in Drosophila for signaling pathways that regulate autophagy under hypoxic conditions – a state associated with many solid tumours. This identified a cell autonomous mechanism in human tumour cells which selectively promotes hypoxia associated autophagy and cell survival. Theses findings therefore represent a paradigm for the targeting of cancer-associated autophagy to cause tumour cell death.
The mechanism of action and context-specific nature of this and other factors identified from our screens will be described and the potential implications for the development and treatment of cancer will be discussed.

Sunday 27 June 2010 17:55–18:45

Radium Hospital Foundation Lecture: Genetic instability

52 Early epigenetic and genetic events in breast carcinogenesis

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The active acquisition of epigenetic changes is a poorly understood but important process in development, differentiation, and disease. Our work has recently demonstrated that repression of the p16/pRb pathway in human epithelial cells, a condition common to stem cells and many tumour cells, induces dynamic epigenetic remodeling resulting in the targeted methylation of selected CpG islands. We hypothesized that cells in this epigenetically-plastic state can be programmed by the microenvironment to acquire epigenetic changes that promote tumourigenesis. Normal human mammary epithelial cells (HMEC), and HMEC with repressed p16 were first transduced with constitutively active Ha-rasV12. In order to mimic the secretory aspects of the extracellular environment, the cells were subsequently cultured in a serum-rich environment. When p16-repressed cells were challenged with oncogenic stress, they failed to undergo the classic proliferative arrest as documented in normal cells. When further stressed by being cultured in a serum-rich environment, they spontaneously immortalized and exhibited phenotypic changes indicative of epithelial to mesenchymal transition (EMT). The EMT was accompanied by *de novo* methylation of the E-cadherin promoter and increased motility. These data demonstrate that signals from the microenvironment can induce phenotypic and gene expression changes that result in *de novo* epigenetic alterations important in tumour progression.

Sunday 27 June 2010 09:45–17:30

Poster Session

General, Molecular and Genetic Epidemiology

53 Assessing interaction between established breast cancer genetic susceptibility loci and selected non-genetic risk factors using data from the Breast Cancer Association Consortium

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Background: Breast cancer is known to have both a genetic and non-genetic etiology. A number of common genetic susceptibility variants has recently been identified by predominantly genome-wide approaches, but it is not known whether the loci involved act independently of established non-genetic risk factors. We aimed to assess interaction between genetic and non-genetic risk factors in the Breast Cancer Association Consortium. We focused on age at menarche, ever having had a live birth, number of live births, age at first birth and body mass index and their interaction with single SNPs within each of 10 established susceptibility loci (CASP8, FGFR2, 8q24, TOX3, MAP3K1, LSP1, 2q35, 5p12, SLC4L1 and COX11) and two additional SNPs (TGFB1 and ESR1) with less clear evidence of association.
Material and Methods: Per-allele odds ratios (OR) for SNPs were estimated by categories of non-genetic variables using logistic regression adjusted for study, and two-way gene-environment interaction was tested for by fitting a single-parameter interaction term for departure from log-additive effects. These analyses were applied to data from 14,600−29,991 cases and 16,188−30,990 controls from the Breast Cancer Association Consortium.
Results: No statistical evidence of interaction was observed beyond that expected by chance, given the number of tests carried out. The analyses were repeated using data from 11 population-based studies only, with similarly null results for interaction.
Conclusions: This is by far the largest study to assess interaction between established common genetic risk factors for breast cancer and age at menarche, parity-related variables and body mass index. Further studies of very even larger samples are required to determine whether these common susceptibility variants are associated with different risks of breast cancer depending on other non-genetic factors.

54 Screening for large genomic rearrangements of the BRIP1 and CHK1 genes in Finnish breast cancer families

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Background: In search for susceptibility genes that could explain a portion of familial breast cancer clustering in Finland, we set out to evaluate the presence of large genomic rearrangements in two candidate genes. BRIP1 (alias FANCJ or BACH1) is a BRCA1 associated protein mutated in a fraction of familial breast cancer and Fanconi anemia (FA) cases. The role of large *BRIP1* deletions in breast cancer predisposition is not well-characterized. CHK1 is a critical maintainer of cell cycle checkpoints and genomic stability, and is also involved in the BRCA1 and FA signaling pathways. Although CHK1 is an essential protein for cell cycle and DNA integrity maintenance control, no mutations in this gene has yet been associated with predisposition to cancer. To our knowledge, this is the first report to determine the existence of large *CHK1* deletions in familial breast cancer or in any disease with hereditary background.
Material and Methods: Blood DNA from affected index persons of 111 northern Finnish breast cancer families was assessed for possible constitutional exonic deletions or amplifications in the *BRIP1* and *CHK1* genes by using the multiplex ligation-dependent probe amplification (MLPA) method.
Results: Neither of the genes examined showed any large genomic rearrangements.
Conclusions: Our current results raise the possibility that germline exonic deletions or amplifications do not serve as a significant inactivating mechanism of the tumour suppressive functions of *BRIP1* and *CHK1* in breast tissue. Together with a PCR-based mutation analysis of the *BRIP1* gene, we conclude that pathogenic germline alterations in *BRIP1* appear not to contribute to breast cancer susceptibility in Finland.

55 Association of mammographic density with selected nutrients in Norwegian women

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Background: Mammographic density has been strongly associated with breast cancer risk. The determinants of mammographic density have been shown to be similar to those of breast cancer risk. Investigating the association between diet and mammography density could shed light on the possible relationship between diet and breast cancer risk.
Material and Methods: In this study we analyzed data of 2250 postmenopausal Norwegian women aged 50−69 years residing in the three largest Norwegian counties who participated in the Norwegian Breast Screening Programme in 2004. We estimated intake of selected nutrients and vitamins using a previously validated 200 item food frequency questionnaire. Mammographic density was assessed on scanned mammograms using a computer assisted method. We used multivariate linear regression to determine the least square mean of percent and absolute mammographic density adjusting for potential confounders. Because of the strong confounding effect of body mass index (BMI) on mammographic density we used different adjustments for BMI, analyses were also carried out for different BMI strata.
Results: The mean percent and absolute mammographic density were 19.2% and 24.5cm^2 respectively. Overall, we observed no strong association between mammographic density and total caloric intake or intake of proteins, carbohydrates, total fat, monounsaturated and polyunsaturated fat, cholesterol or dietary fiber. There was a positive borderline statistically significant association (p for trend=0.07) with saturated fat, which became stronger when the analysis was restricted to women with a normal BMI (23–25.9) (p for trend=0.01).

There was no association between mammographic density and intake of calcium, vitamins A, retinol, B_{12}, C and D and no association between mammographic density and combined intake of vitamin D and calcium. However, when examining mammographic density by month of screening, we observed that mean percent density was higher in women screened in April, May and June (21.5%, 20.5%, and 20.2%, respectively) compared to those screened in September, October and November (19.9%, 17.7%, and 17.1%, respectively), suggesting that vitamin D status may be important.
Conclusions: Overall, we found no association between the selected nutrients and mammographic density, although we observed a positive association with saturated fat in women with a normal BMI (23–25.9). We also observed a seasonal variation in mammographic density.

56 Pre-diagnostic serum 25-hydroxyvitamin D concentrations and the risk of ovarian cancer

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Background: The possible role of vitamin D in the prevention of ovarian cancer has been investigated in ecological and experimental studies and there are suggestions that vitamin D may be protective against ovarian cancer. There is however paucity of epidemiological studies exploiting the use of serum 25-hydroxyvitamin D and ovarian cancer risk even though this may represent the best way to determine if there is any relationship.
Materials and Methods: We investigated the relationship between serum 25-hydroxyvitamin D and ovarian cancer risk in a prospective population-based study nested within the Finnish Maternity Cohort (FMC), Finland. The FMC is a biorepository of serum samples of almost all pregnant women in Finland since 1983. It contains about 1.6 million serum samples. Within the cohort, 201 ovarian cancer cases were selected and for each case, 2 controls were matched for age ($\pm$1 year), parity and sampling season ($\pm$4 weeks). Odds Ratio and 95% CI were calculated using conditional logistic regression appropriate for matched data.
Results: We observed an increased risk, OR 1.8 (95% CI 0.9−3.5) of ovarian cancer comparing women within the lowest quintile of serum 25-hydroxyvitamin D concentrations to those within the highest quintile, but this was not statistically significant. There was also a tendency to a higher risk of ovarian cancer among women with insufficient serum 25-hydroxyvitamin D (<75 nmol/L) compared to those with sufficient concentrations (>75 nmol/L); OR 2.7, 95% CI 1.0−7.9.
Conclusions: Though we did not observe a statistically significant association between serum 25-hydroxyvitamin D and risk of ovarian cancer, there is evidence to suggest that some women (women with insufficient serum concentrations) may be at increased risk. Further studies are needed to investigate this relationship because presently, very few modifiable factors are known to have any impact on ovarian cancer risk.

57 Interaction between RFC1 and MTHFR genes polymorphisms and risk of paediatric acute lymphoblastic leukemia with common somatic alterations

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Background: Folate is an important substance for cell division and for maintaining homeostasis. Its metabolism is crucial for the prevention of chromosomal abnormalities. Depending on the folate intake and on the polymorphisms in folate-related genes, the risk of acute lymphoblastic leukemia (ALL) may be affected. We previously observed different risk patterns of Brazilian acute leukemias associated to *MTHFR 677 C>T* and *MTHFR 1298 A>C* polymorphisms. We now aim to address whether there is an interaction pattern between folate-related genes polymorphisms (*RFC1 80G>A, MTHFR 677 C>T* and *MTHFR 1298 A>C*) and the occurrence of somatic alterations commonly observed in ALL.
Material and Methods: From 2000 to 2009, children (0−14 years-old) newly diagnosed with ALL were included. Control group consisted of unselected children with no previous history of malignancy living in the same regions of cases. At the time of diagnosis, samples were routinely screened and subclassified according to the molecular-cytogenetic biomarkers. DNA from cases and controls were obtained from biological sample, which included fresh mononuclear cells or smears or peripheral blood or buccal cells. Genotyping was performed by standard polymerase chain reaction restriction fragment length polymorphism (PCR-RFLP) technique for determining *MTHFR 677C>T* and *MTHFR 1298A>C* and *RFC1 80G A* genetic variants. Maximum likelihood method was used to estimate the allelic frequencies and the goodness-of-fit of genotype distribution to Hardy–Weinberg equilibrium was ascertained by the chi-square test. Unconditional logistic regression methods were used in univariated and multivariated models. To increase the statistical power, heterozygous and mutant homozygous groups were combined and compared to wild-type groups.
Results: A total of 687 ALL cases [pro-B ALL (n, 122), c-ALL (n, 290), pre-B ALL (n, 140) and T-ALL (n, 42); 93 ALL samples could not be subclassified] and 605 controls were analyzed. 274 cases were diagnosed with somatic alterations, being *MLL* rearrangements (n = 90), *ETV6/RUNX1* (*TEL/AML1*) (n = 53), hyperdiploidy (n = 53) the most commonly observed. Univariate analyses of childhood ALL patients and controls demonstrated that *MTHFR 677C>T* results in a protector factor [OR = 0.60; 95% CI, 0.42−1.0], while the *RFC1 80G>A* genotype showed an increased risk but without statistical significance [OR = 1.90; 95% CI, 0.82–4.42]. A significant association for carriers of 677C>T was demonstrated for leukemias with *ETV6/RUNX1* [OR = 2.41; 95% CI, 1.03–5.62]. No significant associations were evident for either polymorphism with other molecular defined subgroups.
Conclusions: The results indicate that molecularly defined subgroups of leukemias have different etiologies and also confirm the importance of folate pathways in the development of childhood leukemia.

58 Human DNArepair genes and genetic susceptibility to melanoma: a candidate gene approach using sequenom platform

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Background: Cutaneous malignant melanomas (MM) represent aggressive neoplasms and its frequency is increasing rapidly. The key environmental risk factor is exposure to the ultraviolet (UV) component in sunlight, which causes various kinds of DNA damage, including bulky lesions and oxidative damage, which may lead to mutations, if not repaired efficiently. Thus, DNA repair is critical for maintaining the integrity of the genome. The nucleotide excision repair (NER) pathway deals with the main forms of UV induced DNA damage. Polymorphisms on these pathway genes might modulate cancer predisposition.
Materials and Methods: We present a case-control study including 640 Spanish MM patients and 340 control subjects. Phenotypic information was collected using a standardised questionnaire. All studied subjects gave informed consent. Functional (from coding and regulatory regions) SNPs with MAF < 0.5 were selected using HapMap database.
Results: Thirty SNPs in 17 genes belonging to the NER pathway were finally selected. Twenty five have been successfully genotyped using Sequenom platform (16 and 9 multiplexes respectively). The 5 remaining assays failed were designed by Taqman.
Conclusions: Associations with melanoma and pigmentary characteristics such as hair, skin and eye colour will be discussed. These results will confirm the contribution of excision repair genes to genetic predisposition to MM in Spain.

59 Colorectal cancer: candidate gene approach using obesity associated genes that show ancestral susceptibility

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Background: Colorectal cancer (CRC) and obesity are nutrition related, complex diseases which share both environmental and genetic risk factors. A number of studies have shown that complex diseases can be associated with ancestral risk alleles. In the evolutionary context, the mechanism of ancestral-susceptibility can be explained by continuous adaptation to varying environmental conditions. Due to a change in these conditions a former beneficial variant can become disadvantageous. In such a case, positive selection will drive the derived, protective or more beneficial allele to higher frequency. In this study we want to apply this framework to single nucleotide polymorphisms (SNPs) and genes that are associated with an increased risk of obesity to find new candidate genes for CRC.
Methods: To identify candidate SNPs we used a two step selection process. 1. We selected genes, for which ancestral alleles have been associated with increased risk of obesity. 2. We chose SNPs with a minimal allele frequency difference of 60% among the worldwide populations YRI, CEU, CHB and JPT, indicating a selective process. So far, we selected 9 SNPs in 3 genes (ENPP1, GAD2 and MTMR9) to test for an association with CRC. A hospital