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Chapter 1 : Public health genomics - Wikipedia

Genetic susceptibility genes for gastric cancer play very important roles in the development and progression of gastric cancer. Although the pathogenesis and genetic mechanisms of several genes have been elucidated recently, further large-sample studies are required after the meta-analysis of many genes.

Cancer Cancer occurs because of mutations in the genes responsible for cell multiplication and repair. The changes which a cell undergoes in the process of malignant transformation is a reflection of the sequential acquisition of these genetic alterations. This multi-step process is not an abrupt transition from normal to malignant, but may take over 20 years or more. The mutation of critical genes, including supressor genes, oncogenes and genes involved in DNA repair, leads to genetic instability and to progressive loss of differentiation. Tumours enlarge because cancer cells lack the ability to balance cell division by cell death apoptosis and by forming their own vascular system angiogenesis. The transformed cells lose their ability to interact with each other and exhibit uncontrolled growth, invade neighbouring tissues and eventually spread through the blood stream or the lymphatic system to distant organs. According to the World Health Report, about 7. The most prevalent of these cancers include lung, stomach, colon, liver, breast and oesophagus cancer, in that order of occurrence. Combined, these cancers are responsible for over 4. Even though generally considered as an illness of the developed countries cancer is a world wide health problem. Due to demographic changes and changes in life style this percentage is expected to rise in the near future. The roles that genes play differ greatly, ranging from genes that completely determine the disease state disease genes to genes that interact with other genes and environment factors in causing cancer susceptibility genes. Studies have shown that the primary determinants of most cancers are lifestyle factors, such as tobacco, dietary and exercise habits, environment carcinogens and infectious agents, rather than inherited genetic factors. Identification of a germline mutations by genetic testing allows for preventive measures, clinical management and counselling. Since the prevalence of germline mutations such as BRCA1 is very low in most societies, the introduction of mass screening to identify people at risk to develop cancer is not recommended. It is now appreciated that so-called metabolic polymorphisms, that is differences in the way people metabolize chemical carcinogens, explain differences in the susceptibility of individuals to cancer, and that these are controlled in cells by mutations in specific genes. A major research endeavour is now under way to characterize these genetic polymorphisms. It is already clear that there are a multiplicity of such genetic changes, that they are caused by genes of low penetrance, and that the classic Mendelian laws do not apply. However, it seems likely that collectively they explain much of innate susceptibility to cancer, and that therefore their potential contribution to the occurrence of cancer is large. It may eventually be possible to identify those individuals at special risk of tobacco or diet-associated cancers, and also those susceptible to the effects of environmental contaminants. It is also anticipated, but not yet shown, that genetic tests may eventually provide information that will be used to determine the best course of treatment for some cancers. Some cancers currently classified as a single disease may ultimately be classified into different types, each best managed by a different therapeutic strategy. In conclusion genetics may eventually play an important role in the control of cancer, including:

Chapter 2 : 'Novel' Susceptibility Genes ID'd in Breast, Ovarian Ca | Medpage Today

Overview. The Epidemiology and Genomics Research Program (EGRP) is a strong supporter of epidemiology studies investigating genetic susceptibility to cancer across all populations, including family studies, candidate gene studies, genome-wide association studies (GWAS), and use of next generation sequencing techniques to identify variants associated with specific cancers.

Our doctors draft national guidelines on what to test for and when to consider it. We lead the way in testing for lesser-known genetic mutations tied to breast and other cancers. Our cancer genetic counselors have years of experience to support you in choosing the right assessment plan for you. You can target more genes or fewer, or opt out of testing altogether. For assessments involving genetic testing, we use the latest technique to test dozens of genes at once, a standard-setting approach we adopted early on and validated. Our doctors and counselors work together to provide deep insight into your needs. They specialize in interpreting uncertain findings and designing risk management plans tailored to you and your family. Leading research and clinical trials: Our highly published doctors continue to identify genetic mutations that can cause cancer and improve the way hereditary cancer risk is evaluated and managed. Most cancers do not have a hereditary cause. While all cancers have genetic mutations, most changes take place after birth and are not inherited. Some, however, get passed down through families. While they do not always cause cancer, they can place you at higher risk. We help determine whether you face a higher probability of developing cancer and, if so, what your level of hereditary risk is. Throughout the process, our genetic counselors help you understand what the findings and options mean for your lifestyle, mental health, children, and other family members. Our genetic consultations may include: Personal and family histories: We ask about your health and nongenetic risk factors, such as lifestyle. If you have been diagnosed with cancer, we study the pathology. We also take a thorough look at both sides of your family, including ancestry, types of cancer, related conditions, and ages at diagnosis. Keep in mind that relatives may not have told you about a genetic mutation or a cancer, or they may have inadvertently passed along incorrect information. We compare your personal data to collective case histories for a particular cancer or genetic mutation, to predict your risk. We always consider the latest findings. We recommend testing when we think it can help. Although risk assessment and counseling do not depend on testing, it can provide greater insight. We provide you with a range of personalized options for managing your risk and protecting your health. If we find that your family faces an increased risk for cancer, we tell you who is potentially affected. We discuss ways you can let them know, such as partnering with another family member. We also provide an explanatory letter you can share. And we can help find care for relatives if they live in a different part of the state, country, or world. We collaborate with other cancer genetics programs nationally and internationally. State and federal laws protect against genetic discrimination. You do not have to worry about health insurers and employers using your test results against you. Privacy laws prevent us from contacting your family members for you, though they are welcome to reach out to us. We may recommend testing another family member first, if we feel that doing so will provide better answers. Testing options change over time. You may benefit even if you had it done in the past or have not previously had the opportunity. Frequently Asked Questions What is genetics? Genetics is the branch of medicine concerned with how hereditary and genetic factors play a role in causing a disease, birth defect, or inherited susceptibility to a health problem such as cancer. Cancers develop due to alterations mutations in genes, that when working properly promote normal, controlled cell growth. Only a small percentage of cancers involve inherited mutations that are passed from generation to generation. The majority of cancers can be attributed to acquired mutations. These changes occur at the cellular level after birth, as a result of environmental exposures such as smoking , lifestyle behaviors such as eating poorly or not exercising , or chance alone. If mutations affect genes that control cell growth this may cause a cell to grow out of control, and to ultimately become a cancer cell. Therefore, all cancers are genetic, in that they develop because of an accumulation of mutations in genes, but most are not inherited. The percentage of cancers that result from a single inherited factor varies depending on the type of tumor. This monumental achievement will give scientists the building blocks to

determine how diseases such as cancer are caused and hopefully, how to treat them and, ultimately, prevent them. What are chromosomes and how are they inherited? The human body is made up of cells. For example, when you have a sunburn your skin peels, and you are shedding skin "cells. Human chromosomes are located in the nucleus of the cell. A chromosome is a structure in the nucleus that contains your genes. Your genes determine your traits, such as eye color and blood type. The usual number of chromosomes in each cell of your body is 46 total chromosomes, or 23 pairs. You inherit half of your chromosomes one member of each pair from your biological mother, and the other half the matching member of each pair from your biological father. Scientists have numbered the chromosome pairs from 1 to 22, with the 23rd pair labeled as Xs or Ys, depending on the structure. The first 22 pairs of chromosomes are called "autosomes. Females have two "X" chromosomes, and males have one "X" and one "Y" chromosome. A picture of all 46 chromosomes, in their pairs, is called a karyotype. A normal female karyotype is written 46, XX, and a normal male karyotype is written 46, XY. What are genes, and how do they determine physical traits? Genes are what determine your traits, such as eye color and blood type. They are contained on our chromosomes, which normally number 46 total 23 pairs in each cell of our body. There are an estimated 30, to 35, different genes contained on these chromosomes. Genes are made of DNA. DNA stands for deoxyribonucleic acid. DNA is made up of base pairs that provide the codes for making proteins. So, ultimately, a gene, or a section of our DNA, makes a protein. There is also DNA located in between genes, which does not code for anything in particular, but simply serves as "spacer. Genes are found in pairs, just as the chromosomes are. One member of each gene pair is inherited from our mother, while the corresponding member of the gene pair is inherited from our father. Genes are expressed in different ways. For some genes, both copies are needed in order for the protein they make to work properly in the body. For other genes, only one copy is necessary. For yet other genes, how the gene works depends on which parent it was inherited from. This means that both males and females are equally likely to have these genes. The last pair of chromosomes determines gender. Males have one X and one Y chromosome, while females have two X chromosomes. Therefore, women do not have any of the genes present on the Y, and men have only one copy of genes on the X. The idea of inheritance was first described by an Austrian monk whose name was Gregor Mendel. Mendel performed experiments on garden peas to determine patterns of inheritance. These basic patterns are sometimes called "Mendelian" or "traditional" inheritance. The basic patterns of inheritance are: There are many different single gene defects that require clinical care by a physician or other healthcare professional. Listed in the directory below are some, for which we have provided a brief overview. What is autosomal dominant inheritance? Autosomal dominant inheritance means that the gene carrying a mutation is located on one of the autosomes chromosome pairs 1 through This means that males and females are equally likely to inherit the mutation. There are four possible combinations in the children. Two of the four, or 50 percent, have inherited the mutation. The other 50 percent have not inherited the mutation. These four combinations are possible every time a pregnancy occurs between these two individuals. The gender of the children whether they are sons or daughters does not matter. An important characteristic of dominant gene mutations is that they can have variable expression. This means that some people have milder or more severe symptoms than others. In addition, which systems of the body the mutation affects can vary as can the age at which the disease starts, even in the same family. Another important characteristic of dominant gene mutations is that in some cases, they can have reduced penetrance. This means that sometimes a person can have a dominant mutation but not show any signs of disease. The concept of reduced penetrance is particularly important in the case of autosomal dominant cancer susceptibility genes.

Chapter 3 : cancer susceptibility in the mouse: genetics, biology and - Nature - calendrierdelascience.com

Genetic susceptibility to cancer in terms of secondary tumors appearing long after initial successful treatment is also a matter of concern for children. Total-body irradiation resulting from leakage from linear accelerators may further contribute to the risk of secondary cancer.

Public policy in the U. Main public concerns regarding genomic information are that of confidentiality, misuse of information by health plans, employers, and medical practitioners, and the right of access to genetic information. Ethical concerns[edit] One of the many facets involved in public health genomics is that of bioethics. Authors of the document explore four broad categories of ethical and policy issues related to pharmacogenetics: In the introduction to the report, the authors clearly state that the development and application of pharmacogenetics depend on scientific research , but that policy and administration must provide incentives and restraints to ensure the most productive and just use of this technology. SNPs may have no effect on gene expression , or they can change the function of a gene completely. Resulting gene expression changes can, in some cases, result in disease, or in susceptibility to disease e. Some current tests for genetic diseases include: A select few are explored below. Herpesvirus and bacterial infections[edit] Since the field of genomics takes into account the entire genome of an organism , and not simply its individual genes, the stud of latent viral infection falls into this realm. An example of this is found in a study published in Nature , which showed that mice with a latent infection of a herpesvirus were less susceptible to bacterial infections. Murine mice were infected with murine gammaherpesvirus 68 and then challenged with the Listeria monocytogenes bacterium. Mice that had a latent infection of the virus had an increased resistance to the bacteria, but those with a non-latent strain of virus had no change in susceptibility to the bacteria. The study went on to test mice with murine cytomegalovirus , a member of the betaherpesvirinae subfamily, which provided similar results. However, infection with human herpes simplex virus type-1 HSV-1 , a member of the alphaherpesvirinae subfamily, did not provide increased resistance to bacterial infection. They also used Yersinia pestis the causative agent of the Black Death to challenge mice with a latent infection of gammaherpesvirus 68, and they found the mice did have an increased resistance to the bacteria. The suspected reason for this is that peritoneal macrophages in the mouse are activated after latent infection of the herpesvirus, and since macrophages play an important role in immunity , this provides the mouse with a stronger, active immune system at the time of bacterial exposure. The study of variations within microbial genomes will also need to be evaluated to use genomics of infectious disease within public health. The ability to determine if a person has greater susceptibility to an infectious disease will be valuable to determine how to treat the disease if it is present or prevent the person from getting the disease. Several infectious diseases have shown a link between genetics and susceptibility in that families tend to have heritability traits of a disease. During the course of the past[when? The findings from this study raise questions about genetic or other predispositions and how they affect a persons susceptibility to and severity of disease. Continued research will be needed to determine the epidemiology of H5N1 infection and whether genetic, behavioral, immunologic, and environmental factors contribute to case clustering. Infectious diseases in humans appear highly polygenic with many loci implicated but only a minority of these convincingly replicated. It is possible that the human genome has evolved in part from our exposure to M. In the case of M. Systems biology and genomics are natural partners, since the development of genomic information and systems naturally facilitates analysis of systems biology questions involving relationships between genes, their variants SNPs and biological function. Such questions include the investigation of signaling pathways , evolutionary trees , or biological networks , such as immune networks and pathways. For this reason, genomics and these approaches are particularly suited to studies in immunology. The study of immunology using genomics, as well as proteomics and transcriptomics including gene profiles, either genomic or expressed gene mRNA profiles , has been termed immunomics. Accurate and sensitive prediction of disease, or detection during early stages of disease, could allow the prevention or arrest of disease development as immunotherapy treatments become available. Type-1 diabetes markers associated with disease susceptibility have been identified, for example HLA class II gene

variants, however possession of one or more of these genomic markers does not necessarily lead to disease. Lack of progression to disease is likely due to the absence of environmental triggers , absence of other susceptibility genes, presence of protective genes, or differences in the temporal expression or presence of these factors. Combinations of markers have also been associated with susceptibility to type-1 diabetes however again, their presence may not always predict disease development, and conversely, disease may be present without the marker group. Potential variant genes SNPs or markers that are linked to the disease include genes for cytokines, membrane-bound ligands , insulin and immune regulatory genes. Meta-analyses have been able to identify additional associated genes, [10] by pooling a number of large gene datasets. This successful study illustrates the importance of compiling and sharing large genome databases. The inclusion of phenotypic data in these databases will enhance discovery of candidate genes, while the addition of environmental and temporal data should be able to advance the disease progression pathways knowledge. This project is intended to promote international data sharing and collaboration, in addition to creating a standard and framework for the collection of this data. Nonsyndromic hearing loss[edit] Variations within the human genome are being studied to determine susceptibility to chronic diseases, as well as infectious diseases. GJB2 is a gene encoding for connexin , a protein found in the cochlea. Variants in GJB2 are being used to determine age of onset , as well as severity of hearing loss. It is clear that there are also environmental factors to consider. Infections such as rubella and meningitis and low birth weight and artificial ventilation , are known risk factors for hearing loss, but perhaps knowing this, as well as genetic information, will help with early intervention. Information gained from further research in the role of GJB2 variants in hearing loss may lead to newborn screening for them. As early intervention is crucial to prevent developmental delays in children with hearing loss, the ability to test for susceptibility in young children would be beneficial. Knowing genetic information may also help in the treatment of other diseases if a patient is already at risk. Further testing is needed, especially in determining the role of GJB2 variants and environmental factors on a population level, however initial studies show promise when using genetic information along with newborn screening. Genomics and health[edit] Main article: Pharmacogenomics The World Health Organization has defined pharmacogenomics as the study of DNA sequence variation as it relates to different drug responses in individuals, i. Pharmacogenomics refers to the use of DNA-based genotyping in order to target pharmaceutical agents to specific patient populations in the design of drugs. Pharmacogenetics may be used in the near future by public health practitioners to determine the best candidates for certain drugs, thereby reducing much of the guesswork in prescribing drugs. Such actions have the potential to improve the effectiveness of treatments and reduce adverse drug events. This may be through either upregulating or downregulating the expression of certain genes or by a number of other methods. While the field is quite young there are a number of companies that market directly to the public and promote the issue under the guise of public health. Yet many of these companies claim to benefit the consumer, the tests performed are either not applicable or often result in common sense recommendations. Such companies promote public distrust towards future medical tests that may test more appropriate and applicable agents. An example of the role of nutrition would be the methylation pathway involving methylene tetrahydrofolate reductase MTHFR. Increased risk for neural tube defects [16] and elevated homocysteine levels [17] have been associated with the MTHFR CT polymorphism. In , researchers from the Johns Hopkins Bloomberg School of Public Health identified the blueprint of genes and enzymes in the body that enable sulforaphane , a compound found in broccoli and other vegetables, to prevent cancer and remove toxins from cells. This study was the first gene profiling analysis of a cancer-preventing agent using this approach. Study results published in The Journal of Nutrition outline the metabolism and mechanisms of action of cruciferous vegetable constituents, discusses human studies testing effects of cruciferous vegetables on biotransformation systems and summarizes the epidemiologic and experimental evidence for an effect of genetic polymorphisms genetic variations in these enzymes in response to cruciferous vegetable intake. Researchers have found that almost all disorders and diseases that affect humans reflect the interplay between the environment and their genes; however we are still in the initial stages of understanding the specific role genes play on common disorders and diseases. It is therefore likely that the recent rise in the rates of cancer worldwide can be at least partially attributed to the rise in the number of synthetic and

otherwise toxic compounds found in our society today. Thus, in the near future, public health genomics, and more specifically environmental health, will become an important part of the future healthcare-related issues. Potential benefits of uncovering the human genome will be focused more on identifying causes of disease and less on treating disease, through: For some individuals, they will be given the assurance of not obtaining a disease, as a result of familial genes, in which their family has a strong history and some will be able to seek out better medicines or therapies for a disease they already have. Others will find they are more susceptible to a disease that has no cure. Though this information maybe painful, it will give them the opportunity to prevent or delay the on-set of that disease through: As we continue to have advances in the study of human genetics, we hope to one day incorporate it into the day-to-day practice of healthcare. IOM is validating the family history tool for six common chronic diseases breast, ovarian, colorectal cancer, diabetes, heart disease, stroke IOM Initiative. Validating cost effective tools can help restore importance of basic medical practices e. For example, the influenza epidemic of , as well as the recent cases of human fatality due to H5N1 avian flu , both illustrate the potentially dangerous sequence of immune responses to this virus. Also well documented is the only case of spontaneous "immunity" to HIV in humans, shown to be due to a mutation in a surface protein on CD4 T cells, the primary targets of HIV. The immune system is truly a sentinel system of the body, with the result that health and disease are carefully balanced by the modulated response of each of its various parts, which then also act in concert as a whole. The causes of perturbed immune responses run the gamut of genome-environment interactions due to diet, supplements, sun exposure, workplace exposures, etc. Public health genomics as a whole will absolutely require a rigorous understanding of the changing face of immune responses. Newborn screening[edit] The experience of newborn screening serves as the introduction to public health genomics for many people. If they did not undergo prenatal genetic testing, having their new baby undergo a heel stick in order to collect a small amount of blood may be the first time an individual or couple encounters genetic testing. Newborn genetic screening is a promising area in public health genomics that appears poised to capitalize on the public health goal of disease prevention as a primary form of treatment. Most of the diseases that are screened for are extremely rare, single-gene disorders that are often autosomal recessive conditions and are not readily identifiable in neonates without these types of tests. Therefore, often the treating physician has never seen a patient with the disease or condition and so an immediate referral to a specialty clinic is necessary for the family. Most of the conditions identified in newborn screening are metabolic disorders that either involve i lacking an enzyme or the ability to metabolize or breakdown a particular component of the diet, like phenylketonuria, ii abnormality of some component of the blood, especially the hemoglobin protein, or iii alteration of some component of the endocrine system , especially the thyroid gland. Many of these disorders, once identified, can be treated before more severe symptoms, such as mental retardation or stunted growth, set in. Newborn genetic screening is an area of tremendous growth. In the early s, the only test was for phenylketonuria. In , roughly two-thirds of states in the US screened for 10 or fewer genetic diseases in newborns. Traditional healers associated specific body types with resistance or susceptibility to particular diseases under specific conditions. Genomics, by associating genotypes with the phenotypes on which these practices were based, could provide key tools to advance the scientific understanding of some of these traditional healing practices.

Chapter 4 : WHO | Genes and human disease

The Laboratory of Genetic Susceptibility (LGS) performs interdisciplinary research on cancer genetics and susceptibility. Research Mission. The LGS mission is to understand the biological basis for genetic susceptibility to cancer, including.

Comparative analysis of whole-exome sequencing in 11, unrelated patients with breast or ovarian cancer, or both, and in 3, controls without cancer, showed that ATM, a non-BRCA gene associated with breast cancer, was correlated with a two- to three-fold increased risk of ovarian cancer odds ratio [OR] 2. The data also supported MSH6, which has a significant association with ovarian cancer, as a weak breast cancer susceptibility gene OR 2. In an accompanying editorial , Lucy E. This includes the prediction of future cancer risks among healthy relatives in families with hereditary breast or ovarian cancer. Study Details For the study, the researchers examined the frequency of known cancer susceptibility genes in a total of 15, patients. From to , the group of 11, patients with breast or ovarian cancer, or both, had been referred to 1, hospitals and clinics across the U. Many of the patients were BRCA gene-negative with a family history of cancer and early onset, bilateral, or triple-negative breast cancers. The 3, unrelated controls were referred for conditions other than cancer during the same time period. Of the 9, patients with breast cancer, 3, Other breast cancer subtypes included invasive ductal, invasive lobular, hormone receptor-positive, and hormone receptor-negative. In addition, breast cancer patients 1. Out of 2, women with ovarian cancer, The gene associations were confirmed in multiple sensitivity analyses using the Genome Aggregation Database gnomAD as a set of reference controls, and in case-control analyses among white patients and women. The study showed that the breast cancer-associated risk with MSH6 was seen with breast cancer, early-onset breast cancer, and with the invasive lobular carcinoma subtype associated with MSH6. This finding is partly in keeping with a prior study , the researchers noted. The data confirmed three other susceptibility genes associated with increased breast cancer risk: When associations with clinical features of breast cancer were examined, the findings revealed that patients who were ATM and CHEK2 carriers were more likely to have estrogen-progesterone receptor-positive disease than estrogen-progesterone receptor-negative disease. The researchers pointed out that although the study had a large sample size and analyzed accurate next-generation sequencing data designed for clinical diagnostic use, it also had a number of limitations. In addition, since the analysis was based on the aggregation of both protein truncating and known pathogenic variants, the cancer risk associated with less-studied genes may have been underestimated. This study was funded by Ambry Genetics. Li and co-authors reported being employees of the company at the time of the study. Side and co-authors reported having no conflicts of interest.

Chapter 5 : Cancer Genetics Salt Lake City, Utah

Various laboratories now offer a variety of panels (see Table 1), from disease-specific panels, such as a breast panel, to "pan-cancer" panels, which test multiple genes that may increase cancer susceptibility for a variety of cancers and inherited cancer syndromes.

Adapted with permission from REF. BACKCROSS A cross between one animal that is heterozygous for alleles that are obtained from two parental strains and a second animal that is homozygous for one of those alleles. Recent analysis of such data resulted in evidence that genetic predisposition contributes to the development of a large proportion of non-familial cancers. These and other data showed that many â€" perhaps most â€" cancers develop in genetically predisposed individuals. In an elegant study, Pharoah et al. These large differences in individual susceptibility make it obvious that targeting the individuals with the highest risk for preventive measures could be an effective strategy for reducing the rates of non-familial cancers. A second important conclusion from these and other analyses10,11 is that genetic predisposition to cancer in humans is largely a polygenic phenomenon; that is, it involves many genes with relatively small effects. Consequently, the collective impact of low-penetrance genes on cancer morbidity and mortality is larger than the effect of strong genes that cause familial cancer syndromes. However, the strategy that was used to identify genes that cause familial cancer syndromes cannot be used to identify these low-penetrance susceptibility genes: The alternative strategy is to first identify these unknown genes in laboratory animals and then to analyse their human homologues. In fact, inbred strains of mice and rats with large differences in susceptibility have provided ample direct evidence for low-penetrance cancer-susceptibility genes over the past decade13â€" Mapping of cancer-susceptibility loci in mice Inbred strains of mice and rats that differ widely in susceptibility to different types of tumour provide the parental strains for the crosses that are needed to map tumour-susceptibility genes through segregation analysis. Such inter-strain differences are common and, in many cases, large: These strain differences are often organ specific. This organ-specific pattern of cancer susceptibility was thought to show that different susceptibility genes were active in different organs. However, a new study indicates that there might be another explanation: This finding, if confirmed, would considerably reduce the estimates of the total number of susceptibility genes and speed up their identification in mice and subsequently in humans. The rank order of susceptibility of mouse strains to a specific tumour is, in many cases, independent of the inducing agent various chemical carcinogens, radiation or no agent at all. This indicates that the various tumour-induction procedures mostly enhance the preexisting genetic predisposition as reviewed for lung tumours in REF. Mapping design and analysis. Mice are then phenotyped for the relevant character for example tumour number, tumour size or latency period and are genotyped at marker loci microsatellites or single nucleotide polymorphisms that are polymorphic between the two parental strains. The correlation between the distribution of marker alleles and the susceptibility phenotypes allows susceptibility loci to be mapped to chromosomal locations. Rapid screening of the genome has been made possible by the introduction of microsatellite markers23, The only low-penetrance cancer-susceptibility gene that was mapped before the microsatellite era is the susceptibilty to colon cancer 1 Scc1 locus These loci affect various quantitative aspects of the tumour-susceptibility phenotype, such as tumour number, size, prevalence, latency period and survival time. Some authors prefer to name the loci by their specific phenotypic effect. However, the same locus might affect different aspects or several aspects of the tumour phenotype, depending on the cross and the test system. For example, Kras2 or a closely linked gene affects lung tumour numbers in some crosses26 and lung tumour size in others27, Therefore, it might be preferable to refer to these loci by a neutral term that indicates that they control susceptibility to a certain type of tumour.

Chapter 6 : Cancer Susceptibility Genes - Genetics

Cancer Susceptibility Genes We suspect that a family may have inherited a mutation in a cancer susceptibility gene when we see one or more of the following: Several people in the family with similar or related cancers.

Chapter 7 : Cancer Genetic Testing and Counseling | Stanford Health Care | Stanford Health Care

cancer development in the future and to identify carriers (individuals who do not have the cancer but have a copy of a gene which has been associated with the development of cancer). Genetic testing for CA susceptibility is considered medically necessary when all of the following criteria.