ABSTRACT

We have entered a transformative period in cancer prevention (including early detection). Remarkable progress in precision medicine and immune-oncology, driven by extraordinary recent advances in genome-wide sequencing, big-data analytics, blood-based technologies, and deep understanding of the tumor immune microenvironment (TME), has provided unprecedented possibilities to study the biology of premalignancy. The pace of research and discovery in precision medicine and immunoprevention has been astonishing and includes the following clinical firsts reported in 2015: driver mutations detected in circulating cell-free DNA in patients with premalignant lesions (lung): clonal hematopoiesis shown to be a premalignant state; molecular selection in chemoprevention randomized controlled trial (RCT; oral); striking efficacy in RCT of combination chemoprevention targeting signaling pathway alterations mechanistically linked to germline mutation (duodenum); molecular markers for early detection validated for lung cancer and showing promise for pancreatic, liver, and ovarian cancer. Identification of HPV as the essential cause of a major global cancer burden, including HPV16 as the single driver of an epidemic of oropharyngeal cancer in men, provides unique opportunities for the dissemination and implementation of public health interventions. Important to immunoprevention beyond viral vaccines, genetic drivers of premalignant progression were associated with increasing immunosuppressive TME; and Kras vaccine efficacy in pancreas genetically engineered mouse (GEM) model required an inhibitory adjuvant (Treg depletion). In addition to developing new (e.g., epigenetic) TME regulators, recent mechanistic studies of repurposed drugs (aspirin, metformin, and tamoxifen) have identified potent immune activity. Just as precision medicine and immune-oncology are revolutionizing cancer therapy, these approaches are transforming cancer prevention. Here, we set out a brief agenda for the immediate future of cancer prevention research (including a “Pre-Cancer Genome Atlas” or “PCGA”), which will involve the inter-related fields of precision medicine and immunoprevention – pivotal elements of a broader domain of personalized public health. Cancer Prev Res; 9(1); 2–10.

© 2016 AACR.

A Time of Transformation

Immense breakthroughs in understanding the progression of genomic events and inflammatory microenvironment that drive premalignancy provide unprecedented possibilities to transform cancer prevention. Although opinions about the current state of cancer prevention science are still wide-ranging (1–5), as is characteristic of emerging fields, we stand on the cusp of opportunity. Just as precision therapy and immunotherapy are transforming cancer treatment, precision medicine and immunoprevention are now moving to the clinic with great promise. Additional gains, such as identification of tractable molecular targets, more sophisticated risk stratification strategies and algorithms, better preclinical models, earlier detection of premalignant lesions and early-stage cancers, new agents, rational development of combinatorial chemopreventive interventions, current availability of 14 FDA-approved drugs and vaccines for application to cancer prevention (5) and advances in implementation science (defined as the application of what we already know), all point to a strong possibility to reduce cancer...
incidence, morbidity, and mortality in the near future. Given that the global burden of cancer is enormous and increasing (the number of diagnosed cases is expected to grow worldwide from 13.3 million in 2010 to 20 million by 2030; ref. 6), cancer prevention (including early detection) is essential to our ability to lessen the burden of cancer in our lifetime. The optimism surrounding progress in cancer therapeutics is propelling investigation into applications of enabling technologies and extrapolation of effective interventions in established disease to the more difficult challenges of cancer prevention or interception (7).

Here, we set out a brief agenda for the near-term future of this exciting field through the inter-related disciplines of precision medicine and immunoprevention — elements of a broader domain of personalized public health.

Biology of Premalignancy

There has been increasing focus on the molecular origins of cancer over the last several years (8). In contrast to studies in malignancy, however, genome-wide analyses of premalignancy have been rare. Remarkable technological advances in next-generation sequencing (NGS, requiring only nanograms of starting DNA/RNA from minute biopsies down to single cells), computational biology, and high-throughput functional screening have now provided us with very real possibilities to deeply probe the biology of premalignancy. Recent studies in lung squamous premalignancy of single nucleotide polymorphism arrays identified losses of tumor suppressors RNF20 and SSBP2 and amplification of the RASGRP3 oncogene (9) and RNA-seq analyses identifying 3q26.33–3q29 (including SOX2) amplification/overexpression (10). Surprisingly, circulating DNA containing cancer driver mutations has been detected in circulating cell-free DNA in patients with atypical adenomatous hyperplasia, preinvasive (premalignant) lesions of the lung, which could be used for early detection and to follow the effects of preventive interventions (11). Studies of the airway field of injury have detected EGFR mutations in adjacent histologically normal epithelium of EGFR-mutant lung adenocarcinoma (12), and whole-genome expression profiling has identified other activated oncogenic signaling pathways (e.g., PI3K/AKT) in the airway of smokers with premalignant lesions and/or lung cancer (13) and in the cytologically normal bronchial airway of smokers with premalignant lesions, potentially enabling genomic approaches to monitoring the preventive effects of PI3K inhibitors (14). This precision genomics approach is currently being tested in a phase IIb prevention trial of myo-inositol among high-risk smokers with premalignant lesions.

Recent studies support the model that a specific sequence of acquired genomic events over many years characterize the transition from normal epithelium to invasive carcinoma and that
specific “driver” events, acquired in a particular order, enable cells to progress from benign growth to an invasive phenotype. A study sequenced 293 cancer-relevant genes in primary melanomas and their adjacent precursor lesions to study the succession of genetic alterations during melanoma progression (15). Whereas benign nevi harbored \( \text{BRAF} \) \( \text{V600E} \) mutations exclusively, this study identified an intermediate (premalignant) category of melanocytic neoplasia characterized by additional mutations, including TRIST, TERT, and NRAS mutations, and found a mutational signature implicating ultraviolet radiation as a major driver of melanocytic neoplasia progression. Ultra-deep sequencing of 74 cancer genes in 234 biopsies of sun-exposed eyelid epidermis revealed mutations similar to those seen in many malignancies, including NOTCH1 and FAT1 genes (16). NOTCH1 driver mutations have also been detected in oral premalignancy (17). Studies in breast lobular carcinoma in situ, pancreatic mucinous cysts, and Barrett esophagus have identified genomic patterns of premalignant progression to cancer, which have important implications for risk prevention and early detection (18–20). Some data suggest that driver mutations in early neoplasia can differ from those in the corresponding cancer. A critical next step for this field will be developing systematic approaches for whole-genome profiling of premalignant lesions followed longitudinally as they progress toward cancer—the proposed initiative “Pre-Cancer Genome Atlas” or “PCGA” (21). This initiative will provide critical insights into the molecular events (and possible sequence) in premalignant cells and their microenvironment that drive progression to invasive cancer (Fig. 1), enabling precision approaches to cancer prevention and early detection.

As described above, the proposed PCGA focuses on solid tumors of epithelial origin; however, it also applies to hematological neoplasia. The Cancer Genome Atlas (TCGA) did include one blood cancer [acute myelogenous leukemia (AML)]. Recent genomic studies suggest that clonal hematopoiesis is a pre-malignant state. Somatic mutations observed mostly in three genes (\( \text{DNMT3A}, \text{TET2}, \) and \( \text{ASXL1} \)), known drivers of hematologic malignancies, have been identified in the blood of people without a known hematologic disorder. The prevalence of these mutations, termed clonal hematopoiesis of indeterminate potential, increases with age (22) and is associated with increased risk of progression to a blood cancer (23). Somatic mutations typical of myelodysplastic syndrome (MDS) and AML have been found in up to 40% of patients with idiopathic cytopenias of undetermined significance (24) who may be at greatest cancer risk. Clonal hematopoiesis detected by deep sequencing was identified in aplastic anemia (25) and associated with risk of developing therapy-related MDS or AML (26). Several prospective studies of ICUS and CCUS have been initiated to identify patients with preclinical MDS (27) most likely to progress and therefore potential candidates for early treatment or prevention. Related hematologic neoplasia work is studying the monoclonal gammopathy of undetermined significance (MGUS)—multiple myeloma sequence, including smoldering myeloma, which has an overall risk of progression to malignancy (multiple myeloma) of 10% per year (compared with 1% per year for MGUS). Recent genomic and immune studies of MGUS progression are providing novel targets for precision and immune prevention (28).

**Precision Medicine**

**Chemoprevention**

The status of this field, including RCTs, has been recently reviewed (4, 5) and includes notable successes (e.g., with selective estrogen receptor modulators and aromatase inhibitors in breast cancer) and failures (vitamin E and selenium in prostate cancer). Two important new RCTs (29, 30) include a positive trial of oral nicotinamide (which enhances DNA repair) in nonmelanoma skin cancer, typically caused by UV-induced DNA damage (29); this provocative result is consistent with an earlier report of topical DNA repair enzymes in xeroderma pigmentosum, a germline DNA repair disorder (31). The first precision medicine RCT in chemoprevention (EPOC) was reported just two months ago (32), beginning a new era of molecular selection in this field (33). Perhaps the most promising current precision medicine approach to change standard of care in cancer prevention involves molecular selection (based on prostaglandin pathway studies) for the repurposed (and now established) chemopreventive drug aspirin in colorectal neoplasia. In September 2015, the US Preventive Services Task Force (USPSTF) recommended low-dose aspirin for colorectal cancer (CRC) prevention based on age and risk (34), a major milestone for the field of cancer prevention. The USPSTF’s recommendation for aspirin use in this setting acknowledges the substantial body of data that now exists supporting aspirin’s efficacy for the prevention of CRC. Given aspirin’s potential adverse effects (e.g., bleeding), further tailoring aspirin use is a high priority. A series of recent reports based on studies of colorectal neoplasia, prostaglandins, and aspirin mechanism support a precision medicine approach in this setting: (i) high urinary PGE-M levels were prognostic (associated with advanced adenomas risk) and predictive for aspirin and/or NSAID preventive activity (35); (ii) aspirin reduced colorectal cancer risk in patients with high 15-hydroxyprostaglandin dehydrogenase mRNA expression in the normal mucosa adjacent to cancer (36); and (iii) aspirin, NSAIDs, or both were associated with reduced colorectal cancer risk and the association of these agents with risk differed based on an SNP at chromosome 12 that could potentially affect prostaglandin synthesis (37). A related study reported that \( \text{SLCO2A1} \) mutation carriers develop early-onset colon neoplasia and are NSAID resistant, suggesting for the first time that disordered prostaglandin catabolism can mediate inherited susceptibility to colorectal neoplasia in humans, mimicking the phenotype of the related HPGD-null mouse (38). \( \text{SLCO2A1} \) encodes the prostaglandin transporter, shown to play a critical role in colorectal neoplasia (39). Related \( \text{NSAID} / \text{CRC} \) clinical trial data include: \( \text{PIK3CA} \) mutation in CRC (genetic driver also detected in adenomas) may predict aspirin efficacy (40), 5-aminosalicylates (related to NSAIDs but poorly absorbed) were associated with reduced colorectal neoplasia risk in the inflammatory bowel disease ulcerative colitis (41), and recent standard-of-care-changing RCTs in hereditary CRC (see Germline mutations below).

**Early detection**

Developing and validating precision medicine approaches for early cancer detection remains a critical challenge in the prevention field. Standard, conventional screening includes mammography (and MRI for high-risk women, e.g., with \( \text{BRCA} \) mutation carriers or Li-Fraumeni syndrome), colonoscopy and fecal occult blood tests, PAP and HPV tests, and low-dose computed tomography for breast, colon, cervical, and lung tumors, respectively. Newer screening approaches in clinical development to detect premalignant disease include the following hepatic studies: MRI and magnetic resonance elastography (42), 3D molecular MRI collagen imaging (43), and plasma eicosanoid lipidomic
profiling (44) detecting the fibrosis and inflammation characterizing non-alcoholic steatohepatitis or NASH, a precursor of liver cancer, the fastest-rising epithelial cancer in the US. This NASH work has important implications for liver cancer surveillance and prevention (45).

Current screening tests detect lesions with a very wide spectrum of natural behavior from those with lethal potential to completely benign lesions. There is an urgent need to develop precision molecular tests to: (i) identify individuals at highest risk who should undergo these screening tests (i.e., screening biomarkers), (ii) distinguish benign versus malignant lesions found on imaging modalities in order to determine which of these lesions should undergo invasive biopsy (i.e., diagnostic biomarkers), and (iii) distinguish biologically indolent versus aggressive tumors that should be treated (i.e., prognostic biomarkers). Advances in computational biology and NGS technology are revolutionizing our ability to discover genomic biomarkers in relatively accessible biosamples. Nucleic acids, both noncoding RNA and DNA mutations, can now be measured in circulating blood due to rapid advances in liquid biopsy technology. These approaches were initially focused on known mutations in commonly altered genes but are now being extended to de novo mutations through unbiased analyses via genome-wide approaches (46). Early stage cancers and precancers may shed some DNA into the circulation (11), but detection of somatic genetic alterations in the circulation in this setting has been challenging and still requires much optimization in terms of the sensitivity and specificity of the assays. RNA-seq bioinformatics algorithms and high-throughput isoform-level RT-qPCR recently identified ovarian cancer-specific mRNA isoforms, suggesting the amazing possibility of ovarian cancer early detection by PAP test (47). Furthermore, several mRNA isoforms encode proteins with unique primary structures, which could be targeted by peptide or T cell-based vaccines.

These rapid advances in biomarker discovery science have struggled to translate into the clinic due, in large part, to the challenge in designing and implementing prospective studies to validate the biomarkers in the clinical setting in which the tests would be used. Two recent genomic biomarkers for early cancer detection have overcome this important hurdle and successfully translated to the clinic. A highly sensitive stool DNA test was validated as a screening tool for CRC (48). Gene-expression alterations identified in the cytologically normal epithelium from the mainstem bronchi of smokers with lung cancer (14), led to a bronchial airway genomic classifier validated as a highly sensitive tool for lung cancer detection in two prospective, multicenter trials (49). This next generation of molecular testing holds the promise to detect biologically aggressive lesions, which would be transformational.

Germline mutations in cancer predisposition genes

Precision prevention may also involve risk stratification, early detection, and risk reduction in patients carrying cancer predisposition genes, including both rare high-penetrance mutations and – more common lower-penetrance – genetic variants. Surgical prevention by removal of at-risk tissues is effective but may come at a high cost in quality of life, such as prophylactic pneumonectomy. Many hereditary syndromes feature predisposition to tumors of multiple sites or include prominent involvement of sites not amenable to surgical risk reduction (e.g., Li Fraumeni, Cowden’s, VHL or RASopathies). Strategies exploiting specific molecular defects in malignancies developing in the setting of predisposition genes can provide insights into cancer prevention and therapy (50, 51).

Tumor testing for mismatch repair (MMR) deficiency in CRC (e.g., microsatellite instability [MSI]) establishes a new model of targeted screening based on a cancer predisposition gene. Lynch syndrome (LS), caused by a germline MMR gene mutation, accounts for ~3% of CRC characterized by MSI. A growing body of data indicates that this tumor testing of all newly diagnosed CRC (universal tumor screening) could identify LS families and patients shown to benefit from intensive surveillance (e.g., colonoscopy) and risk-reducing surgery to prevent primary and second primary CRC (52, 53). Aspirin has also been shown to reduce LS CRC risk in RCT (54). 2015 US estimates are that universal tumor screening will identify ~21,000 people with LS, producing substantial public health benefits (cancers prevented, lives saved and cost effective). Of note, 12-15% of newly diagnosed CRC tumors are MSI-positive, but only 3% have LS. The MSI-positive patients (including LS-negative patients not recommended for increased surveillance) were recently shown to benefit from anti-PD-1 therapy (55), providing even greater support for this tumor tissue screening approach.

A clinical breakthrough for this field is the very recent RCT reporting striking efficacy of combination chemoprevention in familial adenomatous polyposis (FAP). Targeting the convergence between Wnt and EGFR signaling pathways and COX-2 activity (alterations mechanistically linked to the germline adenomatous polyposis coli [APC] mutation causing this disease) with sulindac and erlotinib produced a highly significant reduction in duodenal adenoma burden (56), far more active than single agent sulindac or aspirin (57). This finding has major implications on standards of care for this devastating disease, which can be associated with thousands of colorectal adenomas and a near 100% cancer risk. After prophylactic colectomy (standard of care), duodenal adenocarcinoma is the leading cause of cancer death for these patients.

Seminal work showing that BRCA1/2 mutations induce defects in DNA repair, which confer sensitivity to PARP inhibitors across associated tumor types, including breast, ovary, prostate, and pancreas, establishes a new paradigm of targeted therapeutics in the cancer predisposition setting (58). The possibility of specific therapies for BRCA mutation carriers has led to incorporation of BRCA germ-line characterization for all ovarian and triple-negative breast cancers into the National Comprehensive Cancer Network (NCCN) guidelines. Opportunities for medical risk reduction for BRCA mutation carriers may target DNA-repair defects and/or capitalize on other site-specific data, such as tamoxifen in breast cancer prevention (59). The application of genome-wide association study data as modifiers of high-penetrance genes or more complex risk models of common less-penetrance genes offers promise for more precise personalized risk estimates (60). Loss of heterozygosity screening of oral brushings may help stratify head and neck cancer risk in Fanconi anemia, a rare DNA repair disorder associated with an extremely high risk of oral cancer (61). Novel vaccine prevention strategies in Lynch syndrome and BRCA1/2 carriers are discussed in the next section.

Immunoprevention

Viral vaccines

A successful example of immunoprevention is the nationwide hepatitis B virus (HBV) vaccination program in Taiwan
that began in 1984 and produced an 80% reduction in the incidence of hepatocellular carcinoma (62). Expanding world-wide access to HBV vaccination is a harbinger of benefits to come. Global perspectives on the patterns of human papillomavirus (HPV)-related cancers (e.g., oropharyngeal) and preventing virally related cancers with vaccines, including efforts to make these vaccines available to countries experiencing financial hardships, highlight the burden and challenges of these viral diseases (63, 64). EBV vaccine development has been challenging due in part to complex viral antigen expression patterns.

The standard three-dose schedule of prophylactic HPV vaccine given before infection has 90–100% efficacy in preventing HPV infection and associated anogenital neoplasia (vulva, vagina, cervix, anus and penis), and limited data from secondary analysis of RCT in women reported vaccine protection for oral HPV infection (60). For preventive vaccines, very high antibody concentrations have been reported in HPV-vaccinated younger populations receiving two doses, which is now the schedule recommended by the WHO for girls under 15 years (65). RCTs in Costa Rica and India suggest that even a single HPV16/18 vaccine dose could induce a sustained antibody response (66, 67). Of great public health significance, planning is now underway for an RCT specifically designed to evaluate the protection of one versus two doses in Costa Rica and a US immunobridging study (including males) done in parallel. Another preventive vaccine approach is to eradicate existing premalignant lesions where the pathway to transformation is known. The first vaccine tested clinically in premalignant HPV disease (vulvar intraepithelial neoplasia) was composed of long peptides derived from HPV16 E6 and E7 oncoproteins and produced major activity and strong T-cell responses (68). This therapeutic vaccine approach has produced histopathologic regression and viral clearance in a phase II RCT in cervical intraepithelial neoplasia (69).

A number of prevention studies have focused on the growing public health epidemic of HPV-associated oropharyngeal cancer (70), including two early-detection research studies: oropharyngeal "PAP" smears (71) and influence of childhood tonsillectomy effect on subsequent oropharyngeal cancer (72). The dramatic cancer disparity of blacks versus whites in HPV-positive oropharyngeal cancer (73) is well established; updated data suggest that these patterns may be changing over time (74). No premalignant lesions have been identified in this setting, but current prevention work is focusing on oral HPV16 infection, which tracks closely to oropharyngeal cancer, e.g., both are 4-fold higher and increasing in men compared to women (75). A recent report on the long-term persistence of oral HPV16 infection in men (75) adds important new data to the scarce natural history information currently available. Genomic and imaging studies to identify high-risk groups and early neoplasia in the setting of persistent oral HPV16 infection are ongoing.

Non-viral vaccines

Recent clinical success of HPV (including therapeutic) vaccines for prevention and checkpoint inhibition (proving that immunity can inhibit cancer growth) for therapy has generated tremendous enthusiasm for non-viral vaccine immunoprevention. The immune-checkpoint inhibitors (e.g., targeting CTLA-4 or PD-1), which act on previously induced T cells, are producing durable remissions in some patients with metastatic, previously treated cancers. Their utility in prevention, however, is limited by their serious autoimmune toxicities. Furthermore, it is not clear that these checkpoint signals are important in early TME. Vaccines are an immune approach that is broadly available, specific, cost-effective, and work best in immunocompetent individuals. Vaccines targeting cancer-associated antigens have been studied extensively over the last 30 years in thousands of patients and have been shown to have a very favorable safety profile setting the stage for prevention vaccines, and limited dosing should improve implementation and adherence. Tumor-specific antigens (TSAs), such as KRAS and p53 mutations exclusively on tumor/premalignant cells, have safety advantages as vaccine targets compared with tumor-associated antigens (TAA)s present on tumor and normal cells because of potential for less autoimmune toxicity.

Although more complex and recent than the development of vaccines against foreign pathogen-associated viral targets (e.g., hepatitis B), vaccines against the less-immunogenic neoantigens (genetic drivers and other tumor antigens) are showing promise in preclinical prevention models (e.g., KRas in pancreas models; activating EGFR mutations in lung adenocarcinoma; refs. 76–78) and have now entered early-phase clinical trials (e.g., HER2 and MUC1). This focus is very timely, as evidenced by a major new initiative by Cancer Research UK, which just issued a £20M Grand Challenge that includes a charge to develop vaccines to prevent non-viral cancers (79). The first clinical trial of a preventive vaccine based on a tumor antigen was in patients with advanced colorectal adenomas (80). The vaccine consisted of the 100-mer peptide derived from the tandem repeat region in the TAA MUC1 extracellular domain and adjuvant, toll-like receptor (TLR)-3-agonist Poly-LICIC. It elicited a strong humoral and cellular MUC1-specific immunity and increased IgG levels after a booster injection at one year, demonstrating induction of immune memory. Patients who did not respond (i.e., no increase in MUC1 IgG antibody) had high levels of circulating myeloid-derived suppressor cells (MDSCs) before vaccination, providing the first clinical evidence suggesting that non-infectious/viral vaccines will require adjuvants/immune modulators that decrease immunosuppression (e.g., reduce suppressive immune cell populations like MDSCs and Tregs at the time of vaccination). The vaccine was well tolerated without any toxicity or evidence of autoimmunity. Currently, this vaccine is being tested for efficacy (prevention of adenoma recurrence) in a multicenter RCT (NCT02134925).

Classic adjuvants are stimulants such as non-specific bacterial extracts and newer subtype-specific TLR stimulants. More recently, GEM model studies indicate that the first genetic alterations can initiate a cascade of genetic, epigenetic, and inflammatory changes that lead to an immunosuppressive TME (consistent with the clinical data discussed above; ref. 80), suggesting need for inhibitory adjuvants for vaccine preventive efficacy. This hypothesis was supported when Kras vaccine efficacy (reduced pancreatic intraepithelial neoplasia progression) in the Kras-p53-Cre mouse model required Treg depletion. Recent studies in pancreatic models found that metformin and aspirin can modulate inflammatory pathways within the early TME that promote tumorigenesis, suggesting their potential as adjuvants to enhance vaccine efficacy (81, 82). Current work in this context is developing more specific adjuvants (e.g., miRNA or other epigenetic regulators) to reverse the functional (tumor
promoting/immunosuppressive) immune cell polarity to inhibit the immunosuppressive TME.

Genomic technologies and large data sets are helping identify vaccine targets for cancer prevention, including early genetic drivers in premalignancy. Preclinical studies demonstrate that multi-antigen vaccines are more effective than single-antigen vaccines by inducing immunity to more antigens, generating more activated T cells homing to the premalignant lesion (83). A multi-antigen vaccine for colon cancer, targeting several immunogenic proteins that are upregulated in adenomas and conserved through carcinoma (84), is moving toward the clinic. Preliminary studies of single-antigen vaccines are encouraging in reducing polyp formation in AOM-treated mice and APCmin mice. Important to CRC prevention is the finding that aspirin (recently recommended for CRC prevention by the USPSTF; see above) can increase tumor-trafficking CD8 T cells to enhance immunosurveillance and reverse immune escape (and modulate early TME inflammatory pathways) in premalignant lesions, suggesting the significant potential of combining aspirin with CRC vaccines (81, 82, 85).

Gene amplification resulting in abnormal overexpression of non-mutated self-antigens is an early event in the malignant transformation of many solid tumors. A three-antigen vaccine (targeting IGFBP2, IGF-1R, and HER2—all upregulated in high-risk breast lesions from DCIS to atypical hyperplasia) was shown to be safe and effective in transgenic mice (83) and will start phase I clinical trials in the first quarter of 2016. A five-antigen vaccine targeting breast cancer stem cells (immunizing against CD105/Yb-1/SOX2/CDH3/ and MDM2) called STEMVAC is currently in clinical trials (NCT02157051). Further clinical development of these vaccines will be based on immunogenicity in the phase I trials. A prophylactic lung cancer vaccine, using the same approach in terms of genomic screening and then functional screening to identify candidate proteins upregulated in dysplasia and conserved in stage I/II disease, is in development.

Immunoprevention may also involve patients carrying cancer predisposition genes. A novel example of this approach involves a vaccine targeting hTERT under development for BRCA carriers (86). This vaccine is being tested clinically now in the adjuvant setting with plans to move to BRCA1/2-healthy carriers initially in a window trial before prophylactic surgery. A vaccine targeting mutations that define Lynch syndrome to prevent the development of cancer is under development (87) and is extremely exciting and promising given the striking efficacy of immunotherapy approaches in the treatment of colorectal cancer in this context (55).

Implementation Science

Expanded efforts to refocus on implementation science will be essential to further progress in cancer prevention. More than 50% of cancers are preventable through lifestyle modifications, including increased physical activity, reduced obesity, and elimination of cigarette smoking (88). Standard screening tests (mammography and CRC screening) are unevenly distributed from state to state and also county to county (89). Greater use of effective medical interventions across all sectors of society adds to the potential to prevent the majority of cancer and reduce disparities. A renewed focus on and funding of implementation science in cancer (of note, >90% of NCI funding in this field is focused on prevention; ref. 90) is due to the growing recognition of the difficulty translating evidence into practice. Recent advances include new models, methods, metrics, and measurement tools to study the complex, multi-level factors (e.g., organizational) that influence effective adoption and maintenance and acceptance of study designs beyond RCTs. The importance of implementation science also applies to precision medicine and immunoprevention as briefly discussed below. For example, uptake of CRC universal tumor screening for Lynch syndrome is limited despite data showing clear public health benefits (discussed in detail above in Germline mutations section) and recommendations of several professional organizations, including NCCN. Tamoxifen (and related FDA-approved agents) produces durable reduction of breast cancer risk by 75% (91) in atypical hyperplasia (10% of patients with a biopsy for benign breast disease; invasive cancer risk of 30% at 25 years [92], similar to BRCA mutation carriers). Appalling under-use in this high-risk subset suggests that providers and patients are not fully aware of the clinical risks and benefit in this setting.

Identification of HPV as the cause of a major global cancer burden, including as a necessary driver of cervical cancer (the leading cause of cancer deaths in women in many developing countries) and a dramatically increasing subset of oropharyngeal cancer among men in the US and other developed countries, provides exceptional prospects for implementation of public health interventions (70). Three HPV vaccines – bivalent (HPV 16 and 18), quadrivalent and 9-valent – have been FDA-approved (first in 2006), but the uptake remains slow in parts of the US and world. In 2013, only 38% of girls and 14% of boys in the US were fully vaccinated despite recommendations from the CDC, American Academy of Pediatrics, and other groups. HPV vaccination in the US is lower in areas of high cervical cancer incidence and mortality and among non-Hispanic Blacks, helping direct public health implementation efforts (93). Major global efforts are now focusing on implementing HPV vaccination programs in countries where the burden of disease is highest, including through school-based programs in low-income countries (65, 94). Recent RCTs suggest that a single vaccine dose can provide durable protection against HPV infection (66, 67), which if confirmed by the planned definitive RCT, would dramatically improve vaccine implementation and uptake globally.

Conclusion

Remarkable advances in NGS (including single cell sequencing), liquid biopsy technology, computational biology methods and algorithms, and high-throughput functional screening are transforming cancer prevention through the inter-related fields of precision medicine and immune oncology. These extraordinary tools provide unprecedented opportunities to interrogate the biology of premalignancy, including site-specific genomic events that initiate a cascade of genetic and epigenetic changes and an inflammatory (increasingly immunosuppressive) TME, driving premalignant progression to cancer. These studies are identifying driver mutations in the blood of patients with epithelial premalignant lesions (11) and premalignant states for blood cancer (23, 24) and are providing molecular targets for prevention (including vaccines) and early detection, including a bronchial airway genomic classifier validated for lung cancer (49) and promising leads for pancreatic, liver, and ovarian cancer (43, 44, 46, 47). Prostaglandin pathway studies may help personalize standard aspirin CRC prevention (34–38) and possibly other agents targeting this pathway such as iloprost, the most promising lung cancer chemopreventive agent...
based on positive phase II RCT [95]. Study of the biology of tumors that develop in individuals carrying predisposition mutations has led to recent paradigm-changing therapy (e.g., PARP and immune checkpoint inhibitors in BRCA carriers and LS; refs. 55, 58, 96) and prevention (e.g., chemoprevention, screening, and vaccines in LS and FAP; refs. 53, 54, 56, 86, 87). Clinical success of HPV vaccines for cancer prevention (including encouraging RCT data supporting single-dose prophylactic vaccine [66, 67] and therapeutic vaccine for cervical premalignancy [69]) and checkpoint inhibitors for cancer therapy has generated tremendous enthusiasm for immunoprevention, including developing vaccines targeting premalignant genetic drivers (EGFR, Kras, and Hras mutations; refs. 76–78). Targeting the TME has shown promise in GEM models, including arresting progression of intraepithelial neoplasia (97) and as adjuvants for non-viral vaccines (98). Potential vaccine adjuvants include repurposed drugs (aspirin and metformin; refs. 81, 82, 85, 98) and new agents under development (e.g., epigenetic regulators). Even tamoxifen (FDA-approved for breast cancer prevention) was just shown to have striking off-target immune effects (99). Finally, studies of microbiome effects on inflammatory and immune mechanisms influencing cancer development are also providing novel insights into and directions for cancer prevention (100, 101). Just as precision therapy and immunotherapy are transforming cancer treatment, precision medicine and immunoprevention approaches are being translated to the clinic and showing great promise. We stand at the edge of a new frontier that will include comprehensively characterizing the molecular and cellular events that drive premalignant progression (e.g., the PCGA). The technology and science are evolving rapidly and herald a new era of precision medicine and immunoprevention in cancer prevention that will require new paradigms for implementation into clinical practice.

Acknowledgments
The authors express their appreciation to Drs. Graham Colditz, Nora Disis, Karen Emmens, Olivera Finn, Heather Hampel, Elizabeth Jaffe, Ki Hong, and Brian Kreamer for helpful discussions.

Grant Support
This work was supported in part by grant NIH/NCI P30 CA023100 28.

Published online January 7, 2016.

References


Transforming Cancer Prevention through Precision Medicine and Immune-oncology

Thomas W. Kensler, Avrum Spira, Judy E. Garber, et al.


Updated version
Access the most recent version of this article at:
http://cancerpreventionresearch.aacrjournals.org/content/9/1/2

Cited articles
This article cites 88 articles, 5 of which you can access for free at:
http://cancerpreventionresearch.aacrjournals.org/content/9/1/2.full#ref-list-1

Citing articles
This article has been cited by 10 HighWire-hosted articles. Access the articles at:
http://cancerpreventionresearch.aacrjournals.org/content/9/1/2.full#related-urls

E-mail alerts
Sign up to receive free email-alerts related to this article or journal.

Reprints and Subscriptions
To order reprints of this article or to subscribe to the journal, contact the AACR Publications Department at pubs@aacr.org.

Permissions
To request permission to re-use all or part of this article, use this link
http://cancerpreventionresearch.aacrjournals.org/content/9/1/2.
Click on "Request Permissions" which will take you to the Copyright Clearance Center's (CCC) Rightslink site.