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Chapter 22

Pre-malignant Disease in the Prostate

Alastair D. Lamb, Anne Y. Warren, and David E. Neal

Abstract Carcinoma of the prostate (CaP) is the most common non-cutaneous cancer in men and the second most common cause of cancer related death. Mortality remains high despite improvements in diagnosis in the developed world. A better understanding of the mechanisms involved in the development of prostate cancer should allow targeted diagnosis, prevention and treatment, and may improve mortality. In this chapter, we outline the two principal pre-malignant histological types, prostate intraepithelial neoplasia (PIN) and atypical small acinar proliferation (ASAP) and the likelihood of progression to CaP if these diagnoses are made. We then assess current understanding of factors contributing to the initiation of pre-malignant disease and progression to CaP as they relate to stem cells, inflammation, diet and specific genetic mutations or aberrant pathways. Finally, we discuss the translational potential of these factors in early detection and prevention of CaP.

Introduction

Carcinoma of the prostate (CaP) is the most common non-cutaneous cancer in men and the second most common cause of cancer related death, killing approximately 10,000 men annually in the UK [1]. The majority of prostate cancer deaths occur in men aged 65 and over (Fig. 22.1); however, the disease is also found amongst younger men, with prevalence rates of up to 30% in 30–50 year olds reported on post-mortem analysis [2]. There is a 15-fold variation in prostate cancer mortality rates worldwide, and although North America ranks first in terms of incidence, mainly owing to high levels of PSA testing, it is eighth for mortality, with the highest mortality rates being recorded in the Caribbean (Fig. 22.2). Countries with higher levels of PSA testing detect a greater proportion of early stage disease, the consequent lead-time bias

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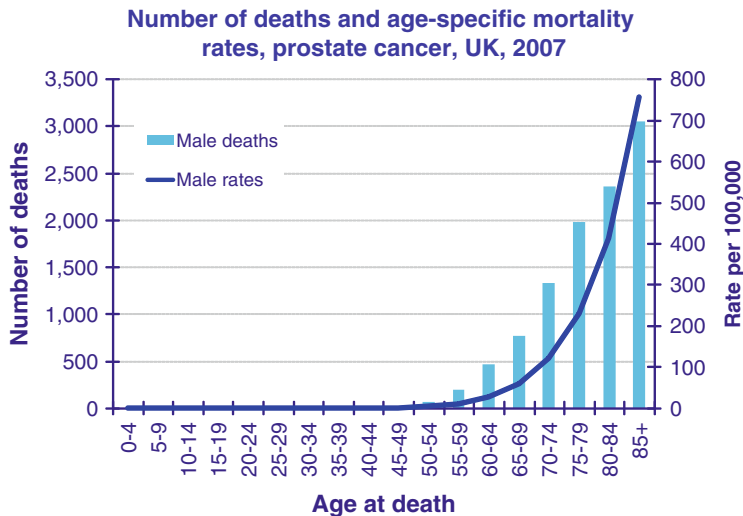


Fig. 22.1 UK age-specific mortality rates in 2007

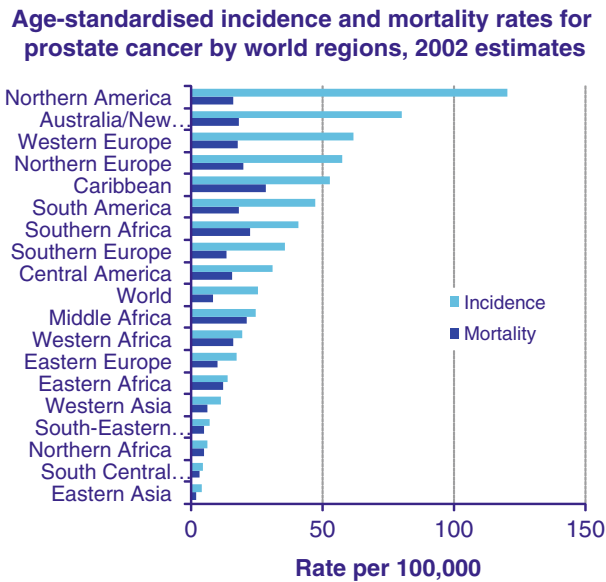


Fig. 22.2 World age-standardised incidence and mortality in 2002

giving higher survival rates compared to incidence [3]. Overall in the United Kingdom, prostate cancer mortality was fairly stable, but began to increase in the early 1980s. Mortality peaked in the early 1990s when the age-standardised death rate reached 30 per 100,000 in 1992. Since then there has been a slight fall in rates and in 2007, the age standardised rate was 25 per 100,000 (Fig. 22.3) [4]. Prostate cancer mortality remains high despite improvements in diagnosis in the developed world.

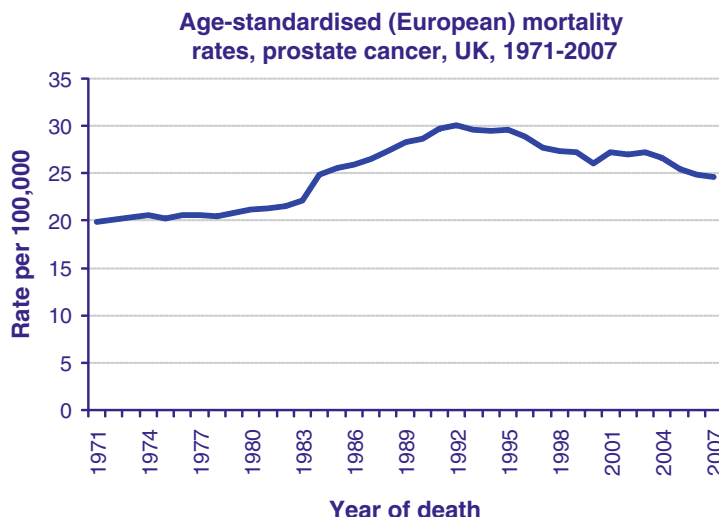


Fig. 22.3 UK mortality rates for three decades with age standardised to European averages

A better understanding of the mechanisms involved in the development of prostate cancer would allow targeted diagnosis, prevention and treatment, and may improve mortality.

Prostate cancer is a heterogeneous, often multifocal disease with numerous factors contributing to its initiation and progression. In this chapter, the two principal pre-malignant histological types will be outlined and current understanding of factors contributing to development of CaP will be assessed as they relate to stem cells, inflammation, diet and specific genetic mutations or aberrant pathways. Finally, the translational potential of these factors in early detection and prevention of CaP will be discussed.

Normal Prostate

The prostate is an accessory sexual organ with *exocrine* and *endocrine* functions, responsible for production and storage of 25–30% of constituents of the seminal fluid. Prostatic fluid is alkaline, which protects spermatozoa in the acidic environment of the vagina. The protein content of prostatic secretions is less than 1% and includes proteolytic enzymes, prostate acid phosphatase and prostate specific antigen as well as minerals such as zinc (free and protein bound) which has antimicrobial and semen coagulant effects [5, 6].

The prostate develops as part of the urogenital sinus (endodermal in origin) with contributions from the *Wolffian ducts* and from the surrounding mesenchyme. The prostate consists of branching ducts and *acini* which are often referred to as prostate glands collectively. The cells lining ducts and acini are identical with the exception of the larger peri-urethral ducts that have a urothelial lining. There are four main

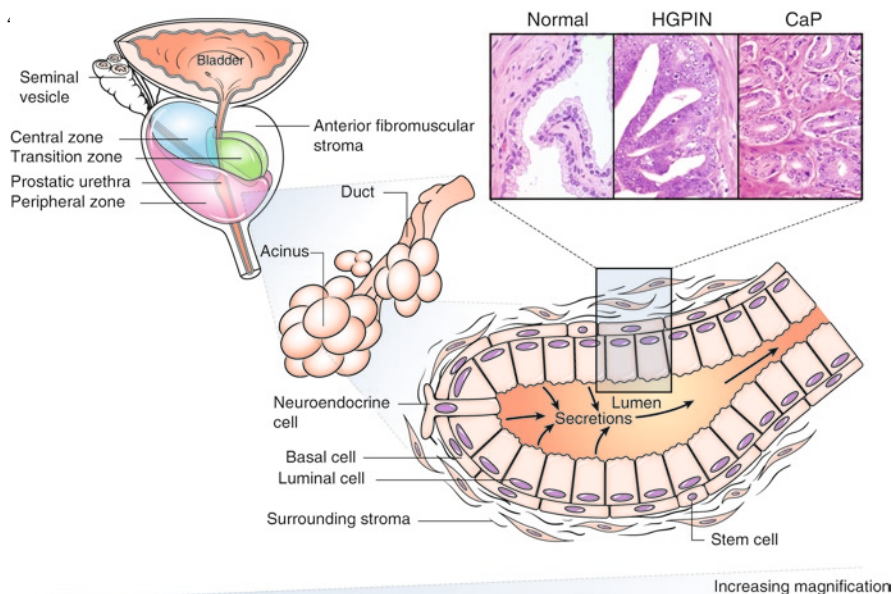


Fig. 22.4 Schematic of the prostate from organ to glands (ducts and acini). Different cell-types shown. Haematoxylin and Eosin sections show normal prostate, prostatic intraepithelial neoplasia (PIN) and Gleason score 6 carcinoma

anatomically distinct cell types (Fig. 22.4). First, prostate basal cells form a largely structural basal layer encircling each prostatic duct or acinus. Second, luminal (or glandular) cells form a columnar layer that make up the functional secretory surface of the glandular lumen. Third, rare neuroendocrine cells are interspersed between the basal and luminal cells. These are endocrine and sensory cells thought to share structural, functional and metabolic properties with neuronal cells found in the prostate. They secrete neuroendocrine peptides that support epithelial growth and viability [7]. Fourth, stromal cells surround the prostate glandular structures to guide and support growth and differentiation of the epithelium. Stromal cells include fibroblasts, myofibroblasts and smooth muscle cells and are derived from mesenchyme. Stem cells are generally thought to reside in the basal layer of the prostate contributing to all epithelial cell types of the prostate. The significance of prostate stem cells in development of prostate cancer will be discussed.

Prostatic Intraepithelial Neoplasia

Prostatic intra-epithelial neoplasia (PIN) is defined as the presence of cytologically atypical cells within a generally normal ductal or acinar outline in the presence of a basal layer of cells. PIN is conventionally divided into low grade (LG) and high grade (HG). Morphologically, HGPIN is identified by enlarged, crowded, often multilayered nuclei with irregular spacing, prominent nucleoli and amphophilic

cytoplasm, features also found in high *Gleason* grade carcinoma (Fig. 22.4) [8]. The essential distinguishing feature between HGPIN and carcinoma is the presence of basal cells, which, though often patchy in HGPIN are always present [9]. LGPIN, by contrast, shows a lesser degree of atypia and lacks prominent nucleoli. Clinically, LGPIN is not reported as such because of poor reproducibility and uncertain diagnostic significance, instead being classified as benign prostatic tissue [10]. Genetic and molecular factors contributing towards the development of PIN will be discussed in subsequent sections.

There is strong histological evidence implicating HGPIN as a pre-neoplastic lesion. Morphologically, HGPIN is primarily found in the peripheral zone, in proximity to invasive CaP [11], is multifocal and similar in cytological appearance to CaP [6], and it generally precedes CaP by at least 10 years, consistent with a linear progression [2, 12]. At a cellular level, HGPIN displays similar chromosomal abnormalities to early invasive CaP [13] as well as similar markers of differentiation [14]. However, the question remains open as to whether PIN is truly a precursor lesion of CaP or whether the two conditions are simply commonly associated.

A diagnosis of PIN has important clinical implications. There is general consensus regarding the diagnosis of HGPIN and also regarding the general relationship of HGPIN to CaP [8, 15, 16]. The reported incidence of HGPIN on transrectal ultrasound (TRUS) biopsy varies considerably at 0.6–24% (mean 7.7%), largely dependent on variation in the population under study, with HGPIN incidence increasing with age [17]. There is less consensus regarding the actual risk of diagnosing CaP on repeat biopsy with figures ranging from 50% from studies in the 1990s compared to 20% in recent studies, which is little different from the risk after a “normal” biopsy [17, 18]. The explanation lies in the extent of HGPIN and timing of biopsy. HGPIN that is multifocal and present throughout the gland, as determined by involvement of multiple (two or more cores) biopsies, is associated with a 39–80% risk of CaP depending on the study [19, 20]. Similarly, delaying biopsy has been reported to increase the detection rate of CaP from 25% at 6 months to 44.6% at 1 year [21]. This has led to the advice that patients with HGPIN in more than one core should have repeat biopsies after a 1 year interval [22].

Atypical Small Acinar Proliferation

Atypical small acinar proliferation (ASAP) describes a group of small, often closely packed, acini that are regarded by the pathologist as being atypical, but lacking in sufficient morphological abnormalities to be regarded as unequivocally diagnostic of carcinoma. Although generally used to indicate a suspicion of malignancy, this term encompasses a range of pathological conditions including benign mimics of CaP such as atypical adenomatous hyperplasia (AAH) in the transition zone, reactive atypia and atrophy, high grade PIN and acini that are cytologically suspicious, but too few in number to allow a confident diagnosis of malignancy [8, 23]. ASAP is detectable in a mean of 5% of biopsies and is accepted as being

highly predictive for CaP on subsequent biopsies, with a 34–60% second biopsy detection rate [17, 24]. Advice at the time of writing is for repeat biopsy in the presence of ASAP within 3–6 months [22].

The Role of Stem Cells in the Initiation of Prostate Cancer

Stem cells or early progenitors in the prostate are thought to reside in the basal layer of the prostate. This is based on the observation that there is preferential survival of the basal layer of the prostate during androgen ablation with apoptosis of androgen receptor (AR)-expressing differentiated luminal cells [25]. It is supported by findings that mice null for the basal cell marker p63 are born without prostates (or mammary glands) [26, 27]. The existence and site of prostate stem cells has been most recently elucidated following studies incorporating murine renal-subcapsular grafting of a single adult mouse prostate stem cell defined by *Lin⁻Sca-1⁺CD133⁺CD44⁺CD117⁺* and located in the periurethral prostate. These cells are able to generate functioning secreting prostate tissue with long term self renewal capacity as demonstrated by serial transplantation in vivo [28]. This prostate tissue contains all three epithelial cell-types including neuroendocrine cells, dispelling previous notions that this rarer prostate cell may have a distinct cell of origin, common with surrounding neuroectodermal or stromal cells (Fig. 22.5) [7]. The peri-urethral region in the mouse prostate is rich in basal cells and characterized by a morphologically distinct band of smooth muscle rich in TGF- β , known to promote stem cell quiescence, consistent with this site being a prostate stem cell niche [29]. However, the site of prostate stem cells remains controversial, with another recent paper identifying cells in the luminal epithelium with full regenerative potential, defined by *NKX3-1⁺CK18⁺AR⁺* [30], and these studies are yet to be replicated with human tissue. This debate has important implications for the cell of origin in prostate cancer.

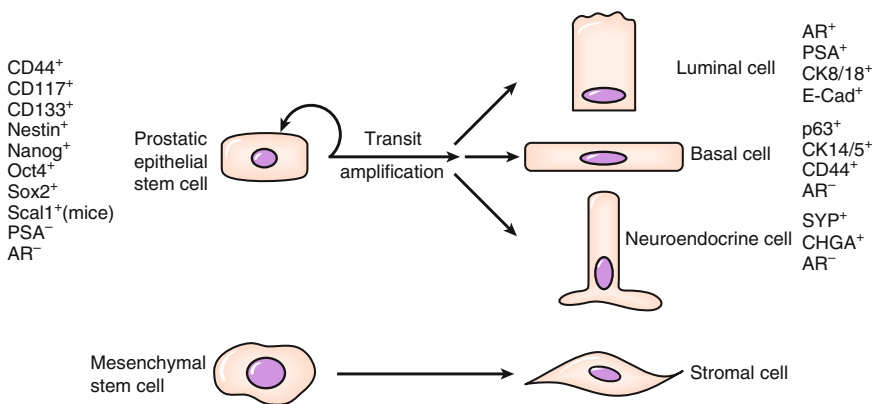


Fig. 22.5 Cell lineages of the prostate. The three epithelial cell types of the prostate are derived from a single epithelial stem cell. Stromal constituents are independently derived. Surface markers for different cell types as shown

The current dogma of stem cells as quiescent, slow-cycling cells, able to self-renew and pluripotent provides a strong case for these cells being the cell of origin in cancer. This was originally proposed in acute myeloid leukaemia [31], and subsequently many epithelial cancers including prostate [32–34]. Pathways that normally govern self-renewal or proliferation – such as PI3K [35], Wnt [36], SHh [37] and Notch [36] in haematopoietic, neural and epithelial systems – if dysregulated can contribute to tumorigenesis, for example in colon and mammary cancer, medulloblastoma, leukaemia and CaP. There are two main reasons for this. First, because stem cells have activated machinery for self-renewal, maintaining this activation may be easier than turning it on *de novo*. Second, if a number of mutations are required for neoplastic transformation to take place, then cells with longer lifespans have greater potential to accumulate these mutations and drive cancer [38]. The specific mutations involved in prostate cancer will be discussed later in this chapter.

Several properties of human prostate cancer suggest the disease may arise from a stem-like cancer initiating cell. The progression to androgen independent castrate resistant prostate cancer (CRPC) during androgen ablation therapy is consistent with prostate tumours containing populations of androgen-independent cells that survive and can expand in the absence of androgen. Given their androgen independent nature, prostate stem cells are a possible candidate. If the population of cells with such tumour regenerative potential is small this would fit with conventional wisdom regarding a precursor stem cell. However, it is also possible that a larger proportion of cells in a prostate tumour retains stem-like potential (a tumour is, after all, by definition, not fully differentiated), and when stressed by androgen ablation these cells alter their phenotype in a manner that is advantageous to their survival. One example of this is the propensity for castrate resistant prostate cancer to display a luminal to neuroendocrine shift [39].

Sub-populations of cells within prostate cancer cell lines with increased proliferative capacity *in vitro* and increased tumour initiating and metastatic capacity *in vivo* have been shown to possess a CD44⁺CD133⁺CD117⁺ profile similar to prostate stem cells [34, 40, 41], as well as expressing $\alpha\beta 1$ integrin consistent with membrane adhesional properties encouraging metastasis [34], and demonstrate higher levels of Oct4, Sox2, Nanog, Nestin [41–43], all markers of “stemness” or pluripotency. They are predominantly AR⁺. However, they are also p63⁺ [24, 41], suggesting that cancer stem cells are probably an intermediate cell type; not luminal, but not truly basal either.

In summary, prostate cancers are heterogeneous and contain subpopulations of cells that have increased tumorigenic potential compared to surrounding cells. These cells are characterised by markers that are similar, if not identical to those thought to define prostate stem cells. These “cancer stem cells” are thought by some to be the sites of initiation and maintenance of prostate cancer.

There are several questions that still need to be answered. First, most work on prostate cancer stem cells has been performed on cells that are already malignant – if prostate cancer stem cells really are transformed normal prostate stem cells then what is or are the initiating event/s? Which factors dysregulate the self-renewal pathways in normal prostate cancer stem cells? Second, can it be assumed that prostate cancer

stem cells really are dysregulated normal prostate stem cells? Or, are they committed progenitors/transit amplifying cells which retain some self-renewal and multipotent properties? Or are they de-differentiated terminally differentiated (luminal) cells that re-acquire stem-like properties and phenotypic versatility when stressed (e.g. by androgen deprivation)? Third, if prostate cancer stem cells are the initiating event in prostate cancer, and the source of repopulation in recurrent tumours, is there a unifying pathway that can be targeted therapeutically either to destroy the stem cells with malignant potential, or to prevent expansion of their malignant progeny? There is no clear answer to any of these three questions at the time of writing.

The Role of Inflammation in the Initiation of Prostate Cancer

Chronic inflammation is implicated in the development of a diverse range of human cancers, with evidence causally linking it to several cancers of the gastrointestinal tract, bladder and lung [44]. In these cancers, inflammation often collaborates with environmental exposures such as dietary toxins to increase the risk further [45]. The molecular mechanisms that underlie the pathogenesis of inflammation-associated cancer are complex and involve both the adaptive and innate immune system [46–48]. The release of highly reactive compounds such as hydrogen peroxide, nitric oxide and superoxide by activated phagocytic cells of the innate immune system damages DNA in epithelial cells, leading to increased cell division to replace these damaged cells, these dividing cells then being further exposed to mutagenic agents. The release of cytokines by inflammatory cells promotes cell proliferation and stimulates angiogenesis further enhancing tumorigenesis. In addition, during chronic inflammation, T and B cell-mediated antibody activity of the adaptive immune response can cause excessive and prolonged activation of innate immune cells [47].

The prostate has been shown to harbour focal areas of epithelial atrophy, sometimes associated with inflammatory infiltrates. These are common in the ageing prostate and often encompass a large fraction of the peripheral zone [49]. Despite the atrophic architectural appearance, there is an increased fraction of epithelial cells in such lesions. One term that has been used to describe those which are also associated with an inflammatory infiltrate is proliferative inflammatory atrophy (PIA) [50]. These areas of PIA have been observed to transition to HGPIN and adenocarcinoma in morphological studies [51–54], although some debate persists regarding this continuum and the validity of the separation of PIA from other forms of atrophy [55, 56].

In most cases, the precise cause of prostatic inflammation is unclear. However, potential sources include (Fig. 22.6):

- Infectious agents (viral or bacterial)
- Reflux of urine into the prostatic ducts
- Hormonal agents (e.g. oestrogen)
- Dietary factors [57]

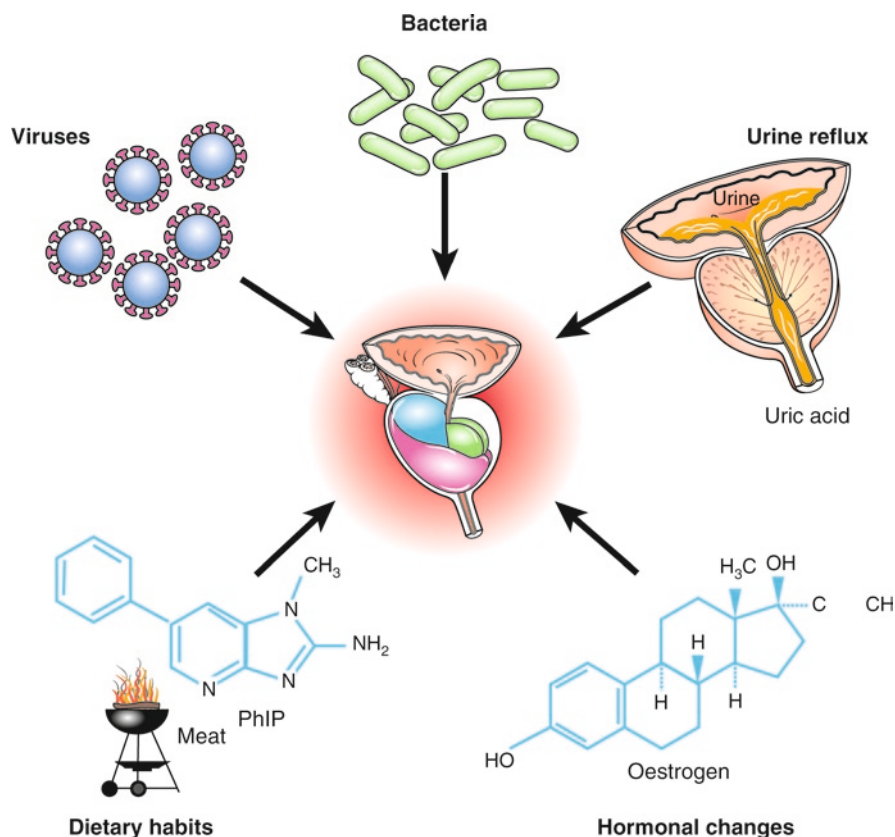


Fig. 22.6 Causes of inflammation in the prostate

Infectious agents. Sexually transmitted organisms that are known to infect the prostate include *Gonorrhoea* [58], *Chlamydia* [59], and *Trichomonas vaginalis* [60], while non-sexually transmitted bacteria include Gram-negative organisms such as *Escherichia coli* [61]. These can cause acute or chronic prostatitis, however severe acute inflammation and formation of prostatic abscesses is rare with antibiotic treatment, although TRUS biopsy of the prostate does increase this risk [62]. Nonetheless, asymptomatic infection and inflammation can still occur [58]. Viruses such as human papillomavirus (HPV) [63], cytomegalovirus (CMV) [64] and human herpes simplex virus (HSV) [65] have been detected in the prostate, although the extent to which they elicit an inflammatory response is largely unknown. It is possible that, in analogy to *H. pylori* in gastritis, there is a previously unidentified causative organism for PIA [57]. There is limited evidence linking specific infectious organisms with prostate cancer risk. This amounts to a lack of data rather than negative data per se, most likely due to the difficulties in assaying colonisation of the prostate. With prostatic massage being the only means of accurately

obtaining prostatic fluid cultures directly from the prostate it is difficult to accurately identify and quantify the extent of prostatic colonisation [66] and to correlate causative organisms with prostate cancer risk. There is also no evidence of an association between clinical prostatitis and prostate cancer, although this may be due to the complex nature and classification of clinical prostatitis which is not a true reflection of histological prostate inflammation [67]. The link is implicit. Infectious agents cause inflammation in the prostate, often chronic, and chronic inflammation causes PIA which is associated with prostate cancer risk.

One recent development has been the discovery of Xenotropic murine leukaemia-virus related virus (XMRV) in human prostate cancers. Gammaretroviruses have well-characterised oncogenic effects in animals but this is the first such virus known to infect humans. XMRV infection has been shown to be associated with a common polymorphism of the RNASEL gene [68]. XMRV transcripts and protein, when present, have been found to be predominantly expressed in malignant epithelial cells, especially more aggressive tumours [69]. This is, at present, still only an associative link.

Urine reflux. Chemical or traumatic irritation have been linked with inflammation in the prostate [70] for example, uric acid has been shown to directly engage inflammasomes, pro-inflammatory intracytoplasmic complexes in cells of the innate immune system, especially macrophages, resulting in recruitment of other inflammatory cells [71]. A rat model of partial urethral obstruction has shown increased Cox-2 levels in response to intraprostatic urinary reflux [72]. In addition the retrograde movement of spermatozoa into the prostate has been found in association with prostatic inflammation probably due to the adaptive immune response to these immune privileged cells [73].

Hormonal influence – oestrogen. Increased levels of oestrogens have long been seen to affect the growth and development of the prostate, which is known to express oestrogen receptor- α (ER α) primarily in the stroma and oestrogen receptor- β (ER β) in the epithelium [74, 75]. Administration of oestrogens to neonatal rodents induces developmental defects, but also results in inflammation as well as hyperplasia, dysplasia or PIN [51]. It is therefore reasonable to associate oestrogens with chronic inflammation and prostate cancer risk in the adult prostate, although further work needs to be done.

In summary many mechanisms might lead to prostate epithelial inflammation. Continuous exposure to the stimulating agent can set up a sustained or chronic inflammatory response leading to PIA and potentially to cancer. Questions that still need to be answered include: first, does the breakdown of prostate epithelial cells (e.g. in response to chemical injury) release antigens that either initiate an autoimmune response or reduce tolerance to future injuries? Indeed, a T-cell immune response to PSA in patients with chronic prostatitis has already been reported [76]. Second, do the endogenous inflammatory cells present in normal prostate, such as T-lymphocytes contribute to PIA and carcinogenesis? Methods such as automated quantitative image analysis are crucial to answer this [77]. Third, are there specific

polymorphisms or mutations in inflammation-related genes that predispose an area of PIA to initiation of prostate cancer? Aspects of this last question will be answered later in this chapter.

The Role of Diet in the Initiation of Prostate Cancer

Epidemiological studies have revealed a link between prostate cancer incidence and mortality and the consumption of red meat and animal fats [78]. North-east Asian and Northern Atlantic populations have the lowest international prevalence of prostate cancer and yet they assume western risk profiles within two generations on migration [79]. This is generally thought to be due to dietary factors. Saturated and monounsaturated animal fat as well as linoleic acid have been associated in a number of case control and cohort studies with a higher risk of prostate cancer [80, 81]. By contrast, Japanese studies have demonstrated a negative association with soybean products, isoflavones, and long-chain polyunsaturated fatty acids such as eicosapentaenic acid (EPA) and docosahexanoic acid (DHA) [82]. In addition trace metals such as zinc supplements in the VITamins And Lifestyle (VITAL) cohort have been associated with a decreased risk of advanced prostate cancer [83].

Studies of the Mediterranean diet (Greece in particular) have revealed a protective effect for lycopenes, selenium, vitamin E, pulses and high plasma 1,25-dihydroxyvitamin D levels. Foods high in calcium such as milk, which is also rich in insulin-like growth factor-1 (*IGF-1*), increase the risk of prostate cancer [84].

Mechanisms by which dietary fat could affect CaP development include effects on insulin IGF-1 [85], steroid hormone metabolism, free radical damage and fatty acid metabolism pathways. Transgenic mice fed with low versus high fat diets have shown a significant delay in progression from mouse PIN to CaP and a reduction in AKT activation consistent with an IGF-mediated role (see explanatory box) [86]. This study used the *probasin* directed Hi-Myc model of mouse CaP; as yet, it has not been replicated in other models.

One mechanism by which meats might stimulate cancer development is through the formation of heterocyclic amines (HCAs), molecules produced by cooking red meat at high temperatures, and which can be metabolised to DNA damaging agents. Rat exposure to the most abundant HCA, 2-amino-1-methyl-6-phenylimidazo[4,5-b]pyridine (PhIP), results in intestinal carcinomas, mammary tumours and CaP [87, 88]. PhIP has also been shown to recruit epithelial macrophages and stromal mast cells and induce PIA before inducing PIN and CaP [89].

Recently, it has been shown that genistein, the major isoflavone of soy, and resveratrol, a polyphenolic phytoalexin found in red wine and grape-derived products, suppress the development of CaP in transgenic rat models when administered either alone or in combination. These nutritional polyphenols reduce cell proliferation and induce apoptosis by reducing levels of growth factors such as IGF-1 and steroid signalling proteins such as SRC-3 [90].

In summary, although conclusive evidence is limited, it is possible that a diet high in soybean products, fish, fruit and vegetables, and low in red meat, dairy products and calcium, similar to the Japanese or Greek diets may reduce the risk of prostate cancer [91]. However, well-designed epidemiological studies such as nested case-control studies with nutritional analyses of blood samples are needed to confirm these associations. In addition further laboratory studies in vivo models of prostate cancer are required to elucidate the mechanisms.

The Role of Specific Genetic Mutations and Pathways in the Initiation of Prostate Cancer (Table 22.1)

NKX3-1/8p. The NKX3-1 homeobox gene regulates prostate epithelial differentiation. One of the commonest events in prostate carcinogenesis (in ~80% of CaP) is loss of specific regions of chromosome 8p which encodes NKX3-1 [92]. Fluorescence in situ hybridisation (FISH) and allelic imbalance analysis studies concur that loss of 8p12-21 is an early event, while 8p22 is more common in advanced CaP [93]. Chromosome 8p deletions are also present in lung and colorectal tumours, but NKX3-1 expression is restricted to the prostate in adult tissues. NKX3-1 homozygous mutant mice develop PIN by 1 year of age [94]. In the intact adult mouse prostate, all luminal cells and 10% of basal cells express Nkx3-1. Expression is virtually abolished on castration and quickly restored after androgen re-administration. The small number of residual Nkx3-1 expressing cells has been further characterised with serial single cell transplantation and with lineage-marked Nkx3-1 knock-in mice to show that HGPIN and CaP develops from these cells in an inducible PTEN deletion mouse model of CaP. Nkx3-1 is therefore proposed as a marker of a cell of origin for CaP. As discussed earlier in this chapter, these cells also express the androgen receptor (AR) and keratin 18 (CK18) consistent with a luminal origin [30].

PTEN. Mutations involving phosphatase and tensin homolog deleted on chromosome 10 (PTEN) are common with loss of function mutations being reported in ~30% of primary cancers and ~60% of metastatic lesions [95]. PTEN dephosphorylates phosphatidylinositol 3,4,5-triphosphate (PIP3) which is a product of phosphoinositide 3-kinase (Pi3K) activity. Increased levels of PIP3 in PTEN-deficient conditions alter the rate of protein translation, susceptibility to apoptosis and *anoikis*, entry in the cell cycle, differentiation and motility [35]. Key downstream effectors of PIP3 are PDK1, AKT and mTOR1&2, which play a fundamental role in supporting cancer cell metabolism, growth and survival [96]. Deletion of PTEN in the developing murine prostate leads to early onset and rapidly progressive neoplasia [97]. Cre-recombinase mediated PTEN excision in the murine prostate gland after puberty instead leads to a gradual onset of pre-malignant conditions within 16–20 weeks, following by progression to CaP at 1 year [98]. The delayed latency occurred despite evidence of prominent AKT/mTOR activation from the time of PTEN deletion. This indolent evolution of the disease after PTEN deletion in the mature mouse is reflective of disease initiation and progression in humans and is

Table 22.1 Common genetic and somatic changes in initiation of CaP

Gene	Location	Notes
Nkx3-1 [30, 117, 118]	8p12-22	Homeodomain transcription factor. Prostate specific – suppresses growth of epithelial cells/maintains prostate stem cells. One allele frequently deleted in primary tumours. Possible marker of CaP cell of origin
PTEN [98, 119]	10q23.31	Lipid phosphatase that suppresses cell proliferation and increases apoptosis. One allele lost in ~30% of primary tumours. Mutations in 60% of metastatic lesions. Constitutive PTEN deletion in mouse prostates leads to rapid CaP. Post-pubescent deletion leads to PIN and slow development of CaP at 1 year
AKT [99]	14q32.32	Pi3K pathway. Inhibited by PTEN. Activation of murine AKT induces uniform highly penetrant PIN. Only progresses to CaP if there is a secondary hit (e.g. p27)
Myc [107, 108, 120]	8q24	Transcription factor with multiple regulatory roles in epithelial proliferation, senescence, apoptosis and metabolism. Overexpression can directly transform cells. Amplified in ~70% of castrate resistant tumours
ERG	21q22.3	Encode ETS transcription factors. Fusion transcripts with androgen-regulated TMPRSS2 present in ~50% of CaP at all disease stages. Particularly implicated in progression of PIN to CaP
ETV 1-4 [101, 103, 104] (ETS)	7p21.2 19q13.12 1q21-q23 17q21.31	
p27 [99, 121] (CDKN1B)	12p12.3	Cell cycle regulator – regulates cyclin-CDK to inhibit cell cycle progression. Reduced levels observed in CaP progression. Ablation of p27 in mouse PIN induces CaP
Rb [122]	13q	Cell cycle regulator. Infrequently mutated in humans but homozygous mutant mice develop hyperplasia, dysplasia and CaP
Telomerase [123]	Chromosome termini	Maintains chromosomal stability. Shortened telomeres found in >90% of PIN and CaP
E-cadherin [124]	16q22.1	Cell adhesion. Prevents migration of epithelial cells. Reduced expression in PIN and CaP
c-Met [125, 126]	7q31	Tyrosine-kinase receptor. Overexpressed in PIN, CaP and metastasis. Levels repressed by normal AR signalling
FGFs [127, 128]	7:15q15-21.1 8:10q24 10:5p12-13	Growth factors. Regulators of prostate growth. FGF7 & 10 associated with progression in TRAMP mice. FGF8 enhances cell migration
p53 [118, 129]	17p13.1	Regulates apoptosis/senescence in response to DNA damage or telomere dysfunction. Mutations less common in primary CaP but occur in 50% of castrate resistant cancers
AR [130]	Xq11-12	Expressed in most primary CaP. Amplified or mutated in ~30% of castrate resistant tumours

consistent with PTEN deletion being one of the key genetic modifications accumulated in the development of prostate cancer. Inactivation of PTEN leads to deregulated PI3K signalling and subsequent AKT activation. Transgenic overexpression of AKT1 in luminal cells of the ventral murine prostate has been shown to induce PIN with increased expression of senescence markers which are proposed to limit progression to CaP. Only on genetic ablation of p27^{Kip1} does progression occur. Similarly, in humans, senescence markers such as p27 are seen to be elevated in PIN that does not progress to CaP as opposed to cancer-associated PIN and CaP [99]. This is consistent with the need for a double hit: lesions initiated by PTEN deletion and upregulation of AKT also need inactivation of cell cycle limiters such as p27 in order for progression to CaP to take place.

TMPRSS2-ETS. Gene fusions involving members of the ETS family of transcription factors occur frequently in human CaP. The TMPRSS2-ERG fusion gene is generated by an interstitial deletion on chromosome 21 or by reciprocal translocation and is the most common rearrangement in CaP, being found in ~50% of localised tumours [100]. Cell line experiments suggest that the androgen-responsive promoter elements of TMPRSS2 mediate overexpression of ERG (or other ETS family members) [101]. Microdissection and fluorescence in situ hybridisation (FISH) studies have shown that, when present, the fusion is detected in essentially all the malignant cells within a focus of tumour, as well as in adjacent PIN. However, it is less commonly found in premalignant PIN when there is no tumour present [102]. Mice with probasin driven overexpression of ERG alone do not develop premalignant changes [103]. However, when TMPRSS2-ERG fusion mice are crossed with PTEN deletion/AKT activation, all mice develop PIN at 6 months, and CaP by 10–12 months [104]. This suggests that PI3K pathway changes are necessary for disease initiation and development of PIN, while ETS fusion rearrangements play a role in disease progression from PIN to CaP.

Myc/8q24. Chromosome 8q24 is an established risk locus for many common epithelial cancers, including prostate, colon, breast and bladder. It was originally discovered by fine mapping of a prostate cancer linkage peak from a family based study [105]. Most of the *single nucleotide polymorphisms* (SNPs) at 8q24 are contained within an approximately 500 kb sequence devoid of well-characterised genes. However, c-Myc, a well known oncogene in these cancers is nearby [106]. Copy number gain and amplification of 8q24 and increased c-Myc activity has been shown as an early event in some prostate cancers and in a high proportion of resistant tumours [107,108]. c-Myc has been shown to have varying oncogenic/tumour suppressor effects, from direct malignant transformation of benign cells in culture and induction of a pro-resistance phenotype [109] to increases in cell proliferation rates and recruitment of quiescent stem cells into rapidly dividing intermediate progenitors [91], to induction of apoptosis and senescence via effects on p53 and p21 [110, 111]. Overexpression of c-Myc in mouse prostates under the control of probasin (Lo-Myc) and probasin/AR promoters (Hi-Myc) leads to development of murine PIN and rapid development of invasive CaP within 6–12 months. These mice were also found to have a distinct loss of Nkx3-1 expression at the transition

from PIN to CaP but Nkx3-1 is not directly regulated by c-Myc [108]. With c-Myc having such varied effects it remains crucial to delineate its direct targets in prostate carcinogenesis and to clarify its interaction with the other pathways mentioned here. Cooperativity between c-Myc and PTEN deletion has been recently shown in development of HGPIN and CaP. PTEN deletion alone in mouse prostates was shown to activate p53, thought to have a “protective” senescent effect to limit the extent of malignant transformation. However, concomitant c-Myc activation suppressed the protective effect, probably by regulation of p21, to magnify the proliferative and tumorigenic effect [109].

SNPs/GWAS. Genome-wide association studies (GWAS) have emerged as a powerful approach to identify common disease alleles without prior knowledge of position or function. Genotype frequencies are compared between cases and controls at large numbers of single nucleotide polymorphisms (SNPs), chosen to report on most known common variants in the genome [112]. This technique has identified several interesting loci associated with CaP. Most recently, analysis of around 500,000 SNPs in 2,000 cases and controls, followed up with analysis of smaller numbers of SNPs in greater numbers of cases (4,000 cases in the second stage; 16,000 in the third) have revealed prostate cancer susceptibility loci in 14 separate chromosomal regions [112, 113], as well as eight loci in the 8q24 region [114] (Table 22.2) and it is expected that more will soon follow. These studies confirm that CaP is genetically complex and

Table 22.2 Single nucleotide polymorphisms (SNPs) associated with prostate cancer

Chromosome	SNP Marker	Potentially causative genes
3 [111]	rs2660753	<i>CHMP2B, POU1F1</i>
6 [111]	rs9364554	<i>SLC22A3, SLC22A2, LPAL2, LPA</i>
7 [111]	rs6465657	<i>LMTK2, BHLHB8</i>
10 [111]	rs7920517, rs10993994	<i>MSMB</i>
11 [111]	rs7931342	
19 [111]	rs2659056, rs266849, rs2735839	<i>KLK2, KLK3(PSA)</i>
X [111]	rs594561	<i>X NUDT10, NUDT11, GSPT2, MAGED1/4B/4, CTD-2267G17.3, XAGE2/1C/1D/5/3, SSX8/7/2/2B, SPANXN5, TMEM29B/29</i>
8q24 [113]	rs12543663, rs10086908, rs1016343, rs13252298, rs6983561, rs620861, rs6983267, rs10090154	<i>c-Myc</i>
2p21 [112]	rs1465618	<i>THADA</i>
2q31 [112]	rs12621278	<i>ITGA6</i>
4q32 [112]	rs17021918	<i>PDLIM5</i>
4q24 [112]	rs7679673	<i>TET2</i>
8p21 [112]	rs2928679, rs1512268	<i>NKX3-1</i>
11p15 [112]	rs7127900	<i>IGF2, IGF2AS, INS, TH</i>
22q13 [112]	rs5759167	<i>TLL1, BIK, MCAT, PACIN2</i>

Potentially causative genes coded by or regions of regulation associated with these SNPs as shown

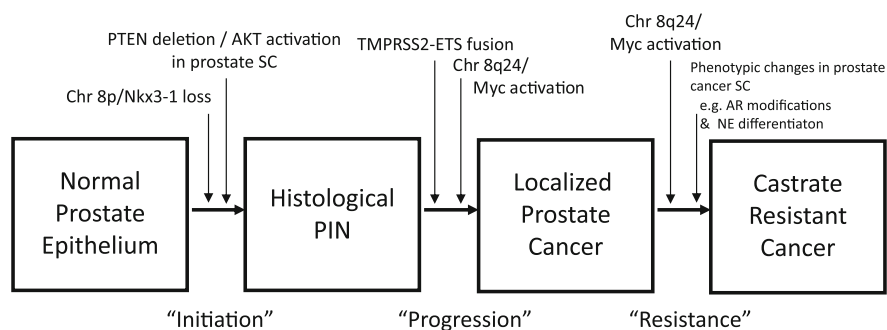


Fig. 22.7 Summary of current knowledge of the key steps involved in the initiation and progression of prostate cancer, as well as in development of resistant disease (not covered in this chapter). SC stem cell; AR androgen receptor; NE neuroendocrine

help to clarify the genetic architecture of CaP. Few of these loci are located directly within exon coding sequences (with the exception of MSMB and LMTK2) suggesting that diverse regulatory pathways are likely to be involved.

In summary, there are multiple specific genetic and regulatory pathway changes that occur in the development of CaP, some of which have been outlined here (Fig. 22.7). There is no doubt that there is parallel and chronological heterogeneity with a variety of factors interacting alongside each other in initiation of PIN and at subsequent progression to CaP and also to more resistant disease. A more complete understanding of these changes and their interactions will provide biomarkers for disease risk and deliver targets for therapeutic manipulation.

Implications for Early Detection and Prevention of Prostate Cancer

Specificity in therapeutic targeting of cancer stem cells will always be difficult. We are in a unique position with prostate cancer in that the patient population who develop the disease are rarely in need of their prostate. Therefore, a treatment targeted specifically to prostate stem cells, even if not specific to prostate cancer stem cells, is a viable option. However, few of the markers for prostate cancer stem cells discussed in this chapter is specific to the prostate. There is one exception: NKX3-1 is specific to the prostate after puberty and is a putative marker for the cell of origin for prostate cancer. If the cells that accumulate the genetic changes responsible for initiation and progression of prostate cancer could be destroyed then prostate cancer would not develop/progress. No compounds capable of this have yet been developed.

By contrast, treatment of inflammation is well established. The results of multicentre randomised controlled trials are awaited, for example studying the effect of non-steroidal anti-inflammatories (NSAIDs) in prevention of CaP.

However, a recent study of neoadjuvant celecoxib in clinically localised prostate cancer reported no difference in primary or secondary outcomes [115]. The search continues for an effective way to manipulate CaP risk by anti-inflammatory treatment: a randomised trial assessing the effect of treatment at the pre-malignant stage is needed. The discovery of viruses associated with CaP such as XMRV also raises the possibility of using vaccines or anti-retroviral drugs to treat CaP-associated infections and lower the risk the disease. Given its association with higher risk disease, XMRV might also serve as a useful marker to identify patients that would most benefit from early treatment [69].

Biomarkers of disease risk and likelihood of recurrence and progression will be an important means of targeting appropriate treatment. Biomarker information can be readily obtained from serum or urine samples, attractive to patients because of their non-invasive nature. In addition, more detailed analysis of prostate biopsy material with particular attention to field tumourigenesis of 'near normal' tissue [115], will allow more information to be obtained from currently available material. Functional understanding is not a prerequisite for a biomarker to be useful in providing diagnostic and prognostic information when candidates have been rigorously validated by correlation of tissue expression and clinical outcome. For example, microseminomaprotein-beta (MSMB) expression is consistently high in normal prostate tissue and PIN, but lost in CaP [116]. This could be useful in assisting TRUS biopsy diagnostics and in directing the need for repeat biopsy. However, given the heterogeneity of prostate cancer development, a more complete knowledge of the key genetic players and their functional interactions will be required and this will most likely lead to a validated panel of diagnostic and prognostic markers for use in the clinical setting.

The identification of prostate cancer susceptibility genes by GWAS has a variety of clinical implications. The location of SNPs within regions that directly code for MSMB and LMTK2 suggest that these proteins might have a role in prostate cancer screening or provide potential therapeutic targets [111]. There are also implications for risk counselling although the relative risks conferred by each loci is modest (odds ratio of 2 at best) suggesting that "at-risk" SNP identification will be most useful at a population rather than individual level.

Conclusion

Prostate cancer is a heterogeneous disease with multiple factors contributing to the development of pre-malignant lesions and progression to adenocarcinoma. The role of cancer stem cells, inflammation, diet and certain specific genetic changes have been discussed in this chapter. With the identification of specific dietary factors contributing to the development of CaP the outlook is positive for lifestyle modification making a significant difference to the impact felt by this disease. It may be that targeting particular high risk populations identified through SNP profiling could lead to early preventative interventions. Prostate cancer research is a

rapidly developing field with a healthy commitment of personnel and resources and new genetic players are being identified all the time. The jigsaw of heterogeneity is beginning to be pieced together and, it is hoped, will soon provide us with exciting new additions to the currently available diagnostic and therapeutic options.

Comment Boxes

Exocrine: Exocrine glands secrete their products (excluding hormones and other chemical messengers) into ducts (duct glands) which lead directly into the external environment. They are the counterparts to endocrine glands, which secrete their products (hormones) directly into the bloodstream (ductless glands) or paracrine glands that release hormones that affect only target cells nearby the release site. Examples include the sweat and salivary glands (exocrine), stomach, liver, pancreas, and prostate (mixed).

Wolffian duct: The Wolffian duct is a paired organ found in mammals during embryogenesis. It was named by Caspar Friedrich Wolff in 1759. It connects the primitive kidney to the cloaca and serves as a clustering site for embryonic cells of the reproductive tracts. The Wolffian duct goes on to form the epididymis, vas deferens and seminal vesicles.

Acinus: Acinus refers to the cluster of cells that make up the termination of an exocrine gland such as the prostate. Acinus is Latin for berry.

Gleason: The Gleason staging system is based upon the microscopic architectural appearance (size, spacing and irregularity) of the prostate glands. The pathologist assigns a grade (from 1 to 5) to the most common tumour pattern and a second grade to the next most common. The combined score is the Gleason score. In practice the lowest score commonly allocated is 6 and the highest score is 10.

Lin⁻Sca-1⁺CD133⁺CD44⁺CD117⁺: Cells can be sorted according to the presence of cell surface proteins which act as specific markers for different groups of cells. These particular cell surface markers have been proposed as the unique signature of stem cells in the mouse prostate.

IGF-1: Insulin-like growth factor (IGF-1) is a protein hormone similar to insulin in molecular structure. It has an important role in child growth and continues to have anabolic effects in adulthood. It is stimulated by growth hormone. 98% is protein bound by one of 6 binding proteins (IGF-BP). It binds to IGF-1 receptor (IGF1R), a tyrosine kinase receptor, to initiate intracellular signalling and is one of the most potent activators of Pi3K/AKT signalling and has been implicated in carcinogenesis.

Probasin (PB): Probasin (PB) is a prostate-specific nuclear and secreted protein found in differentiated luminal epithelial cells. The probasin promoter is used in

mouse and rat models to direct transgene expression specifically to prostate epithelial cells. This commonly-used technology may not allow for tumour initiating events that occur in undifferentiated prostate stem cells.

Anoikis: Apoptosis triggered by detachment of anchorage-dependent cells from surrounding extracellular matrix. Metastatic tumour cells resist anoikis to allow survival and attachment at distant sites. Anoikis is a Greek derivative meaning “the state of being without a home”.

SNPs: A single-nucleotide polymorphism (SNP, pronounced *snip*) is a DNA sequence variation occurring when a single nucleotide in the genome (or other shared sequence) differs between members of a species (or between paired chromosomes in an individual). For example, two sequenced DNA fragments from different individuals, AAGCCTA to AAGCTTA, contain a difference in a single nucleotide.

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