Table A

Mean values	Control	Active/ Short	Inactive/ Short	Inactive/ Long	p value
t-STAT3, % IECs ⁺	23.4	79.3	35.2	61.3	0.001
p-STAT3, % IECs⁺	0	59.4	15.4	32.5	0.001
IL-1β (pg/ml)	0	0.6	0.1	14.3	0.01
IL-2	0	9.3	4.8	383.5	0.001
IL-6	1.1	12.1	6.6	43.8	0.001
IL-8	10	53.5	16.7	132.1	0.001
IL-17	0	2.9	1.1	101.1	0.001
TNF-α	0.2	45.7	9.4	3.7	0.001

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 $\begin{array}{l} \mbox{Genetic polymorphism of inflammation response} \\ \mbox{genes TNF-α -308g > A and TL-8 -251 T > A \\ \mbox{and their influence on colorectal cancer} \\ \mbox{predisposition risk in malaysian population} \\ \mbox{MM AMINUDIN,}^1 \mbox{ MS SITINURFATIMAH,}^1 \\ \mbox{AA HMADAIZAT,}^1 \mbox{ RN VENKATESH,}^3 \mbox{ BM BISWAL,}^2 \\ \mbox{Z ZAIDI,}^4 \mbox{ AMS SHANWANI,}^4 \mbox{AH MOHAMMAD RADZI,}^5 \\ \end{array}$

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Introduction Several lines of evidence including animal models and epidemiological observations suggest that a continuous inflammatory condition predisposes to CRC. Study was designed to investigate the association of IL-8T251A and TNF- α -308G > A with CRC susceptibility risk. *Method* In this case control study, peripheral blood samples of 118 normal controls and 116 CRC patients were collected, genomic DNA was extracted and genotyped employing allele specific PCR.

Results Investigation on the association of the variant genotypes with CRC susceptibility risk, IL-8T251A showed significantly increased risk with OR 3.524 (CI 1.318–9.424, P = 0.012) and TNF- α -308G > A showed significantly increased risk with OR 2.622 (CI 0.985–6.942, P = 0.050). The risk was pronouncedly higher when the homozygous variant genotypes were combined. (OR 9.000 CI 1.087–66.914, P = 0.041).

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Genetic polymorphisms of xenobiotic metabolizing enzymes cytochrome P450 1A2 in Malaysian population and colorectal cancer susceptibility risk

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Introduction Genes encoding xenobiotic metabolizing enzymes especially CYP1A2 play an important role in determining the out come of carcinogen exposure and Colorectal Cancer susceptibility risk. Functional polymorphisms of G3860A, T739G and C729T of CYP1A2 gene have been identified.

Aims A case control study was designed to genotype the Malaysian normal controls and CRC patients to determine the variant allele frequencies of three polymorphisms of CYP1A2 and to evaluate whether variant genotype has any association either singly or in combination with CRC susceptibility risk.

Material & method Genotyping of the 3 polymorphisms (G3860A, T739A & C729T) CYP1A2 genes was performed using polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) on 111 sporadic histopathologically confirmed CRC patients and 123 normal healthy controls.

Result When the 3 polymorphisms G3860A, T739G and C729T were analyzed singly, there was no significant association. When the risk association was evaluated using combination genotypes, the combination of G3860A / T739T genotype showed statistically significant risk with OR 1.75.

Endoscopy

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Quantitative perfusion analysis with contrastenhanced harmonic EUS facilitate distinguishing autoimmune pancreatitis (AIP) from pancreatic cancer

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Background AIP may present as mass lesion and be misdiagnosed as pancreatic cancer (PC). Recently, contrast-enhanced harmonic EUS (CH-EUS) with second generation ultrasonographic contrast (Sonazoid) was shown to be useful for diagnosis of pancreaticobiliary malignancies.

Study aims To evaluate if the quantitative perfusion analysis with CH-EUS facilitate differentiation of AIP from PC.

Methods Consecutive patients with PC or AIP who underwent CH-EUS from January 2009 to March 2010 were analyzed. An electronic radial echoendoscope, ALOKA ProSound alpha10 processor and Sonazoid were used. CH-EUS was performed with intravenous administration of 0.015 ml/