in the cohort. The incidence of oesophageal malignancy overall (per 100 person years of follow-up) was 0.26; for patients with intestinal metaplasia the risk was 0.40 (95% confidence interval (CI) 0.26 to 0.59) and for those without intestinal metaplasia the risk was 0.06 (95% CI 0 to 0.32). In other words, if intestinal metaplasia was absent in biopsy specimens, the risk of oesophageal malignancy was not significantly higher than that in the normal population. Further, we found 93% concordance among the 2969 patients between intestinal metaplasia status on the first biopsy and that on any subsequent biopsy (unpublished data). Intestinal metaplasia seems to be either there from the start or absent. Given that these data are derived from ''real world practice'', where probably few biopsy specimens per patient were taken and hence sampling error might have occurred, it is reassuring to find that the risk of malignancy in patients in whom intestinal metaplasia was not shown was low. These patients may have a ''patchy'' distribution of intestinal metaplasia in the segment of columnar mucosa that is biologically distinct from those where the distribution of intestinal metaplasia is uniform, but this is purely speculative.

Patients with Barrett's oesophagus are at low risk of oesophageal adenocarcinoma; refinement of surveillance programmes is needed to focus resources on those most likely to benefit from surveillance—perhaps concentrating on those patients in whom intestinal metaplasia is evident at initial endoscopy is one way to do this?

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Effect of bowel preparation and colonoscopy on post-procedure intestinal microbiota composition

There is growing interest in the potential contributions of distortions in intestinal microbiota to human intestinal disease.[1–5] Our understanding of intestinal microbiota complexity and dynamics is evolving, but is still in its infancy.[6–8] We have previously shown that microflora profiles are (1) unique to an individual; (2) stable over a period of at least 8 weeks; and (3) not affected by minor short-term changes in diet.[9]

Little is known about (1) changes in microbiota in patients undergoing a screening colonoscopy; (2) if and when microbiota returns to its normal pre-colonoscopy composition; and (3) whether short-term distortions increase disease risks.

We investigated microbiota changes in five patients undergoing screening colonoscopy. Colon preparation was adequate and polyps were detected in two patients (A and E); congested mucosa with chronic inflammation and lymphatic infiltrate was detected in patient B, and the remaining two patients (C and D) had no abnormalities.

Analysis of the faecal microbiota by denaturing gradient gel electrophoresis (DGGE) using primers against both the V3 and the V6–V8 regions showed unique profiles for each patient (fig 1). In three of the five patients, the two profiles detected after the colonoscopy were more similar to each other and clearly different from the precolonoscopy profile; in the two other patients, we found less of a difference between the precolonoscopy and postcolonoscopy profiles.

Archaeal DNA was detected by PCR in one patient and was not detected in three patients at all time points; in the remaining patient, it was detected only in the sample collected following the colonoscopy. 7α-Dehydroxylase was detected in four of five patients: in two patients at all three time points and in the other two patients only after the colonoscopy. Dissimilatory sulphite reductase was detected in three patients: in patient D before and after 6–8 weeks, in patient E at both time points after the colonoscopy and in patient C only once after the colonoscopy.

Fluorescent in situ hybridisation analysis indicated considerable variation in the proportions of bacteria hybridising to the

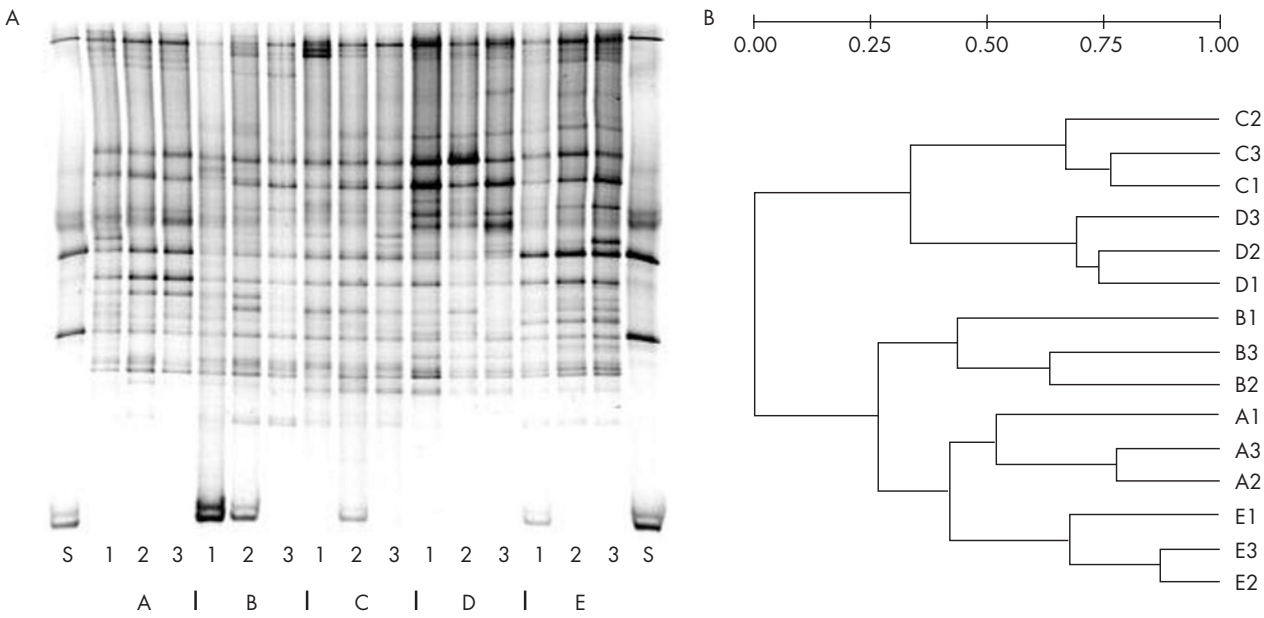

Figure 1 (A) Denaturing gradient gel electrophoresis (DGGE) profiles of five patients before and after colonoscopy. Each lane on the gel represents the faecal microbiota profile from a patient at one time point. Each band represents a molecular species characterised by unique denaturation characteristics. S, standard lane; A–E, patients at time points 1, 2 and 3. (B) Dendogram of the DGGE profiles from five patients (A–E) before (A–E1) and after (A–E2 and A–E3) colonoscopy (Ward's algorithm, Dice coefficient). Branch length indicates differences in the correlation coefficients in the distance matrix, generated using the Diversity Database software (Bio-Rad, Hercules, CA, USA).

Table 1 Proportion of bacterial groups (number of cells hybridising to probe/total number of 4′,6-diamidino-2-phenylindole-2HCl-stained cells) as determined by fluorescent in situ hybridisation

Sample		FISH					PCR		
		Erec482	Bac303	Bif164	LAB158	EC1531	Archaea	7αDH	DSR
A	1	0.11	0.31	0.04	0.012	ND	−	−	−
	2	0.24	0.42	0.06	0.019	ND	+	+	−
	3	0.21	0.97	0.06	0.013	ND	−	−	−
B	1	0.06	0.09	0.02	0.009	D	−	−	−
	2	0.15	0.27	0.05	0.041	D	−	−	−
	3	0.33	0.21	0.01	0.013	D	−	+	−
C	1	0.15	0.07	0.04	0.008	D	+	−	−
	2	0.11	0.05	0.04	0.007	ND	+	−	+
	3	0.28	0.13	0.05	0.049	D	+	−	−
D	1	0.17	0.33	0.05	0.016	ND	−	+	+
	2	0.16	0.22	0.02	0.022	D	−	+	−
	3	0.67	0.32	0.04	0.034	D	−	+	+
E	1	0.28	0.09	0.04	0.020	ND	−	+	−
	2	0.15	0.14	0.02	0.005	ND	−	+	+
	3	0.16	0.23	0.03	0.005	ND	−	+	+

Bac303, *Bacteroides-Prevotella* group; Bif64, *Bifidobacterium*; D, detected; 7αDH, 7α dehydroxylases; DSR, dissimilatory sulphite reductases; EC1531, *Escherichia coli*; Erec482, *Eubacterium rectale-Clostridium coccoides* group; FISH, fluorescent in situ hybridisation; LAB158, *Lactobacillus* and *Enterococcus* group; ND, not detected; PCR, polymerase chain reaction with primers against archaea; +, detected; −, not detected.

group-specific and species-specific probes, with no trends detected in precolonoscopy and postcolonoscopy samples.

We analysed 96-clone libraries from all three stools per patient (GenBank DQ904637–DQ905931, DQ905933–DQ905956). By using the ∫–Libshuff programme,[10] we determined which of the libraries originated from the same source, and whether they were subsets or were derived from different sources. For none of the patients did all three libraries derive from the same source, indicating variation in microflora composition. For patient A, the libraries before and 6–8 weeks afterwards originated from the same source ($\Delta C_{X1,Y3}$ and $\Delta C_{Y1,X3}$ >0.009), and the library before was a subset of the library detected 2–4 weeks afterwards. For patient B, all libraries originated from different sources (all $\Delta C_{X,Y}$ and $\Delta C_{Y,X}$ <0.009). For patient C, the libraries at 2–4 and 6–8 weeks after the procedure originated from the same source ($\Delta C_{X2,Y3}$ and $\Delta C_{Y2,X3}$ >0.009). For patient D, the library generated after 6–8 weeks was a subset of both other libraries ($\Delta C_{Y1,X3}$ and $\Delta C_{Y2,X3}$ >0.009). For patient E, the libraries after the procedure were a subset of the precolonoscopy library ($\Delta C_{Y1,X2}$ and $\Delta C_{Y1,X3}$ >0.009) and the library 2–4 weeks afterwards was a subset of that after 6–8 weeks ($\Delta C_{Y3,X2}$ >0.009).

Our observations with different methods did not agree in many details, probably due to different biases inherent in each method. However, all methods indicated that microbiota composition is disturbed in patients undergoing screening colonoscopy, which might have implications for potential health effects that we do not yet understand. Simple DGGE profiling, with universal and group-specific primer sets, might currently be most efficient for monitoring the complex human microbiota composition over time. There is a clear need for improving our understanding of the dynamics in microbiota composition.

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BOOK REVIEW

The political economy of healthcare; a clinical perspective

Authored by Julian Tudor Hart. Published by The Policy Press, Bristol, £14.99 (hardback £55), pp 336. ISBN 1-86134-808-8

At last, a coherent alternative to the healthcare agenda promoted by all political parties! A distinguished general practitioner draws on erudite sources and vivid personal experience to analyse British healthcare. The core principle of the National Health Service (NHS), he argues, is an exponentially expanding knowledge base, which has been translated to benefit everyone within a framework of consensus and solidarity (despite the odd greedy doctor or patient). The NHS transformed British hospitals ''by distributing medical labour away … from university cities to provide all … specialty functions everywhere in Britain''. Will profit-driven multinationals (which are substantially more expensive to administer than state-run healthcare) ensure that this continues? No other economy has achieved comprehensive healthcare for so little. Critics of the old NHS