NATIONAL BREAST CANCER COALITION

ARTEMIS PROJECT

ANNUAL MEETINGS
MARCH 13-16, 2025

I. INTRODUCTION

The National Breast Cancer Coalition (NBCC) was formed in 1991 to end breast cancer through the power of grassroots action and advocacy. Since that time, NBCC has built a strong coalition of advocates and organizations that advance its mission. Launched in 2010 to support the NBCC's research goals, the Artemis Project®, under NBCC leadership, brings together leading researchers and trained advocates who set priorities and design and implement research plans that focus on two areas:

- **Primary Prevention:** How do we stop women and men from getting breast cancer?
- **Prevention of Metastasis:** How do we stop them from dying of breast cancer?

The Artemis Project reports from previous annual meetings, found at www.stopbreastcancer.org/what-we-do/research/artemis-project/, lay out the history of the Artemis Project. This report provides a summary of discussions and recommendations made at the 2025 annual Artemis meeting. This meeting had 25 participants, including advocates and scientific expertise ranging from immunology, biomedical engineering and genetics to molecular biology, radiation oncology and clinical oncology.

2025 ANNUAL MEETING PARTICIPANTS

Michele Atlan Research Advocate and Board Member, Breast Cancer Care & Research Fund

Joe Camardo, M.D. Independent Medical Professional

Jayanta Debnath, M.D. Distinguished Professor and Chair, Department of Pathology, University of California San Francisco; Member, Helen Diller Family Comprehensive Cancer Center

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Steve Elledge, Ph.D. Gregor Mendel Professor of Genetics and Medicine, Department of Genetics, Harvard Medical School, Division of Genetics, Brigham and Women's Hospital

Silvia C. Formenti, M.D. Chair, Department of Radiation Oncology, Weill Cornell Medical College; Radiation Oncologist-in-Chief, New York Presbyterian/Weill Cornell Medical Center

Zev Gartner, Ph.D. Professor of Pharmaceutical Chemistry, University of California San Francisco

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II. BACKGROUND

The Artemis Project Meetings began Thursday evening, March 13, 2025. The Thursday session included attendee introductions, a general NBCC update, a review of Artemis' background and the previous year's outcomes, and a general discussion on current key questions in breast cancer. Friday, March 14, included background talks on both prevention of metastasis and primary prevention. The work on prevention of metastasis began in the afternoon and ended Saturday afternoon, March 15, followed by a brief vaccine update and then work on primary prevention. The meeting ended midday on Sunday, March 16.

III. ARTEMIS PROJECT ON PREVENTION OF METASTASIS AND PRIMARY PREVENTION

March 14, 2025

BACKGROUND PRESENTATIONS

Bytes, Bench, Bedside: Translating Mutational Signature Insights Into Patient Benefits

Serena Nik-Zainal

The project meetings opened with a talk by Serena Nik-Zainal.

Cancer research has focused primarily on identifying a small number of driver mutations while labeling the many thousands of nondriver mutations as "passengers" and considering them mutational noise. However, each tumor is different, and each has its own set of mutational signatures. We can use cancer genome profiling, especially whole genome sequencing, to identify common mutational signatures across patients. Serena presented three similar mutational profiles from three unrelated patients who were BRCA-deficient in different ways. One had a germline inherited BRCA1 mutation; one had an acquired somatic BRCA1 mutation; and one did not have a BRCA1 mutation at all but had an epigenetic promoter hypermethylation of BRCA1.

Many signatures have been validated in human cellular models, and machine learning has been used to classify tumors based on mutational signatures. The difficult but very important part is showing their clinical prognostic and predictive value. There may be an untapped potential for preventing metastasis through hitting targets more precisely at an early stage (e.g., metastases we are not treating effectively, like the 12% of BRCA-ness tumors not detected), identifying specific targets for precise intervention strategies and targeting resistance mechanisms.

Participants raised issues around technical variance within the same patient and spatial variance within the tissue. They asked why any particular signature would be enriched in samples. Participants asked if these mutational signatures could be detected in circulating tumor cells (CTCs) or disseminated tumor cells (DTCs), and whether mutational signatures can distinguish between a primary tumor and a metastasis. Participants asked about histological correlates associated with the signatures, and whether mutational burden is associated with host human leukocyte antigens (HLAs).

How Do We Understand and Block Changes in Tissue Structure During Breast Cancer Progression?

Zev Gartner

Traditional models of cancer progression have described a stepwise process in which cells acquire mutations, form tumors and then invade surrounding tissue. But newer evidence suggests the process can be more complex, with disease sometimes spreading earlier than expected or progressing without the classic changes seen in the traditional model. Zev proposed looking at cancer progression through the lens of tissue structure and the microscopic dynamics that shape it.

Two key processes—surface tension and lineage—shape positional changes in structure. By analyzing a tissue's overall surface energy, researchers can predict when structural rearrangements are likely. Three main variables, specifically mechanical potential, entropy of different cell arrangements and effective tissue "temperature" govern this energy balance. Different combinations of these factors could be manipulated to prevent cancer cells from moving, changing their fate and acquiring more dangerous basal phenotypes, thus preventing metastasis and keeping tumors in situ.

Identifying general strategies for how structure is disrupted could reveal new strategies to correct it. For example, making luminal cells more basal enables them to stay near the basement membrane longer, increasing the likelihood of invasion. Importantly, the processes that keep luminal cells "in" are not necessarily the same as those that keep immune cells "out," so stopping basal cells from invading should not automatically disrupt immune cell activity.

Participants discussed whether it is possible to measure the metabolic costs of rearrangements, noting the challenge of disentangling a cell's fate from its position in a tissue. They also raised the influence of the surrounding microenvironment, pointing out that clinical examples such as microinvasion in ductal carcinoma in situ (DCIS) and the widespread changes to the breast tissue composition after menopause suggest that host factors may create the conditions that enable these events.

Can Cancer Cells Transfer Their Genetic Code of Malignancy to Benign Cells in the Microenvironment for Immune Evasion?

Simon Knott

The last introductory talk was delivered by Simon Knott.

Simon presented findings from a recent paper showing that cancer cells can transfer their mutated mitochondria into T cells in the tumor microenvironment, altering immune cell metabolism. Co-culture and in vivo experiments found that mutated mitochondria from cancer cells carry mitophagy-inhibitory molecules that protect them from degradation, while cancer-derived reactive oxygen species (ROS) promote mitophagy of the T cells' healthy mitochondria, ultimately replacing the immune cells' normal mitochondria. Tumor-infiltrating lymphocytes (TILs) with mutated mitochondria have lower tumor-cell-killing capabilities, lower programmed cell death protein 1 (PD-1) expression, high rates of apoptosis and higher rates of terminal differentiation. Reanalysis of existing clinical data revealed that tumors with mitochondrial DNA mutations responded poorly to immune checkpoint inhibitors as compared to those without.

Simon also described recent work published by his colleague, Dan Theodorescu, and him on Y chromosome loss in male tumors (e.g., bladder). Y chromosome loss is frequent in male cancers and correlated with poor prognosis. They developed a predictor to identify Y chromosome loss in single-cell data and found that Y chromosome loss in epithelial cells was correlated with Y chromosome loss in TILs and peripheral blood mononuclear cells (PBMCs). They then looked at data from a large clinical cohort with long-term follow-up and found that concurrent loss of Y chromosomes in both epithelial cells and TILs was associated with worse cancer patient outcomes. These findings highlight how cancer genome alterations can appear in the microenvironment and impair immune cell function.

Participants discussed the proportion of T cells acquiring mutated mitochondria, whether immune cells contain more mitochondria than other cell types, and skepticism about whether small numbers of mutated mitochondria could replace the entire mitochondrial network. They also questioned the relevance of Y chromosome loss to women, whether the loss itself or the process causing it was more important and proposed experiments in immune-deficient mice to test the persistence of Y chromosome loss. Other points included natural age-related Y chromosome loss, possible accelerated aging phenotypes, selective pressure for Y chromosome loss in other cells and links to cachexia.

IV. SUMMARY OF ARTEMIS PROJECT ON PREVENTION OF METASTASIS

March 14-15, 2025

The first set of breakouts focused on the prevention of metastasis. The participants formed four groups.

The H&E Whisperer

Jayanta Debnath, Judi Hirshfield-Bartek, Simon Knott, Christopher Li, Michelle Tregear

Can a metastatic signature be predicted at the time of histologic diagnosis of a primary cancer, and how early can that signature be found? These are critical clinical questions, as they could help inform medical decisions such as how intense follow-up and observation need to be and whether and when to start treatments. The group proposed the use of digitized pathology stains (hematoxylin and eosin [H&E]) to identify features that put particular patients at a high (or higher) risk of metastasis. This could guide interventions to avoid overtreatment and identify physical structures that need to be interrupted to change outcomes.

Key research concept:

The group proposed employing both a prospective analysis with fresh-frozen tissue and retrospective analyses with older formalin-fixed, paraffin-embedded samples currently available.

Short-term plan:

The group's initial goal is to gather enough samples to run computational foundation models and cluster the derived features. This information will be used to train secondary machine learning models to predict DTC-positive and metastasis-positive outcomes in each set.

The key questions at this stage are whether the outcomes can be cross-validated; that is, how well does the model for DTCs predict metastasis, and how well does the model for metastasis predict DTCs? The answers to these questions could hold insights regarding the bottlenecks of metastasis.

The group members will thus collaborate with each other and with external researchers to be able to look at as many stains as possible to localize features that are most informative in the prediction models, as well to randomly select some noninformative regions to learn what makes a region predictive. The models will be continuously improved, as each new H&E will add additional information.

Long-term vision:

Assuming the basic models can be validated, the work could be extended to layer information and provide multiple validations against electronic medical records, clinical data, treatment histories and basic annotated medical histories. This could possibly include extensive genomic, proteomic and other relevant "-omic" data. Clinically, the use of clustered H&E data should result in faster and better treatment (or nontreatment) decisions to prevent metastases.

Hit Snooze

Zev Gartner, Cyrus Ghajar, Christopher Gregg, Alana Welm

Following from observations in nematode, yeast and mouse models of growth arrest from lack of nutrients, the group focused on the problem of how to put potentially metastatic tumor cells into such a deep state of dormancy that they can never emerge to cause metastases.

Key research concept:

The group proposed creating an irreversible dormant state by understanding what enables metabolic flexibility. This would be dependent on finding the evolutionarily conserved states defined by nutrient availability and determining if they are

co-opted by disseminated breast cancer cells to enter, maintain, adapt and exist from dormancy.

Short-term plan:

The immediate goal is to determine if there would be the possibility that human breast cancer DTCs could be controlled by dormancy, as they might be in other species.

The group identified three key questions: 1) Do DTCs display hibernation signatures that are present in other species? 2) Do DTCs reflect nutrient availability states, and if so, does this predict a dormant cell's capability of initiating overt metastasis? and 3) Can these states be toggled to induce a deep dormant state in tumor cells that are incapable of waking up?

Answering those questions will require a knowledge of hibernation and dormancy signatures from model organisms, additional mouse studies and access to human tissue (for example, from rapid autopsy samples or DTCs from bone marrow). This will be done by comparing already-available hibernation signatures to DTCs in bone marrow and rapid autopsies using bioinformatics, and then extending this comparison to dormancy signatures in other species (some are already available, and some will need to be developed). Taken together, these analyses will then allow the determination, at least in a mouse model, of which DTCs can be locked into dormancy and which cannot.

Long-term vision:

The longer the cells are dormant, the less likely they are to wake up. However, in humans, the mechanisms for keeping cells in a dormant state have not been defined. Methods that work in lab models—such as depriving cells of nutrients—can't be applied to the whole human body. Long term, the work would need to focus on how to maintain a dormant-like environment in specific areas of the body.

TRM Neighborhood Watch

Joe Camardo, Brandon DeKosky, Stephen Elledge, Andrei Goga, Benjamin Goldman-Israelow, Keith L. Knutson, Michele Rakoff, Miguel Reina-Campos, Natasha Sheybani

Tissue-resident memory T cells (TRM) are rare immune cells that reside in tissues, continually surveilling for threats. The group proposed the use of TRM to provide robust surveillance for and prevention of breast cancer metastasis.

Key research concept:

Can the TRM network be bolstered so that cells can easily access and target pre-metastatic tissue?

Short-term plan:

The goal for the first 12-18 months of the project is to address two pivotal concerns to determine whether the use of TRM could be considered as a reasonable treatment option: 1) the full scope of the biology of TRM, and 2) whether TRM are in fact protective against metastasis, with this protection failing only because of the rarity of the cells.

To address the biology, the group will use spatialomics to profile immune networks within healthy human lungs, liver, brain and bone marrow to understand the spatial distribution of TRM, DTCs and other immune populations. This would yield three critical insights: 1) whether there are sufficient numbers of TRM within pre-metastatic tissues to effectively surveil DTCs, 2) if expansion of the TRM network would be necessary for therapeutic intervention and 3) the antigen-specificity of TRM. To address whether the TRM are then protective against metastatic expansion, the group would carry out a mouse experiment, with murine cancer cells expressing a model antigen (ovalbumin). Mice without antigen-specific TRM would be compared to mice that have received adoptive transfer of ovalbumin-specific TRM purified from donor animal tissues. Metastatic burden should be equivalent in all tissues except at sites receiving TRM.

Long-term vision:

If the spatial profile of TRM can be fully worked out, and it is then determined that TRM are protective against metastatic expansion, the group would want to translate these findings for breast cancer patients. The critical point will be whether the expansion of the network is best done specifically, for example with an mRNA vaccine, or nonspecifically with Toll-like receptor agonists or activating cytokines. While the latter is much easier and less expensive to develop, the nonspecific approach can generate unacceptable side effects. This would be tested if there is evidence the mouse observations can be clinically translated.

What's My (Germ)Line?

Michele Atlan, Stephen Elledge, Silvia C. Formenti, Benjamin Goldman-Israelow, H. Kim Lyerly, Serena Nik-Zainal, Sohail Tavazoie, Xiang (Shawn) Zhang

Hereditary variants likely can predict the risk of metastasis. For example, around 30% of women who have a nonpathogenic form of a recently discovered germline genetic variant in a gene called PCSK9 seem to be protected from metastasis, while

about 70% who inherit the pathogenic form of this gene variant show a higher risk for metastasis. To date, most of the focus in breast cancer prevention (both primary prevention and prevention of metastasis) has been on somatic mutations and oncogenes. Any focus on host genetics has been on predisposition to getting cancer and not on host effects on tumors, cancer progression, nor metastasis.

Could this observation be used to construct a mechanism for identifying women born with this hereditary risk and then how to target it?

Key research concept:

Can the host's inherited genetics predict which patients will develop metastasis? Can that information be used to prevent metastasis?

Short-term plan:

The group would work to identify relevant candidate germline alleles, possibly indicating a higher risk of metastasis, using large, annotated databases such as DNA.Land.

The key framing for the inquiry was whether researchers can look at germline mutations of importance in the same way they have looked at, for example, BRCA. Assuming this is the case, the first steps in identifying candidate metastasis-inducing genes might be straightforward. The complexity will come in determining any additional somatic mutations that could be amplifying or mitigating.

Using bioinformatics approaches integrating germline genetics and tumor genetics to inform risk prediction, cells with vulnerabilities to metastasize could be targeted either through precision medicine or through very early interventions.

Long-term vision:

Any ability to identify a lower risk of metastasis allows for the possibility of avoiding overtreatment. Further, by identifying factors that could be targeted for mitigation or exploited if protective, this approach could eventually allow for precision interventions even early in life, rather than needing to wait for the emergence of the tumor to understand the risk of metastasis.

V. SUMMARY OF ARTEMIS PROJECT ON PRIMARY PREVENTION

March 15-16, 2025

The participants formed four groups for the second set of breakouts, here focused on the primary prevention of breast cancer.

Bugs R Us

Stephen Elledge, Silvia C. Formenti, Andrei Goga, Keith L. Knutson, Christopher Li, Michele Rakoff, Sohail Tavazoie

The group discussed the possibility of harnessing the breast microbiome as a novel tool for primary breast cancer prevention, selectively introducing naturally occurring or engineered commensal bacteria to either directly inhibit carcinogenesis or enhance local immunity within the breast.

Key research concepts and short-term plan:

AIM 1: Define the breast microbiome

Map the microbial landscape of healthy and high-risk breast tissue.

Key Questions:

- Do individuals cluster into distinct breast microbiome types?
- How does the microbiome change over a woman's lifetime or with reproductive history?

Planned Activities:

- Analyze bio-banked tissue.
- Perform microbiome analysis using 16S rRNA and other sequencing tools.
- Compare microbiome profiles by breast cancer risk status, lactation history and progression from benign disease to cancer.

AIM 2: Manipulate the breast microbiome

Introduce beneficial bacteria to reshape the breast microbiome in ways that reduce cancer risk.

- What is the best approach for delivery (either topical or local delivery to the nipple/ducts [e.g., via patch, lotion, lavage])?
- What is the longevity of transplanted bacteria?

Challenges to address include ensuring persistence and localization of introduced bacteria and avoiding systemic leakage and competition from endogenous microbiota.

Models to test would include both mouse and rat estrogen-receptor positive (ER+) models and dimethylbenz(a)anthracene (DMBA)-induced heterogeneous models. There was also consideration for the use of canine models for spontaneous tumor development and lactation studies.

AIM 3: Engineer bacteria for preventive function

Use synthetic biology to equip bacteria with cancer-sensing and anti-cancer capabilities.

Some possible functionalities of engineered bacteria could include:

- Sensing: Hypoxia, pH, zinc levels, or other tumor microenvironment signals (e.g., quorum sensing)
- Delivery of payloads: Enzymes to degrade estrogen, produce androgens or deliver therapeutic agents such as antibodies (e.g., anti-human epidermal growth factor receptor 2 [HER2]), interferons or other agents that inhibit cellular proliferation

Long-term vision:

The group would want to develop a window-of-opportunity trial in women with DCIS to test bacterial colonization and short-term changes in response, Ki67 (tumor cell proliferation), inflammation and T cell subsets.

Early DEFLECTION

Jayanta Debnath, Brandon DeKosky, Zev Gartner, Cyrus Ghajar, Judi Hirshfield-Bartek, H. Kim Lyerly, Serena Nik-Zainal

A robust mechanism for preventing primary breast cancer would be to reduce the mutational burden in the breast. A significant increase in that burden occurs during puberty for women. Would it be possible to mitigate that increase? One approach seeks to harness immune-based strategies to identify and eliminate genetic changes that are enriched in aggressive breast cancers before cancer emerges. The second aims to replicate the long-observed protective effect of early pregnancy—without requiring pregnancy.

Key research concept:

Epidemiological studies show that full-term pregnancy before age 30 significantly reduces the risk of hormone receptor-positive (HR+) breast cancer. Mechanistic studies suggest that sustained exposure to high levels of pregnancy-associated hormones (especially estrogen and progesterone) leads to long-lasting transcriptional changes in mammary epithelial cells that reduce their responsiveness to hormonal stimulation—potentially decreasing cancer susceptibility.

Breast epithelial cells accumulate mutations over a woman's lifetime, particularly during cycles of proliferation and regression associated with the menstrual cycle. Certain genetic features are enriched in aggressive or metastatic breast cancers. These could be targeted by the immune system.

Short-term plan

The first goal for the group is to establish the best time in physiological development for an intervention. The group discussed the possibility of an early intervention, around the onset of puberty and compare this to later interventions, up to several decades after puberty.

The group, meanwhile, posed two main questions: 1) Is it possible to generate the protective effects of pregnancy without an actual pregnancy using brief hyperphysiological doses of pregnancy-associated hormones? and 2) Can the post-puberty mutational bursts be targeted with a preventive vaccine?

For the hormone approach, the group will develop in vivo models and protocols to simulate hormone pulsing to test combinations, doses and durations of hormone exposure, along with defining the best delivery mechanisms, as well as assess loss of hormone responsiveness by evaluating transcriptional responses post-treatment.

For a vaccine approach, the group will characterize early mutational burden and clonal expansion, and develop a computational pipeline to identify potential neoantigens in female breast tissue, ages 10-20, and will model vaccine strategies for both universal and personalized approaches. They will then validate immunogenicity of a candidate vaccine and optimize timing for administration alongside optimizing delivery platforms.

Long-term vision:

Even for women who have been pregnant, the protective effect of pregnancy against breast cancer is partial at best. To be able to employ either a one-time vaccine or several limited hormonal interventions at carefully selected times in development could significantly reduce breast cancer incidence for anyone who might otherwise be subject to the disease.

Project Genesis

Michele Atlan, Christopher Gregg, Simon Knott, Miguel Reina-Campos, Natasha Sheybani, Alana Welm

The group focused on the idea of engineering a mouse model that is genetically unable to develop breast cancer. If changes can be made in the germline, both the individual and all generations following would be protected.

Key research concept:

Could we use embryo editing to prevent breast cancer formation over an experimental mouse's lifetime and in any of the generations following? What changes to the genome would be necessary to ensure the prevention of breast cancer?

Short-term plan:

The group determined that, rather than trying to edit all of the genetic drivers in a mouse model of breast cancer, it would be better to construct a mechanism to clear cells expressing tumor-forming drivers at regular intervals. This would be turned on by an agent that the mice are not routinely exposed to. The mechanism would require the detection of a burgeoning cancer.

A key part of the initial research will be to determine which gene products or antigens need to be looked at. This will require high-throughput screening to identify the most effective elements. For example, a molecule like P53 might be an appealing trigger to target when mutated, but at the same time, it has normal physiological functions. This type of analysis would need to be done for any triggering molecule.

Long-term vision:

Although targeted and successful large-scale embryo editing is currently far outside available technologies, the tools for this are rapidly improving. If a successful animal model could be demonstrated, there would likely be interest in applying these technologies for human breast cancer prevention. Even trying such technologies at an experimental (in vitro) level for human cells would, of course, need to be preceded by anticipating safety and efficacy, with a foundation of extensive societal discussions.

Sonic T Cells

Joe Camardo, Benjamin Goldman-Israelow, Christopher Gregg, Natasha Sheybani, Michelle Tregear, Xiang (Shawn) Zhang

Somatic mutations that can lead to breast cancer begin accumulating early in life, particularly around puberty, and continue throughout a woman's life. The group proposes developing a noninvasive, wearable device that uses low-intensity-focused ultrasound as a local breast cancer prevention strategy. The core aim is not to stop inevitable mutations, but to enhance immune surveillance and, ultimately, clearing of mutated cells within the breast tissue—specifically by promoting T cell infiltration and clearance of pre-malignant lesions—thereby reducing the likelihood of tumor formation.

Key research concept:

Use of low-intensity, pulsed ultrasound (akin to that in FDA-approved wearable therapeutic devices for musculoskeletal injuries) could gently disrupt physical barriers (e.g., basement membrane) and stimulate localized immune activity without systemic side effects or inflammation. This could be delivered through a wearable patch or bra-like device used periodically—e.g., once a month during sleep or in sync with menstrual cycle phases.

Short-term plan:

Conduct proof-of-principle preclinical studies in mouse and rat models, including:

- Baseline models and BRCA1 mutation models
- Experiments evaluating:
  - Whether low-intensity ultrasound enhances immune cell (T cell) infiltration
  - Whether it clears precursor lesions
  - Optimal timing, frequency, intensity and duration of treatment
  - Effects of pregnancy and stress on treatment efficacy

Approach:

- Use existing ultrasound equipment adapted for rodents.
- Measure immune activation (e.g., T cell tracers, cytokine changes).
- Track lesion progression, immune infiltration and tumor development.

Long-term vision:

If the proof-of-concept studies are successful, the next steps would include designing a prototype-wearable ultrasound device tailored for human use, considering factors such as breast size; density and safety; and, subsequently, optimal treatment windows. Early-phase clinical trials would then be conducted to evaluate feasibility, safety and early biomarkers of effectiveness and possible integration with health apps. Finally, the team would explore integration with stress-monitoring or cycle-tracking apps to personalize timing of use.

VI. CONCLUSION

Now 15 years into its existence, the Artemis Project has brought together biomedical researchers, advocates, clinicians and many others who might not otherwise have crossed paths, but through the power of the infrastructure supplied by the NBCC, has resulted in collaborative works, advancing extraordinary ideas conceived at the annual Artemis Project meetings.

Even with an Artemis-founded vaccine approaching a trial, and many very large research projects that have come out of work from Artemis, the urgency of ending breast cancer remains. We cannot make assumptions about what will work for preventing primary breast cancer or its metastases. Rather, everyone associated with the Artemis Project continues to work in collaboration to create novel approaches and intensely follow up on earlier Artemis work groups. This has led to remarkable advances in understanding tumor dormancy; improved technologies; and, most importantly, the ability to think about approaches (such as a vaccine) that previously were thought to be impossible or economically unfeasible.

The 2025 meetings continued to produce novel and bold ideas that are also scientifically sound. For example, a collaboration has already been established by a group in the prevention of metastasis session on using histological collections to determine any correlation between early histology patterns in primary tumors to later metastasis. Another group explored how to keep DTCs in such a deep state of dormancy that they never emerge as metastases.

The primary prevention meeting discussions ranged from using existing observations (for example, the breast cancer-protective effect of pregnancy) to novel interventions and looking at possible applications driven by new technologies (e.g., wearable ultrasound devices to stimulate T cells to clear pre-malignant lesions). One notable discussion regarding primary prevention, and a much broader discussion in public health, is to frame interventions for healthy individuals. This framing has been done successfully for preventing infections using vaccines, but what does it mean in cancer beyond suggestions of improving the individual's environment (diet, exercise, community health)?

The goal for the Artemis Project, as for NBCC, is to end breast cancer. In its first decade-plus, Artemis as a project, and the individual researchers and advocates associated with it, has produced remarkable advances that allow us to reasonably think about both primary prevention and prevention of metastasis. A number of the projects proposed by Artemis participants over the years are now being pursued in funded research, or close to clinical trials, and NBCC expects that these applications will begin to achieve the goals laid out originally as part of Breast Cancer Deadline 2020.

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