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TITLE:
Fusion Genes Predict Prostate Cancer Recurrence

PRINCIPAL INVESTIGATOR:

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CONTRACTING ORGANIZATION: Stanford University
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Stanford, CA, 94305

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13. SUPPLEMENTARY NOTES

14. ABSTRACT
Most prostate cancers are indolent and may not require clinical intervention. Only a small fraction of cases progress to metastatic disease if not treated. Prediction of the clinical outcomes of prostate cancer remains a challenge. Recently, we discovered a panel of 8 fusion genes that occurred in aggressive prostate cancer. The presence of these fusion genes correlates 91% chance of recurrence of prostate cancer. In order to make the fusion gene test clinically ready as a predictor, we have modified to test into a semi-quantitative Taqman QRT-PCR. The tests were performed in CLIA certified lab. Four hundred and sixty samples of prostate cancers were collected. Prostate cancer cells were microdissected. Taqman QRT-PCRs were performed on these samples. Significant numbers of samples were found positive for some of these fusion genes. In addition, we have analyzed 150 samples from Stanford University and 155 samples from University of Wisconsin Madison. A training model has been constructed. We are in the process to apply the model to testing sets.

15. SUBJECT TERMS
Prostate Cancer, prognosis, gene fusions, fusion transcripts

16. SECURITY CLASSIFICATION OF:			17. LIMITATION OF ABSTRACT	18. NUMBER OF PAGES	19a. NAME OF RESPONSIBLE PERSON
a. REPORT	b. ABSTRACT	c. THIS PAGE			USAMRMC
Unclassified	Unclassified	Unclassified	Unclassified		19b. TELEPHONE NUMBER *(include area code)*

Major Task 1 : We will conduct analysis of MAN2A1-FER, SLC45A2-AMACR, TRMT11-GRIK2, MTOR-TP53BP1, LRRC59-FLJ60017, CCNH-C5orf30, KDM4-AC011523.2, TMEM135-CCDC67 on 5106 prostate cancer samples collected from University of Pittsburgh, Stanford University and University of Wisconsin Madison. We will first establish prostate cancer recurrence model and short PSADT prediction models either by fusion gene status alone or in combination with nomogram based on the cohort from 600 radical prostatectomy samples from UPMC. This model will be locked in and tested on cohorts from University of Pittsburgh, Stanford University and University of Wisconsin. The prediction accuracy, sensitivity and specificity within each cohort will be evaluated.

Subtask 1: In the first 3 months of the funded period, we plan to establish this test in the CLIA certified laboratory at the University of Pittsburgh Medical Center. Fifty-six FFPE samples that were shown to be positive for at least one fusion transcripts in the matched frozen tissues. These FFPE samples had been tested in non CLIA certified laboratory, and achieved 98.9% sensitivity and 100% specificity. We will repeat the same tests on these samples in CLIA certified laboratories. All PCR products will be analyzed through Sanger's sequencing to confirm the authenticity of the fusion products. In addition, all fusion minigene RNA templates will be serially diluted. TAQMAN QRT-PCR will be performed to evaluate the sensitivity of the test. Detection threshold will be obtained. Random selection of 600 prostate cancer samples with definitive clinical outcomes will be carried out in UPMC campus. TAQMAN QRT-PCR on β-actin will be used as RNA quality control. For sites 2 and 3, all relevant institutional review board exempt protocols will be secured and approved.

Progress: We have procured the CLIA certified lab space in the beginning of the funded period. To accommodate the reality of formalin-fixed and paraffin-embedded tissues, we have designed a set of new primers and Taqman PCR probes for highly fragmented RNA species. These sets of primers and probes were subsequently tested and validated on synthetic mini-fusion genes of MAN2A1-FER, TRMT11-GRIK2, MTOR-TP53BP1, CCNH-C5orf30, KDM4-AC011523.2, SLC45A2-AMACR, TMEM135-CCDC67, and LRRC59-FLJ60017. The probe and primers for β-actin were also revised to accommodate a shorter RNA fragment. The analyses showed that these assays detect as low as 600-1000 molecules of these fusion transcripts. We then analyzed 56 FFPE samples whose frozen counterparts have been previous found to contain at least one fusion gene using these sets of probes and primers. All samples that were positive for these fusion genes were also positive in the new Taqman qRT-PCR assays. The positive match rate is 100%. All participating institutes, including University of Pittsburgh, Stanford University and University of Wisconsin Madison, had obtained the institutional approval for the exempt protocols.

Subtask 2: From month 4-9 of the first funded year, we will perform TAQMAN QRT-PCR and Sanger's sequencing on a randomly selected cohort of 600 samples from phase 1 that have at least 5 years clinical follow-up. These tests will be performed in CLIA certified laboratory of University of Pittsburgh. The prediction models of PCa recurrence and PSADT mentioned will be developed based on this large number of samples. For sites 2 and 3, the first 300 prostate cancer cases from each site will be selected and evaluated for sufficient materials for the assay.

Progress: To create a training set, we performed Taqman qRT-PCR using the primers and probes as mentioned from above on 271 samples from University of Pittsburgh, 155 samples from University of Wisconsin Madison, and 150 samples from Stanford University. The results show surprisingly high positive rate of SLC45A2-AMACR in Stanford and Wisconsin cohort, reaching 96% and 92.6% respectively. Among these fusion genes, the lowest frequent one is TMEM135-CCDC67: A total of 8 samples were found positive. In addition, high positive rate of CCNH-C5orf30 was also found in the prostate cohort from University of Wisconsin. In general, the rates of fusion gene positive samples are comparable among the 3 cohorts (table 1). Subsequent analyses showed that MAN2A1-FER (or normalized MANA1-FER), TRMT11-GRIK2, and mTOR-TP53BP1 gene fusions have the highest odd ratios for predicting the recurrence of prostate cancer for UPMC and University of Wisconsin cohorts (Table 2).

Table 1 Positive rate of fusion in prostate cancers

Cohort	MAN2A1/ FER	TRMT11/ GRIK2	MTOR/ TP53BP1	CCNH/ C5orf30	KDM4B/ AC011523.2	SLC45A2/ AMACR	TMEM135/ CCDC67	LRRC59/ FLJ60017
UPMC	13% (60)	25.8% (119)	2.8% (13)	33.4% (154)	0.4% (2)	50.1% (234)	1% (5)	3.4% (16)
Stanford	18% (9)	20% (10)	10% (5)	12% (6)	4% (2)	96% (48)	6% (3)	22% (11)
UWisc	19% (31)	12.9% (21)	4.3% (7)	76.7% (125)	9.2% (15)	92.6% (151)	0.6% (1)	26% (43)

Table 2
The cutoffs(and OR) of each fusion gene in each cohort

Cohort	MAN2A1/FER	MAN2A1/FER-actin	TRMT11/GRK2	MTOR/TP53BP1	CCNH/C5Orf30	KDM4/AC011523.2	SL45A2/AMACR	TMEM135/CCDC67
UPMC	32(26.3)	0 (25.9)	43(5.53)	42(inf)	39(0.12)	44(inf)	34(1.57)	47(1.54)
Wisconsin	35(14.81)	3(7.57)	42(inf)	40(23.6)	38(0.49)	40(1.5)	31(1.7)	N/A
Stanford	39(1.71)	0(0.34)	39(4.03)	39(inf)				

To establish a prediction model, we combined top 6 fusion genes that have prediction power to construct classification models to predict prostate cancer recurrence. As shown in table 3, all three models (Random Forest, Support vector machine and Linear discriminant analysis) yielded very similar accuracy: 81%, even though the specificity and sensitivity may vary. When combined with gleason's score and TNM pathology staging, the accuracy improves to 84-86%.

Table 3

Model	Fusion genes only					2x2 table		
	Sensitivity	Specificity	Youden	Accuracy	AUC		Recurrent (n=107)	Non-Recurrent (N=164)
RF	0.80	0.81	0.61	0.81	0.862	Positive	TP=86	FP=31
	Top 6, cutoff=0.2					Negative	FN=21	TN=133
SVM	0.71	0.87	0.58	0.81	0.77	Positive	TP=76	FP=21
	Top 4, cutoff=0.2					Negative	FN=31	TN=143
LDA	0.71	0.88	0.59	0.81	0.85	Positive	TP=76	FP=20
	Top 6, cutoff=0.4					Negative	FN=31	TN=144

Table 4

Model	Gleason and TNM stage + fusion genes					2x2 table		
	Sensitivity	Specificity	Youden	Accuracy	AUC		Recurrent (n=208)	Non-Recurrent (N=368)
RF	0.79	0.82	0.61	0.81	0.86	Positive	TP=164	FP=67
	top 5 fusion genes, cutoff=0.2					Negative	FN=44	TN=301
SVM	0.75	0.83	0.59	0.81	0.84	Positive	TP=157	FP=61
	Top 6 fusion genes, cutoff=0.2					Negative	FN=51	TN=307
LDA	0.77	0.85	0.61	0.82	0.87	Positive	TP=160	FP=57
	Top 5 fusion genes, cutoff=0.4					Negative	FN=48	TN=311

When the same models were applied to the dataset from University of Wisconsin, the accuracy rate yielded 75-84%. Interestingly, when combined with

Gleason's grade and pathology TNM staging, the accuracy rate improved to 88-90%. However, the same model fared worse in Stanford data set: 67-68% accuracy was found. Combination with fusion genes, Gleason's grade and pathology TNM staging improves the accuracy to 75%.

When all data were pooled, and 10 fold cross validation was performed. The accuracy of fusion gene prediction rate is 76-77%. When combined fusion genes, Gleason's grading and TNM staging, the accuracy is improved to 81-82% (table 4). In contrast, if prediction is only relied on Gleason's grade and TNM staging, the prediction accuracy is 74-76% across all three data set. As a result, we concluded that fusion contains independent prediction value and can assist in predicting the clinical outcomes of prostate cancer.

Subtask 3: A training model using fusion genes have been established. It appears that the microdissecting samples from UPMC performed the best. Thus, there is some concern on the impact of purity of the cancer samples from Stanford and University of Wisconsin due to uncertainty nature of the needle core samples in terms of % cancer in the samples. The lesson from the project is that we should have unified the sample standard in the very beginning. To address these issues, this join plan is to unify the standard to microdissection so that the results are comparable among the three institutes, and improve the prediction results. In addition, additional methods to examine the fusion genes are proposed to verify the Taqman and Sanger sequencing methods. Other types of samples will be submitted as controls of the assays. As detailed in previous progress reports, we have been investigating whether fusion transcripts described previously are prognostic in localized prostate cancer. The investigators have had ongoing discussions regarding concerns over possible artifacts in the RT-PCR-based assay of these fusions that had temporarily reached an impasse late last fall. The investigators have had considerable correspondence and communications to resolve this impasse and have jointly developed a plan to evaluate and validate the performance of the RT-PCR assay. The experiments agreed upon are outlined below. All the investigators have agreed to the following plan to be carried out at the University of Pittsburgh.

TAQMAN QRT-PCR analysis for the MAN2A1-FER, TRMT11-GRIK2, MTOR-TP53BP1, CCNH-C5orf30, KDM4-AC011523.2, SLC45A2-AMACR, TMEM135-CCDC67 and LRRC59- FLJ60017 fusion genes will be carried out at the CLIA certified lab at the University of Pittsburgh using approximately 200 samples provided by Drs. Brooks and Jarrard. These samples will include negative controls such as human foreskin and non-mammalian samples, normal prostate tissue samples, as well as recurrent and non-recurrent tumors (all blinded). All the normal and cancer tissue samples will be microdissected using H&E stained slides and a scalpel to ensure that they are as pure as possible. The timeline for tissue submission is 50 samples for 3 months from each institute. Thus, the tissue submission will be completed in the first 6 months of the funded period. All Taqman and Sanger sequencing results will be available once the analyses are completed the submission of the tissues. Preliminary analysis will be available shortly after the completion of experiments and the clinical information is obtained. Quarterly progress report will be submitted to DOD.

Once the experiments have been completed, Dr. Luo will provide primary data to Dr. Brooks and Jarrard who will then break the code. A subset of samples (approximately 50) that have been found to be positive for gene fusions, along with appropriate controls, will be further validated by FISH analysis. If necessary, the results can also be validated for a small number of samples by deep sequencing; since this method is very expensive, a source of funds will need to be identified for this purpose. Fifty percent of the results of FISH will be available 6 months after the resumption of the funding. All results will be available 9 months after the resumption of the funding. Deep sequencing will be performed once new funding is identified. The analyses results will be available 2 months after the sequencing.

Once the above experiments have been completed, all the investigators will meet in Pittsburgh to review and discuss the data and devise a plan for future studies. This meeting will be facilitated by the leadership of the University of Pittsburgh School of Medicine.

Progress: Investigators in University of Pittsburgh, Stanford University and University of Wisconsin Madison, had conducted thorough and constructive conversation on the fusion gene test. A consensus had been reached on the selection of samples. Instead of pursuing high number of samples for model validation, we will increase the breadth of the investigation by including other methodologies in the investigation, including FISH and additional RNA sequencing of prostate cancer samples. Dr. Jarrard had submitted 58 samples for the fusion gene analysis. The assays were completed and clinical information was provided. Analysis is ongoing in this sample set, but globally fusions appear more common in the tumor than associated normal tissue. Some fusions are seen commonly in the associated normal tissue (MAN2A1-FER 72%, SLC45A2-AMACR 45%). No fusions for TMEM135-CCDC67 and KDM4B-AC011523.2 were seen in this dataset.

Dr. Brooks had submitted 90 blinded cases for the analysis. We have just completed the first round of analysis. Once the verification round of analysis is completed, the results will be tabulated. We will submit the results to Dr. Brooks for de-identification and to obtain the clinical information of the samples. We have also analyzed the fusion transcripts on 90 samples from UPMC cohort for the validation purposes. The prediction analysis is on-going. All these analyses have been conducted in a blind fashion so that no information of the samples is disclosed to people who conduct the experiments. We have selected 20 samples from UPMC cohort to perform FISH analysis on MAN2A1-FER and SLC45A2-AMACR. The FISH probes have been constructed and labeled. Currently, we are carrying out FISH analysis in the InSitu lab of UPMC. We expect that we will have the results in several weeks.

Once all samples are de-identified, and the relevant clinical information is obtained, we will pool all the results of three cohorts to examine whether status or quantity of fusion genes plays a role in the aggressive behavior of prostate cancer. In addition, we may combine the status of fusion genes with other clinical parameters to evaluate whether fusion transcripts enhance the prediction of these clinical prediction models.

An abstract shall be provided in Block 14 and shall state the purpose, scope, and major findings and be an up-to-date report of the progress in terms of results and significance. Abstracts will be submitted to the Defense Technical Information Center (DTIC) and shall not contain proprietary information. Subject terms are keywords that may have been previously assigned to the proposal abstract or are keywords that may be significant to the research.

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1. **INTRODUCTION:** *Narrative that briefly (one paragraph) describes the subject, purpose and scope of the research.*

Cancer specific fusion genes are the results of chromosome rearrangement in the cancer genomes. The detection of fusion transcripts in cancer cells may reflect the progression of human cancer. Previously, we have identified a panel of 8 fusion genes in prostate cancer. The presence of these fusion transcripts correlated with the aggressive behavior of prostate cancer. In this proposed study, we will conduct large scale analysis to evaluate whether the detection of these fusion transcripts is predictable for poor clinical outcomes.

2. **KEYWORDS:** *Provide a brief list of keywords (limit to 20 words).*

Fusion gene, RNA, Taqman RT-PCR, in situ hybridization, RNA, prostate cancer, cancer relapse, chromosome

3. **ACCOMPLISHMENTS:** *The PI is reminded that the recipient organization is required to obtain prior written approval from the awarding agency grants official whenever there are significant changes in the project or its direction.*

What were the major goals of the project?

List the major goals of the project as stated in the approved SOW. If the application listed milestones/target dates for important activities or phases of the project, identify these dates and show actual completion dates or the percentage of completion.

We will conduct analysis of MAN2A1-FER, SLC45A2-AMACR, TRMT11-GRIK2, MTOR-TP53BP1, LRRC59-FLJ60017, CCNH-C5orf30, KDM4-AC011523.2, TMEM135-CCDC67 on over 1000 prostate cancer samples collected from University of Pittsburgh, Stanford University and University of Wisconsin Madison. We will first establish prostate cancer recurrence model and short PSADT prediction models either by fusion gene status alone or in combination with nomogram based on the cohort from 600 radical prostatectomy samples from UPMC. This model will be locked in and tested on cohorts from University of Pittsburgh, Stanford University and University of Wisconsin. The prediction accuracy, sensitivity and specificity within each cohort will be evaluated.

1) In the first 3 months of the funded period, we plan to establish this test in the CLIA certified laboratory at the University of Pittsburgh Medical Center. Fifty-six FFPE samples that were shown to be positive for at least one fusion transcripts in the matched frozen tissues. Detection threshold will be obtained.

2) From month 4-9 of the first funded year, we will perform TAQMAN QRT-PCR and Sanger's sequencing on a randomly selected cohort of 600 samples from phase 1 that have at least 5 years clinical follow-up. These tests will be performed in CLIA certified laboratory of University of Pittsburgh. The prediction models of PCa recurrence and PSADT mentioned will be developed based on this large number of samples. For sites 2 and 3, the first 300 prostate cancer cases from each site will be selected and evaluated for sufficient materials for the assay.

3) TAQMAN QRT-PCR analysis for the fusion genes will be carried out at the CLIA certified lab at the University of Pittsburgh using approximately 200 samples provided by Drs. Brooks and Jarrard. In addition, validation of selected prostate cancer samples on specific fusion genes using FISH will be performed. Statistical analyses will be performed to evaluate whether the fusion gene status is predicative for the clinical outcomes of prostate cancers.

What was accomplished under these goals?

For this reporting period describe: 1) major activities; 2) specific objectives; 3) significant results or key outcomes, including major findings, developments, or conclusions (both positive and negative); and/or 4) other achievements. Include a discussion of stated goals not met. Description shall include pertinent data and graphs in sufficient detail to explain any significant results achieved. A succinct description of the methodology used shall be provided. As the project progresses to completion, the emphasis in reporting in this section should shift from reporting activities to reporting accomplishments.

1. We have reaffirmed the detection of fusion transcripts in prostate cancer samples.
2. Using sensitive detection methods, we have found that fusion genes are widely present in prostate cancer samples.
3. We have established a preliminary training model for the prediction of the clinical outcomes of prostate cancer.
4. We have found the fusion genes identified in prostate cancer are also present in other human malignancies.
5. We have found that the fusion transcripts are present in the serum samples of human cancers in cell-free RNA form.

What opportunities for training and professional development has the project provided?

If the project was not intended to provide training and professional development opportunities or there is nothing significant to report during this reporting period, state "Nothing to Report."

Describe opportunities for training and professional development provided to anyone who worked on the project or anyone who was involved in the activities supported by the project. "Training" activities are those in which individuals with advanced professional skills and experience assist others in attaining greater proficiency. Training activities may include, for example, courses or one-on-one work with a mentor. "Professional development" activities result in increased knowledge or skill in one's area of expertise and may include workshops, conferences, seminars, study groups, and individual study. Include participation in conferences, workshops, and seminars not listed under major activities.

Nothing to report

How were the results disseminated to communities of interest?
If there is nothing significant to report during this reporting period, state "Nothing to Report."

Describe how the results were disseminated to communities of interest. Include any outreach activities that were undertaken to reach members of communities who are not usually aware of these project activities, for the purpose of enhancing public understanding and increasing interest in learning and careers in science, technology, and the humanities.

Nothing to report

What do you plan to do during the next reporting period to accomplish the goals?
If this is the final report, state "Nothing to Report."

Describe briefly what you plan to do during the next reporting period to accomplish the goals and objectives.

Nothing to report

4. **IMPACT:** D*escribe distinctive contributions, major accomplishments, innovations, successes, or any change in practice or behavior that has come about as a result of the project relative to:*

What was the impact on the development of the principal discipline(s) of the project?
If there is nothing significant to report during this reporting period, state "Nothing to Report."

Describe how findings, results, techniques that were developed or extended, or other products from the project made an impact or are likely to make an impact on the base of knowledge, theory, and research in the principal disciplinary field(s) of the project. Summarize using language that an intelligent lay audience can understand (Scientific American style).

MAN2A1-FER is the first tyrosine kinase fusion genes found to play critical roles in prostate cancer, it opens a new door for the treatment of prostate cancer using tyrosine kinase inhibitors. In addition, we developed a novel approach to treat human cancers that are positive for fusion gene by inserting a suicide gene into the chromosomal breakpoint of a fusion gene in the cancer genome. This could be a new way to treat prostate cancers that are refractory to other modes of the cancer treatment.

What was the impact on other disciplines?
If there is nothing significant to report during this reporting period, state "Nothing to Report."

Describe how the findings, results, or techniques that were developed or improved, or other products from the project made an impact or are likely to make an impact on other disciplines.

Fusion transcripts mentioned in the proposed study was also present in ovarian cancer, breast cancer, colon cancer, lung cancer, liver cancer, GBM and esophageal adenocarcinoma, and may play roles in the development of those cancers.

What was the impact on technology transfer?
If there is nothing significant to report during this reporting period, state "Nothing to Report."

Describe ways in which the project made an impact, or is likely to make an impact, on commercial technology or public use, including:

- *transfer of results to entities in government or industry;*
- *instances where the research has led to the initiation of a start-up company; or*
- *adoption of new practices.*

Nothing to report

What was the impact on society beyond science and technology?
If there is nothing significant to report during this reporting period, state "Nothing to Report."

Describe how results from the project made an impact, or are likely to make an impact, beyond the bounds of science, engineering, and the academic world on areas such as:

- *improving public knowledge, attitudes, skills, and abilities;*
- *changing behavior, practices, decision making, policies (including regulatory policies), or social actions; or*
- *improving social, economic, civic, or environmental conditions.*

Nothing to report

5. **CHANGES/PROBLEMS:** *The PD/PI is reminded that the recipient organization is required to obtain prior written approval from the awarding agency grants official whenever there are significant changes in the project or its direction. If not previously reported in writing, provide the following additional information or state, "Nothing to Report," if applicable:*

Nothing to report

Changes in approach and reasons for change
Describe any changes in approach during the reporting period and reasons for these changes. Remember that significant changes in objectives and scope require prior approval of the agency.

Actual or anticipated problems or delays and actions or plans to resolve them
Describe problems or delays encountered during the reporting period and actions or plans to resolve them.

Nothing to report

Changes that had a significant impact on expenditures
Describe changes during the reporting period that may have had a significant impact on expenditures, for example, delays in hiring staff or favorable developments that enable meeting objectives at less cost than anticipated.

Nothing to report

Significant changes in use or care of human subjects, vertebrate animals, biohazards, and/or select agents

Describe significant deviations, unexpected outcomes, or changes in approved protocols for the use or care of human subjects, vertebrate animals, biohazards, and/or select agents during the reporting period. If required, were these changes approved by the applicable institution committee (or equivalent) and reported to the agency? Also specify the applicable Institutional Review Board/Institutional Animal Care and Use Committee approval dates.

Significant changes in use or care of human subjects

Nothing to report

Significant changes in use or care of vertebrate animals

Nothing to report

Significant changes in use of biohazards and/or select agents

Nothing to report

6. **PRODUCTS:** *List any products resulting from the project during the reporting period. If there is nothing to report under a particular item, state "Nothing to Report."*

- **Publications, conference papers, and presentations**
  Report only the major publication(s) resulting from the work under this award.

Journal publications. *List peer-reviewed articles or papers appearing in scientific, technical, or professional journals. Identify for each publication: Author(s); title; journal; volume: year; page numbers; status of publication (published; accepted, awaiting publication; submitted, under review; other); acknowledgement of federal support (yes/no).*

None to report

Books or other non-periodical, one-time publications. *Report any book, monograph, dissertation, abstract, or the like published as or in a separate publication, rather than a periodical or series. Include any significant publication in the proceedings of a one-time conference or in the report of a one-time study, commission, or the like. Identify for each one-time publication: author(s); title; editor; title of collection, if applicable; bibliographic information; year; type of publication (e.g., book, thesis or dissertation); status of publication (published; accepted, awaiting publication; submitted, under review; other); acknowledgement of federal support (yes/no).*

Nothing to report

Other publications, conference papers and presentations. *Identify any other publications, conference papers and/or presentations not reported above. Specify the status of the publication as noted above. List presentations made during the last year (international, national, local societies, military meetings, etc.). Use an asterisk (*) if presentation produced a manuscript.*

None to report

- **Website(s) or other Internet site(s)**
  List the URL for any Internet site(s) that disseminates the results of the research activities. A short description of each site should be provided. It is not necessary to include the publications already specified above in this section.

Nothing to report

- **Technologies or techniques**
  Identify technologies or techniques that resulted from the research activities. Describe the technologies or techniques were shared.

Nothing to report

- **Inventions, patent applications, and/or licenses**
  Identify inventions, patent applications with date, and/or licenses that have resulted from the research. Submission of this information as part of an interim research performance progress report is not a substitute for any other invention reporting required under the terms and conditions of an award.

Nothing to report

- **Other Products**
  Identify any other reportable outcomes that were developed under this project. Reportable outcomes are defined as a research result that is or relates to a product, scientific advance, or research tool that makes a meaningful contribution toward the understanding, prevention, diagnosis, prognosis, treatment and /or rehabilitation of a disease, injury or condition, or to improve the quality of life. Examples include:
  - *data or databases;*
  - *physical collections;*
  - *audio or video products;*
  - *software;*
  - *models;*
  - *educational aids or curricula;*
  - *instruments or equipment;*
  - *research material (e.g., Germplasm; cell lines, DNA probes, animal models);*
  - *clinical interventions;*
  - *new business creation; and*

- *other.*

Nothing to report

7. PARTICIPANTS & OTHER COLLABORATING ORGANIZATIONS

What individuals have worked on the project?

Provide the following information for: (1) PDs/PIs; and (2) each person who has worked at least one person month per year on the project during the reporting period, regardless of the source of compensation (a person month equals approximately 160 hours of effort). If information is unchanged from a previous submission, provide the name only and indicate "no change".

Example:

Name: *Mary Smith*
Project Role: *Graduate Student*
Researcher Identifier (e.g. ORCID ID): *1234567*
Nearest person month worked: *5*

Contribution to Project: *Ms. Smith has performed work in the area of combined error-control and constrained coding.*
Funding Support: *The Ford Foundation (Complete only if the funding support is provided from other than this award.)*

Name: *James D. Brooks*
Project Role: *Professor*
Nearest person month worked: *1.20 calendar months*
Contribution to Project: *I have supervised the project at Stanford*
Funding Support: *Non-sponsored (designated, endowment, etc). Sponsored (DoD, NIH)*

Name: *Michelle Ferrari*
Project Role: *Research Nurse Manager*
Nearest person month worked: *2.76 calendar months*
Contribution to Project: *Pulled clinical data on all patients. Constructed clinical databases. Communicated blinded clinical data to Dr. Brooks who sends blinded data to Pittsburgh*
Funding Support: *Non-Sponsored (gift, endowment, etc). Sponsored (DoD, NIH).*

Name: *Kieu My Huynh*
Project Role: *Research Technician*
Nearest person month worked: *4.32 calendar months*
Contribution to Project: *Pulled H & E slides with Mrs. Nolley*
Funding Support: *Non-Sponsored (endowment, etc). Sponsored (DoD, NIH).*

Name:	*Rosalie Nolley*
Project Role:	*Pathology Technician*
Nearest person month worked:	*1.80 calendar months*
Contribution to Project:	*Pulled H & E slides. Cored samples. Shipped to U Pittsburgh. Confirmed pathology under supervision of Dr. Brooks*
Funding Support:	*Sponsored (DoD, NIH)*

Has there been a change in the active other support of the PD/PI(s) or senior/key personnel since the last reporting period?
If there is nothing significant to report during this reporting period, state "Nothing to Report."

If the active support has changed for the PD/PI(s) or senior/key personnel, then describe what the change has been. Changes may occur, for example, if a previously active grant has closed and/or if a previously pending grant is now active. Annotate this information so it is clear what has changed from the previous submission. Submission of other support information is not necessary for pending changes or for changes in the level of effort for active support reported previously. The awarding agency may require prior written approval if a change in active other support significantly impacts the effort on the project that is the subject of the project report.

Title: Glycosylation and immune evasion in urologic tumors
1U01CA226051
Effort: 1.20 calendar
Supporting Agency: NIH/NCI
Grants Officer: Karl Kreuger
Performance Period: 05/01/2019-04/30/2024
Funding Amount: $ 404,179
Project Goals: First, because sialic acid is known to be overexpressed on the surface of cancer cells, we will use intact glycoproteomics methods developed in-house to enrich and identify sialoglycoproteins from cancerous and matched healthy tissues from patients. Quantitative comparative analyses will reveal changes in sialoglycoprotein expression and illuminate candidate ligands for sialic acid-binding proteins in the tumor microenvironment that potentially contribute to immune inactivation. Correlation of these glycoproteomic datasets with RNA-seq data focused on glycogene expression will bolster the assignment of specific glycoforms as cancer biomarkers. Second, using immunohistochemistry and CODEX methods, we will analyze expression levels of sialic acid-binding immunoglobulin-type lectin (Siglec) receptor proteins on tumor- resident immune cells and cross-correlate the findings with RNA-seq data as well as immune cell markers. We will also probe for the presence of ligands for various Siglec isoforms on tumor cell surfaces and obtain spatial information about their distribution on immune cells in intact tumor tissue. For any Siglecs identified as prominently displayed on immune cells in the tumor environment, we will develop cell-based assays to probe their contribution to tumor cell immunoreactivity. Third, we will perform a genome-wide screening using CRISPRi to identify genes that facilitate the binding of Siglecs to cancer cells. Finally, we will correlate the datasets from Aims 1, 2, and 3 with patient outcomes in a larger set of tissue samples contained on a tissue microarray and evaluate their utility as prognostic indicators.
PI: Pitteri/Bertozzi/Brooks
Role: Co-Principal Investigator
Overlap: None

Title: Prostate cancer Active Surveillance Study (PASS) Cohort: Infrastructure Support for Cancer Research
Effort: 0.24 calendar
Supporting Agency: NIH/NCI
Grants Office: Joy Kearse
Performance Period: 09/20/2019-08/31/2024
Funding Amount: $16,600
Project Goals: The goal of this proposal is to maintain infrastructure for an active surveillance registry trial

men with localized prostate cancer. The grant supports patient enrollment, follow-up, specimen collection and storage, central pathology review, a statistical core, and specimen sharing with the community. Stanford serves as one of the enrollment sites.
Specific Aims:
Aim 1: Continue follow-up of PASS/CEC participants including the collection of biospecimens in addition to clinical, epidemiological, health-related and long-term outcomes.
Aim 2: Support the PASS/CEC database, biospecimen repository, and central pathology review to continue as a unique resource for research.
Aim 3: Promote and facilitate the use of PASS/CEC data and specimens by the scientific community.
Support for the CEC will: 1) promote accessibility to and utilization of cohort data and biospecimens; and 2) provide the biostatistical, clinical, epidemiological and technical expertise that investigators may need for using data and samples from this unique cohort.
PI: Brooks, James
Role: Site Principal Investigator
Overlap: None

PENDING
Title: Targeting AXL to overcome resistance to taxanes and platinum-based therapy in castrate
Effort: 1.20 calendar
Supporting Agency: NIH/NCI
Performance Period: 11/01/2019-10/31/2021
Funding Amount: $150,000
Project Goals: The project develops preclinical data in mouse PDX models to test whether blocking AXL signaling using a novel soluble AXL (sAXL) decoy receptor will inhibit mCPRC growth in the bone as a single agent and whether this decoy receptor will sensitize cancer cells to docetaxel or carboplatin when used in combination.
Specific Aims:
Aim 1: Determine activity of MYD1-72 Fc as a single agent or as a chemosensitizer on intratibial models of LuCaP CRPC AC and NEPC.
Aim 2: Identification of biomarkers associated with responses to single agent MYD1-72 Fc and/or chemosensitization.
PI: Brooks, James
Role: Principal Investigator
Overlap: None

COMPLETED
Title: IQGAP1 Scaffold-Kinase Interaction Blockade In Renal Cell Carcinoma: A Novel Biomarker And Therapeutic Strategy
W81XWH-16-1-0553
Effort: 0.60 calendar
Supporting Agency: Department of the Army
Grants Officer: Wendy Baker
Performance Period: 09/15/2016-09/14/2019
Funding Amount: $119,794
Project Goals: The goal of this proposal is to test whether the scoffold protein IQGAP plays a significant goal in conventional renal cell carcinoma. Candidate signaling pathways associate with IQGAP will be interrogated. IQGAP will be assessed as a biomarker of disease recurrence. Strategies to block IQGAP function will be evaluated as therapeutic targets.
PI: Leppert, John
Role: Co-Investigator
Overlap: None.

Describe partner organizations – academic institutions, other nonprofits, industrial or commercial firms, state or local governments, schools or school systems, or other organizations (foreign or domestic) – that were involved with the project. Partner organizations may have provided financial or in-kind support, supplied facilities or equipment, collaborated in the research, exchanged personnel, or otherwise contributed.

Provide the following information for each partnership:
Organization Name:
Location of Organization: (if foreign location list country)
Partner's contribution to the project (identify one or more)

- *Financial support;*
- *In-kind support (e.g., partner makes software, computers, equipment, etc., available to project staff);*
- *Facilities (e.g., project staff use the partner's facilities for project activities);*
- *Collaboration (e.g., partner's staff work with project staff on the project);*
- *Personnel exchanges (e.g., project staff and/or partner's staff use each other's facilities, work at each other's site); and*
- *Other.*

Nothing to report

8. SPECIAL REPORTING REQUIREMENTS

COLLABORATIVE AWARDS: *For collaborative awards, independent reports are required from BOTH the Initiating Principal Investigator (PI) and the Collaborating/Partnering PI. A duplicative report is acceptable; however, tasks shall be clearly marked with the responsible PI and research site. A report shall be submitted to* ***https://ers.amedd.army.mil*** *for each unique award.*

QUAD CHARTS: *If applicable, the Quad Chart (available on https://www.usamraa.army.mil) should be updated and submitted with attachments.*

9. APPENDICES: *Attach all appendices that contain information that supplements, clarifies or supports the text. Examples include original copies of journal articles, reprints of manuscripts and abstracts, a curriculum vitae, patent applications, study questionnaires, and surveys, etc.*