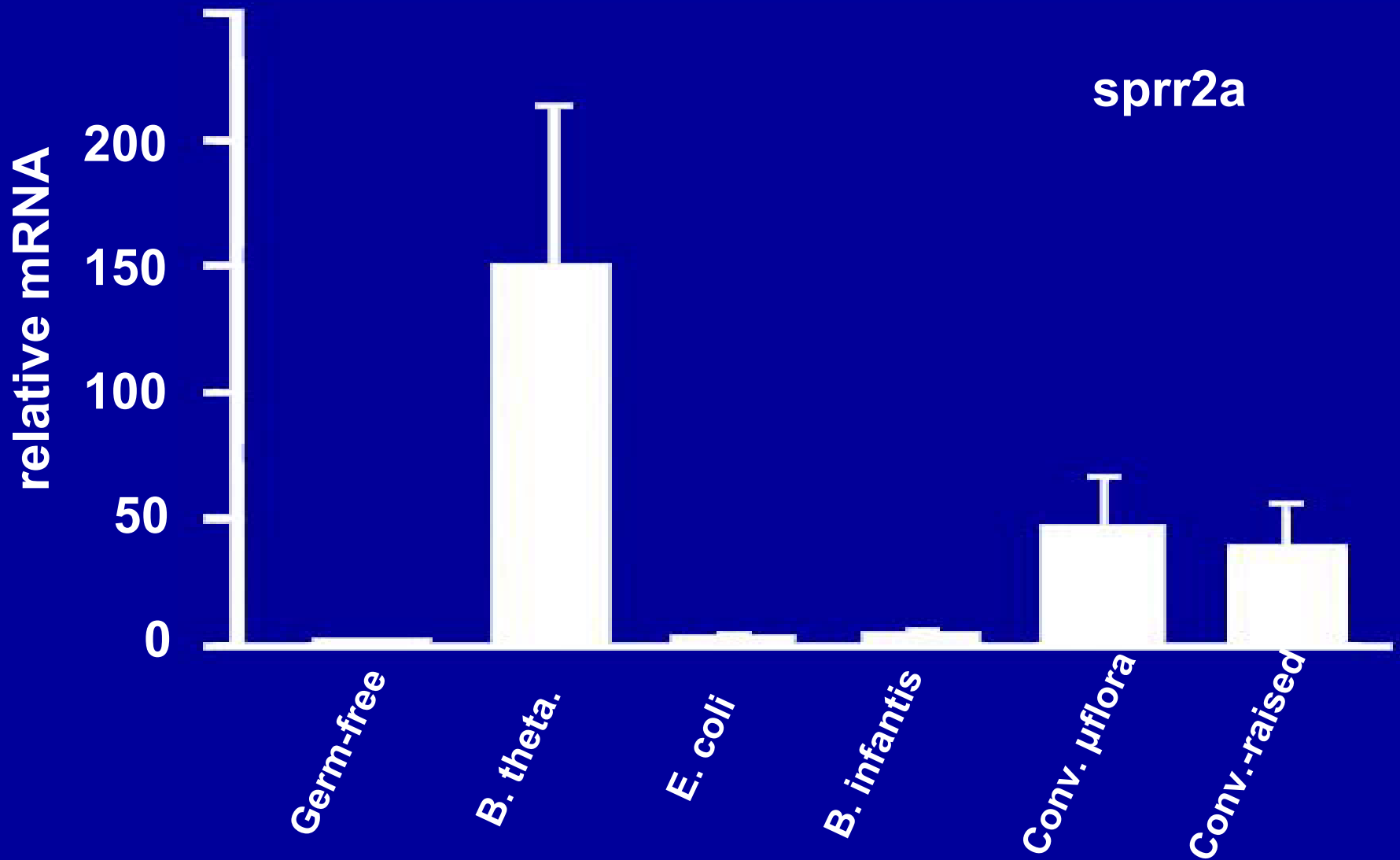


Fig. 2. Specificity of host responses to colonization with different members of the microflora.