AD_____

Award Number: DAMD17-02-1-0412

TITLE: Identification of Novel Inhibitory Peptides of Protein-Protein Interactions Involved in DNA Repair as Potential Drugs in Breast Cancer Treatment

PRINCIPAL INVESTIGATOR: Sitharthan Kamalakaran

CONTRACTING ORGANIZATION: University of Illinois at Chicago
Chicago, Illinois 60612-7227

REPORT DATE: April 2003

TYPE OF REPORT: Annual Summary

PREPARED FOR: U.S. Army Medical Research and Materiel Command
Fort Detrick, Maryland 21702-5012

# REPORT DOCUMENTATION PAGE

*Form Approved*
*OMB No. 074-0188*



| 1. AGENCY USE ONLY (Leave blank) | 2. REPORT DATE | 3. REPORT TYPE AND DATES COVERED |
|---|---|---|
| | April 2003 | Annual Summary (1 Apr 02 - 31 Mar 03) |

**4. TITLE AND SUBTITLE**
Identification of Novel Inhibitory Peptides of Protein-Protein Interactions Involved in DNA Repair as Potential Drugs in Breast Cancer Treatment

**5. FUNDING NUMBERS**
DAMD17-02-1-0412

**6. AUTHOR(S):**
Sitharthan Kamalakaran

**7. PERFORMING ORGANIZATION NAME(S) AND ADDRESS(ES)**
University of Illinois at Chicago
Chicago, Illinois 60612-7227

E-Mail: ksit@uic.edu

**8. PERFORMING ORGANIZATION REPORT NUMBER**

**9. SPONSORING / MONITORING AGENCY NAME(S) AND ADDRESS(ES)**
U.S. Army Medical Research and Materiel Command
Fort Detrick, Maryland 21702-5012

**10. SPONSORING / MONITORING AGENCY REPORT NUMBER**

**11. SUPPLEMENTARY NOTES**
Original contains color plates: All DTIC reproductions will be in black and white.

**12a. DISTRIBUTION / AVAILABILITY STATEMENT**
Approved for Public Release; Distribution Unlimited

**12b. DISTRIBUTION CODE**

**13. Abstract** ***(Maximum 200 Words)*** *(abstract should contain no proprietary or confidential information)*

Protein-protein interactions are critical to almost every cellular process. Disruption of these interactions would effectively interfere with the cell's functions and its ability to grow and divide normally.

The Rad51 and Rad52 proteins are important proteins involved in DNA repair. Rad51 acts as a hexamer binding single-stranded DNA to drive strand exchange during homologous recombination. By blocking Rad51 from multimerization we can theoretically disrupt homologous recombination, and thus decrease the efficacy of DNA repair. Deficiency in DNA damage repair will sensitize cells to DNA damaging agents and thus such tumors can be effectively treated with a lower dose of chemotherapeutic agents/radiation.

Short peptides of a few amino acids (5-10) have been shown to be enough to destabilize protein-protein interactions. Thus a library of random combinatorial peptides of sufficient complexity will in theory have an inhibitory molecule for any protein-protein interaction.

This project will attempt to isolate peptides that inhibit Rad 51 from multimerisation to be used as a chmosensitizing agent during chemo/radiotherapy. We plan to use a modified Yeast two hybrid screen called the reverse two-hybrid system to isolate such peptides.

| 14. SUBJECT TERMS: | 15. NUMBER OF PAGES |
|---|---|
| DNA repair, yeast reverse two hybrid system, random peptide library, Rad 51, Ku70/80, sensitizing agents to chemotherapy | 14 |
| | 16. PRICE CODE |

| 17. SECURITY CLASSIFICATION OF REPORT | 18. SECURITY CLASSIFICATION OF THIS PAGE | 19. SECURITY CLASSIFICATION OF ABSTRACT | 20. LIMITATION OF ABSTRACT |
|---|---|---|---|
| Unclassified | Unclassified | Unclassified | Unlimited |

## Table of Contents

**Identification of novel inhibitory peptides of protein-protein interactions involved in DNA repair as potential drugs in breast cancer treatment**

**Introduction:**

Tumorigenesis is the result of multiple genetic changes. Although cells are subject to a multitude of environmental and chemical factors, the cell's robust repair machinery is able to repair most of the damage and, if not, at least program the cell to undergo apoptosis, thereby preventing uncontrolled proliferation of DNA damaged cells. However, mutations in these check-point genes that diminish the cell's ability to do either of these functions may lead to increased susceptibility to neoplasias. Hereditary Nonpolyposis colorectal cancer syndrome (HNPCC) is an example of such an inherited mutation causing increased susceptibility to cancer [1].

Homologous recombination is one of the important repair pathways that guards against tumorigenesis. While its prominent function is the exchange of information during meiosis, its has been shown to be a key pathway in DNA repair in bacteria and yeast[2]. In bacteria, Rec A is the protein that drives homologous recombination. Rec A acts as a hexamer, binding single-stranded DNA and driving strand exchange. It has been shown that Rec A is a critical component of the SOS response to ionizing radiation. In *Saccharomyces cerevesiae,* the Rad 51 and Rad 52 proteins have been identified as important players in this pathway. Rad 51 is the yeast homologue of the bacterial Rec A protein[3-5]. A mammalian homologue of Rad 51, with high homology to the bacterial Rec A protein, has also been cloned. The high degree of conservation between prokaryotes and high order eukaryotes suggests the importance of this pathway for the cell.

The other major pathway for Double Strand Break (DSB) repair is the Ku70/80-mediated Non Homologous End Joining pathway (NHEJ). DNA lesions are recognized by the Ku70/80 hetrodimeric protein which then recruits the repair complex to the lesion. Important members of the repair complex are XRCC4-DNA ligase4, which joins the broken strands of the complex and the Mre11 nuclease, which cleans the ends for ligation.

BRCA1 and BRCA2 are tumor suppressor genes identified in breast cancer. Although the primary function of these genes has not been fully elucidated, they are thought to have a role in DNA damage repair. BRCA1 has 1863 amino acids and BRCA2 3418 amino acids. There are no homologues for either protein in yeast. A wide spectrum of both mis-sense and truncation mutations have been identified in these genes. Both BRCA1 and BRCA2 knockouts are embryonic lethal in the mouse [6]. BRCA2 has eight repeating motifs named BRCA repeats (BRCT). Both proteins have been shown to be cell cycle regulated, peaking during the S phase of the cell cycle. BRCA2 has also been shown to bind Rad51, underlying the importance of these proteins in DNA repair[7-9].

**Body :**

Protein-protein interactions are critical to almost every cellular process from cellular macrostructures to enzyme complexes and signal transduction. As such,

disruption of these interactions will provide a mechanism of deregulation of the respective pathways and hence a molecular target for drugs.

Most therapeutic agents for breast cancer function by causing DNA damage, either directly (ionizing radiation) or indirectly (topoisomerase inhibitors). The problem with these agents is the generalized toxicity of the treatment. Therefore any agent that can specifically target the breast tumor can be used to sensitize the tumor alone to the DNA damaging agent.

Mice lacking BRCA2 and Rad51 have a Rad51-associated hypersensitivity to gamma radiation (7). However, BRCA2 deficient breast epithelial cells can survive with an unstable genome and thus proliferate, especially if they have another genomic alteration associated with malignancy. We think that loss of function of BRCA2 might increase genomic instability due to increased or error-prone homologous recombination mediated by Rad51. In this context, inhibition of Rad51 function may decrease the proliferative capacity of these cells. Because BRCA1 and BRCA2 mutations are estimated to be responsible in 80% of inherited cases of breast cancer and more than 95% of inherited ovarian cancers, this strong correlation provides an ideal molecular target for treatment of these cases. While normal cells regulate the rates and activities of the homologous recombination (HR) machinery in check through tumor suppressors BRCA1 and 2, tumor cells that are BRCA null will have a deregulated HR pathway. Thus, inhibition of homologous recombination in these cells will preferentially sensitize them to treatment.

Being the primary sensor of this pathway, abolition of Ku activity severely impairs DNA repair ability by NHEJ. The Ku knockout mice have a SCID phenotype and are also sensitive to DNA damage. A dominant negative mutant of Ku70 that can form the ku heterodimer but is deficient in DNA binding has been shown to sensitize HeLa and MCF7 cells to drugs that cause DSB([10-12]).

The DNA repair pathway is thus an obvious target for an agent that disrupts protein-protein interactions. By blocking Rad51 from multimerization we can theoretically disrupt homologous recombination, and thus decrease the efficacy of DNA repair. We can make the same argument for Ku70/80 DNA binding activity and the NHEJ pathway of DNA repair. Deficiency in DNA damage repair will sensitize cells to DNA damaging agents and thus such tumors can potentially be treated with a lower dose of chemotherapeutic agents/radiation.

The crystal structure of the Ku70/80 in complex with DNA has been published[13]. The structure clearly delineates important motifs of the Ku proteins that are responsible for DNA binding activity. The Ku70/80 complex has a preformed ring structure that is of the same diameter as a d.s DNA molecule. The inside of the ring has many positive-charged amino acids which are critical for interactions with the phosphate backbone of DNA.

While our original proposal included only the use of the Yeast two hybrid system to screen for Rad 51 inhibitors we intend to use the data from the crystal structure of Ku70/80 to achieve the overall aim of this project, i.e, to target DNA repair proteins as potential sensitizing agents to chemotherapy (as discussed in the Future Directions part of this report).

**Isolation of Inhibitory Peptides**

Short peptides of a few amino acids (5-10) have been shown to be sufficient to destabilize protein-protein interactions. Thus a library of random combinatorial peptides of sufficient complexity will in theory have an inhibitory molecule for any protein-protein interaction. We proposed to use the reverse two-hybrid system to isolate inhibitory peptides[14]. The system is a modification of the conventional two-hybrid system but selects for a protein that will destabilize a protein protein interaction. This is done by introducing a Ura3 gene under the Gal 4 promoter as one of the reporter genes. Basal expression of Ura3 is inhibited by engineering an Upstream Repressing Sequence (URS1) of Spo13 upstream of Ura3 (2). Ura3 encodes Orotidine 5'phosphate decarboxylase, used in the biosynthesis of Uracil. Ura3 can also catalyze the conversion of 5 Fluoro orotic acid (FOA) into a toxic product, 5 fluorouracil. Accordingly, if we transform this host strain with plasmids harboring genes whose products are known to interact (as fusions with the Gal 4 DNA binding domain and Gal 4-activation domain) the yeast will be able to grow in a media lacking Uracil. However, the strain will be sensitive to the presence of FOA (Fig. 1). Thus, if we now introduce a library of random peptides one of which may potentially inhibit this interaction in this cell, we may suppress the expression of Ura 3. A cell harboring such a peptide will be $Ura^-$ $FOA^R$ and thus can be selected.

The strain we proposed to use was MaV103 (MATalpha leu2-3, 112 trp1--901 his3D200 ade2-101 gal4D gal80D SPAL10::URA3 GAL1::lac Z Gal1::his3@LYS2 can1R cyh2 R) [14]. The host strain has 3 stably integrated Gal4p-inducible genes: SPAL::URA3, integrated at URA3, Gal1::HIS3, integrated at LYS2, and GAL1::LacZ integrated at an unknown locus.

Specifically the plan for year 1 was:

**1.To set up the Reverse Two Hybrid System**

a) Develop a series of plasmids for expressing the Rad51 as fusion protein with Gal4 activation domain(Gal4 AD) and Gal4 DNA binding Domain (Gal4 DB). (Months 1-3)

b) To Transform the fusion constructs in to MV103 and select for transformants. (Month 4)

c) Perform assays to determine the strength of Rad51 association in a two hybrid context using Lac Z assays (Months 5-7).

**d)** Determine Minimum concentration of FOA required for cell killing of the Rad51 fusions transformed MV103 strain (Months 8-11).

**2. To construct Random Nucleotide Library**

a. Perform PCR/ Klenow fill-in reactions on a synthetic oligo purchased from GIBCO –BRL and purify random d.s DNA fragments (Months 8-10).

**b.** Clone the d.s DNA containing the random library in frame with HA tag into vector pHANLS.(Months 10-14)

**Methodology:**

**1. The Reverse Two hybrid Set up:**

The next part of our plan was to set up a two hybrid system of Rad 51 interaction in *S. cerevisiae*. Rad 51 fusions were constructed with the Gal 4 activation domain (Gal4 AD) and the Gal4 DNA binding domain (Gal4 BD). The Rad 51 cDNA was obtained from Dr. Zhiyuan Shen (Univ. of New Mexico). The insert was PCR amplified and cloned into the pGDBMAD vector, also provided by Dr.Shen. This vector is derived from the commonly used pBRIDGE and has two multiple cloning sites for fusion with the Gal4 AD and Gal4 DB and has a Tryptophan selection marker.

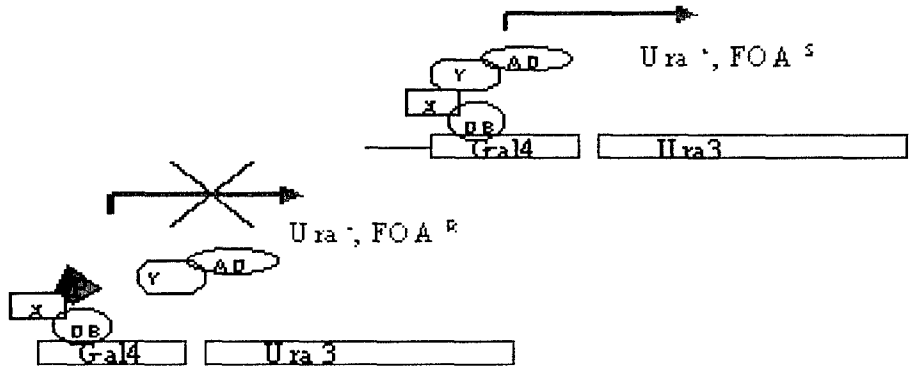


**Fig. 1: Reporter Gene Function.**

Three plasmids were thus constructed:

PGDBMAD/AD51- with Gal4 AD-Rad51 fusion

pGDBMAD/DB51- with Gal4DB-Rad51 fusion

pGDBMAD/MAD51- with Gal4 AD-Rad51 and Gal4DB-Rad51 fusions

The vectors were then transformed into MV103 and the transformants selected on Trp⁻ plates. The clones obtained were then assayed for Lac Z activity (Fig. 2).

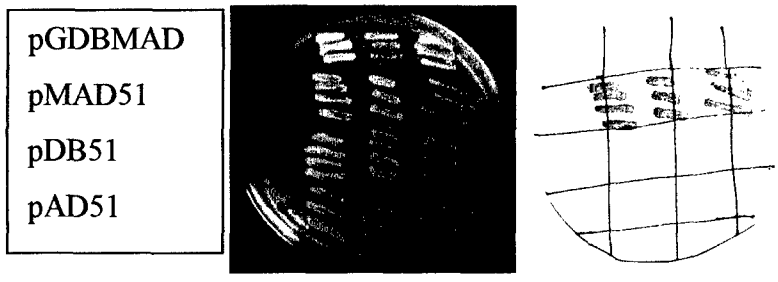


**Fig. 2: Lac Z assay.** 3 clones from each transformation with the respective vectors (pGDBMAD, pMAD51, pDB51 and pAD51) were grown overnight. A colony lift Lac Z assay was then performed and color development was observed after 3 h. Only clones that harbored pMAD51 tested positive.

**Determination of minimum 5 FOA concentration:**

Three clones from each transformation were taken and grown on $Trp^-$ plates containing 0%, 0.05%, 0.1%, 0.16% and 0.3% 5FOA by weight. Clones harboring pMAD51 are sensitive to 5FOA and are killed between 0.05% and 0.1% FOA. In the next step the clones were plated on plates containing 0%, 0.02%, 0.04%, 0.06% & 0.08% FOA. Minimum FOA concentration for cell death in MV103/pMAD51 was 0.06% (Fig. 3).

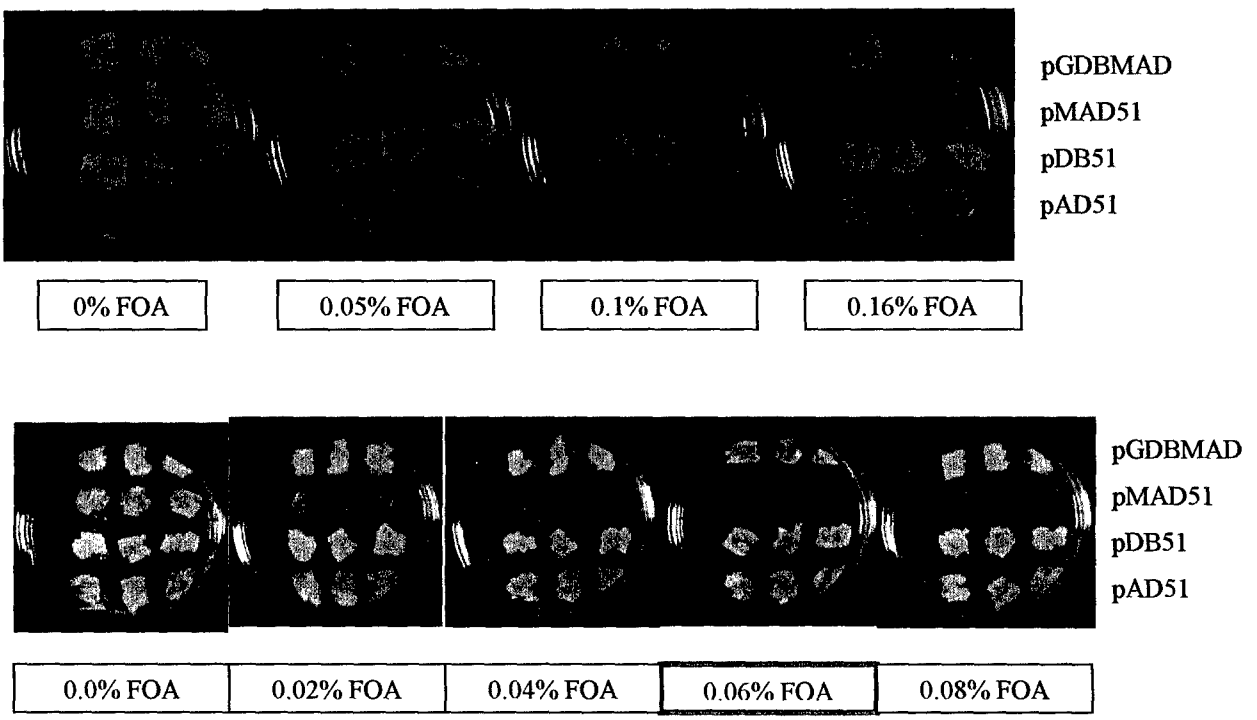


**Fig. 3: Determination of minimum FOA concentration.**

**2. Construction of a combinatorial Library:**

A random DNA library coding for all possible combinations of 15 amino-acid peptides was to be constructed. The vector pHANLS we used was derived from the commercially available pGAD vector. The Gal4 activation domain was removed and a nuclear localization signal (NLS) was added upstream of the multiple cloning site (MCS) at the *Nco I* restriction site. A HA tag was added immediately downstream of the NLS. The vector was constructed by Dr. Shen.

We encountered a variety of unforeseen problems at this stage, so we tried three different approaches (Fig.4).

**Approach 1:**

A template for the library (RanTMP) containing $N_{45}$ flanked by 15 bases on either side for primer binding and restriction was custom synthesised from GibcoBRL. The library was then synthesised by PCR using Ran TMP as template, precipitated using ethanol and then digested at the introduced *EcoR I* and *BamH I* sites and cloned into pHANLS vector. However this approach did not work well and the tranformation efficiency was always low (the maximum complexity obtained was in the order of $10^3$).

**Approach 2:**

During a meeting on Phage Display technologies (MIT, April 7-9, 2001) the PI was able to talk with Dr. Jonathan Blum (Harvard Medical School). He had done some work using combinatorial DNA libraries to isolate peptides with antibacterial action (1). We learned that he had also tried the approach described earlier and had encountered the same problems as we did. He suggested we use Klenow fill-in to generate our library. We then used the same template as before but instead of PCR amplifying the library we used Klenow enzyme and a single primer at the 3' end. The product was then purified as before and the ligation and cloning was carried out. However we encountered new problems at this step. The small insert size (47 bases after restriction) provided a lot of background with no or multiple inserts. So we chose approach 3.

**Approach 3:**

We used a 77 nucleotide DNA fragment custom ordered from GIBCO-BRL as the template for the library. The 3' end of the oligonucleotide is complementary to the vector pHANLS and has 15 repeats of NNK ('N' stands for any nucleotide and 'K' for the base 'A' or 'T'). Each 'NNK' will serve as a codon for amino acid synthesis. Using this oligo as the 3' primer and a 5' primer from the upstream portion of pHANLS we can generate a double stranded DNA fragment with the library at the 3' end. This approach addressed a variety of problems encountered in the previous approaches:

- Accomodating for the degeneracy of the codon usage allowed us to reduce the complexity required to cover the entire sample space by an order of $2^{15}$.
- Incorporating the library as a primer will prevent the amplification bias introduced by PCR.
- This method also allowed us to synthesize the library as a much larger fragment and made it easier to handle and manipulate the library DNA during construction.

Using a restriction site incorporated in oligo primers we were able to directionally clone the library into the vector. Scaling up at this level will give us a library complexity of $10^6$ (Fig. 5 and 6). We are presently fine-tuning the process to increase the complexity of the library to $10^8$.

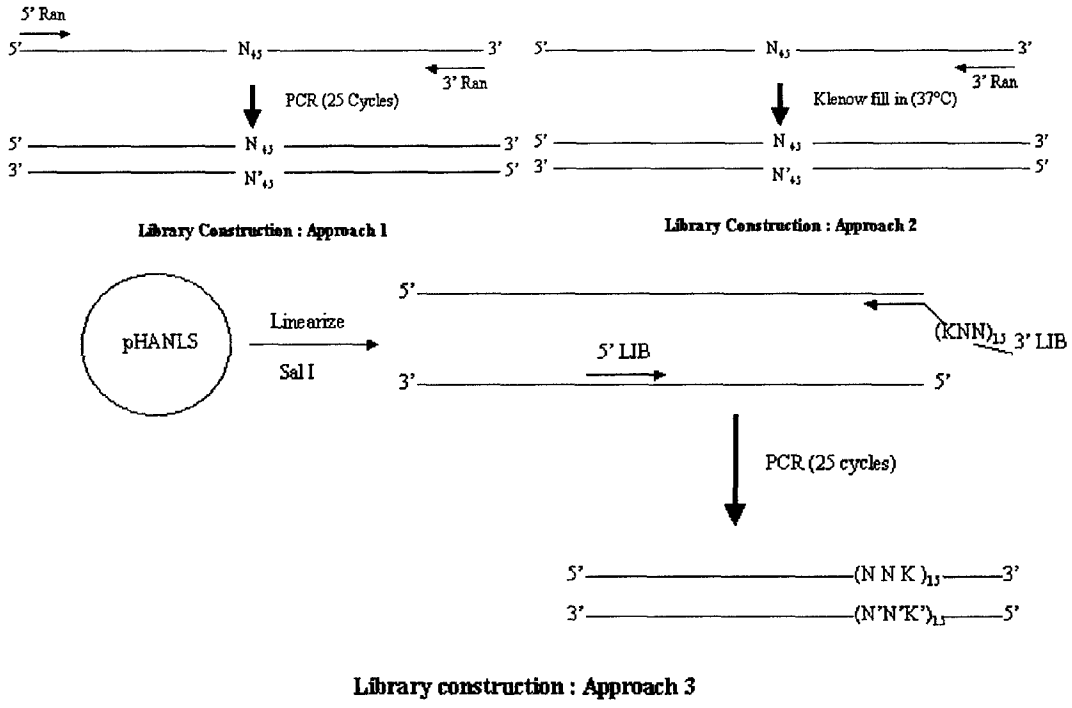


**Fig. 4: Approaches for Library construction.**

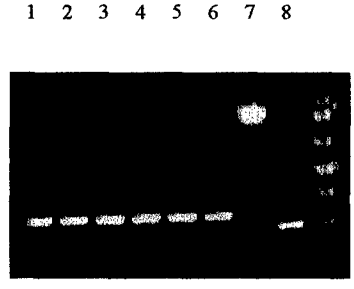


**Fig. 5:** Colony PCR was performed using primers in the vector pHANLS to look for library inserts. A vector with no insert gave a band of length ~280bp (Lane 8) while a plasmid harboring a random nucleotide insert gave a band of length ~330bp(Lanes 1-6). Lane 7 is a positive control (pHANLS harboring a 520bp insert).

```
pHANLS/1 CCGGGGATCCGTCGACCT AAAGCCCCCTCCATCCCCGCAAATTCTGCCACC.ACCACCGCACA  AGATCTATGAATCG
pHANLS/2 CCGGGGATCCGTCGACCT CCCAACGATAATTCCTACCCCCCGCAACATACTACCTCCTCACA   AGATCTATGAATCG
pHANLS/3 CCGGGGATCCGTCGACCT GCCCAACGATAATTCCTACCCCCCGCAACATACTACCTCCTCACA  AGATCTATGAATCG
pHANLS/4 CCGGGGATCCGTCGACCT CTCCGAACCTTCCCCCTCCACCCCTGCCCCTCCGACGCCCCCATA  AGATCTATGAATCG
pHANLS/5 CCGGGGATCCGTCGACCT TTCTCCCCCACCTCCCCCAGCTCCAAACCATGAAACCCAGTCACC  AGATCTATGAATCG
pHANLS/7 CCGGGGATCCGTCGACCT CTCCCCCACCTCAGCCTCACCCCCCCCGGATGCACCTCCCTCTCC  AGATCTATGAATCG
pHANLS   CCGGGGATCCGTCGACCT ..........................................  AGATCTATGAATCG
```

**Fig. 6: Randomness of library as shown by sequencing a few colonies**: 45 bp random insert flanked by vector sequences. Last sequence is empty vector.

**Future Directions (Year 2):**

**Screening for Inhibitory peptides:**

Once we have a library of sufficient complexity (> $10^7$) it will be transformed into the two hybrid set up detailed above and selected for inhibitors of Rad 51 interaction on $Ura^+$ $FOA^+$ plates. The clones harboring the plasmid for inhibitory peptides will then be isolated and the corresponding plasmid extracted.

*Anticipated problems:* The genetic screen we propose to use is not designed to specifically select for peptide inhibitors. The screen may isolate also antisense RNA. We propose to use an additional step to determine if the plasmid isolated from the screen codes for antisense RNA or peptides. This will be done by sub-cloning the construct into a vector PHANLS/stop which has an inbuilt stop codon following the HA tag. If the construct codes for antisense RNA then the new construct will still select in the $Ura^+$ $FOA^+$ media while it will not if the construct codes for a peptide. We also plan to do in-vitro pull down experiments using GST tagged Rad 51 to confirm disruption of Rad 51 interactions by the peptides isolated from the screen.

**Characterization of inhibitory peptides:**

The plasmids that are positive for the selection will be isolated and sequenced. The pHANLS vector has a HA tag attached at its N terminus of the insert. The peptides will be expressed and purified using the HA tag and used in *in vitro* studies to look at their potency to disrupt Rad51 self-association. Also cell survival assays will be performed to determine if the peptides are active in cell culture and if disruption of the HR pathway through dissociation of Rad 51 sensitizes cells to double strand breaks.

We will use the *I-SceI* system previously described by Pierce *at al.*[15] to investigate the efficiency of Rad 51 mediated homologous recombination in cells expressing inhibitory peptides. This system uses a rare cutting endonuclease to induce DSB at specific sites in the DNA in cell culture. The cells have two retrovirally transfected constructs, one encoding Enhanced Green Fluorescent Protein (EGFP), under a constitutive promoter, with a *I-Sce I* restriction site in the coding region and and another vector harboring a promoterless EGFP construct. When *I-Sce I* is expressed, it makes a double stranded cut in the *I-sce I* sites in the genome. The only way for EGFP expression to continue is when the EGFP gene recombines with the promoterless EGFP integrated elsewhere in the genome through homogous recombination. The eficiency of homologous recombination is then studied by assaying for EGFP reconstitution or cell survival.

**Structure Based Design for KU70/80 inhibitors.**

The Ku70/80 crystal structure has recently been published[13]. We would like to make use of these data to address our overall objective i.e to design inhibitors of DNA repair as sensitizing agents to chemotherapy. Having a crystal structure, especially in complex with DNA, simplifies the realization of our primary objective. We can now use the crystal structure of the Ku complex with DNA, to screen for small molecules that should inhibit DNA binding activity. The Ku complex is the primary sensor for the Non Homologous End Joining (NHEJ) pathway of repairing double strand DNA breaks. Blocking Ku 70/80 from binding DNA should effectively inhibit the NHEJ process.

Thus, small molecules that block Ku activity could act as good sensitizing agents to chemotherapies that target DNA. These small molecules can be used as lead compounds for developing more effective and potent inhibitors. We have already mapped the critical interactions for DNA binding activity of the Ku70/80 complex. We have delineated the site on the DNA binding domain which, when targeted by a small molecule inhibitor, would abolish Ku activity (Fig. 7).

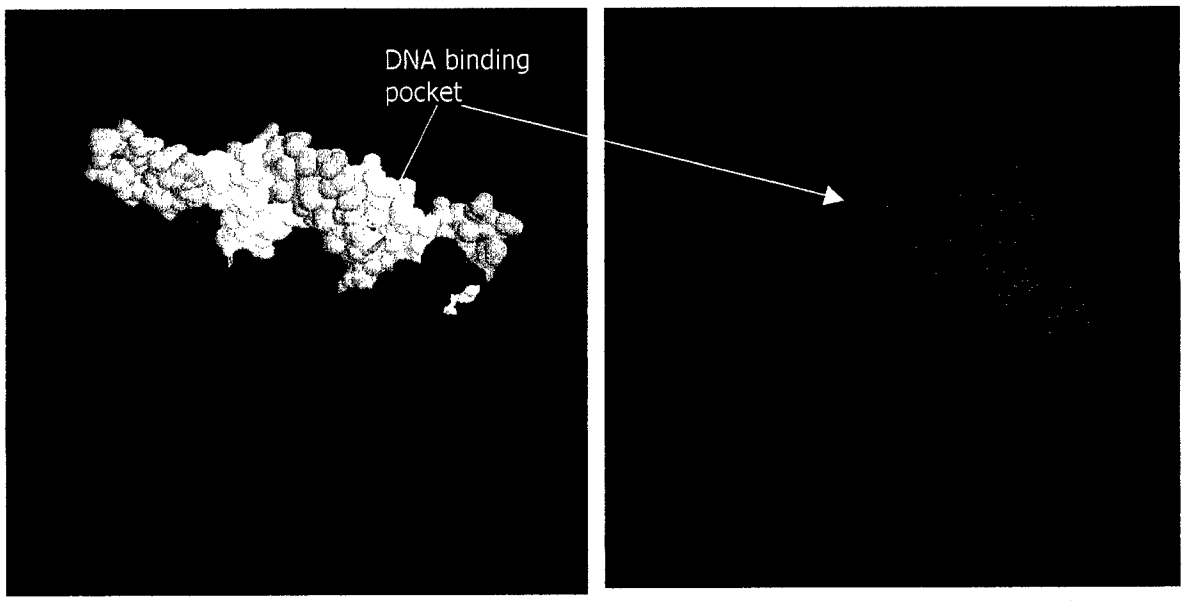


**Fig 7. DNA binding pocket of Ku70/80 dimer (The structure is pared down to show the DNA binding region of the heterodimer clear).**

We plan to use the DOCK 4.0 program to screen small molecule compound libraries for binding affinity to the DNA binding site on the Ku70/80 complex[16-18]. The compound libraries that are available to us are the Available Chemicals Directory (ACD) structure database which has over 300,000 compounds, and the NCI 3D database, which has around 250,000 compounds.

**In this context we would like to modify our proposal to include the following objectives.**

**Proposal for additional objectives for Year 2:**

a. To set up a DOCK screen for small molecules targetting the DNA binding region of the Ku70/80 complex.

b. To select top hits of the screen and verify biochemical activity in the DNA binding assay for Ku70/80 complex described above.

c. To test efficacy of such inhibitors in sensitizing tumor cells to double strand breaks in DNA.

**Key Research Accomplishments:**

- A random DNA library of complexity in the order of $10^6$ encoding 15 amino-acid peptides was synthesized.
- A system to select inhibitors of Rad51 self association in the context of a Reverse Two hybrid System was set up.
- Critical interactions for Ku70/80 DNA bindng activity were mapped.

**Reportable Outcomes:**

- Poster : S. Kamalakaran & WT Beck, Identification of inhibitors for protein-protein interactions involved in DNA Repair as potential drugs in breast cancer, Dept. of Defence Era of Hope Breast Cancer Meeting, Orlando, Fl, Sept 25-29, 2002.

**Conclusions:**

We now have the set up ready for screening inhibitory peptides against Rad51 self association. We have determined the minimum FOA concentration required for the screening at 0.06%. We also have created a combinatorial DNA library coding for 15 aminoacid peptides at a complexity of about $10^6$. We are in the process of increasing the library complexity to about $10^8$. Once we have a library of such complexity we can start screening for inhibitory peptides.

We also intend to move forward with the DOCK screen for identifying potential inhibitors of the Ku70/80 complex. Putative inhibitors predicted by this Chem-informatics analysis will be assayed for biochemical activity.

**References:**

1. Boland, C.R., et al., *Genetic instability and chromosomal aberrations in colorectal cancer: a review of the current models.* Cancer Detect Prev, 1998. **22**(5): p. 377-82.
2. Friedberg, E.C., *DNA damage and repair.* Nature, 2003. **421**(6921): p. 436-40.
3. New, J.H., et al., *Rad52 protein stimulates DNA strand exchange by Rad51 and replication protein A.* Nature, 1998. **391**(6665): p. 407-10.
4. Shinohara, A. and T. Ogawa, *Stimulation by Rad52 of yeast Rad51-mediated recombination.* Nature, 1998. **391**(6665): p. 404-7.
5. Benson, F.E., P. Baumann, and S.C. West, *Synergistic actions of Rad51 and Rad52 in recombination and DNA repair.* Nature, 1998. **391**(6665): p. 401-4.
6. Sharan, S.K., et al., *Embryonic lethality and radiation hypersensitivity mediated by Rad51 in mice lacking Brca2.* Nature, 1997. **386**(6627): p. 804-10.
7. Tarsounas, M., D. Davies, and S.C. West, *BRCA2-dependent and independent formation of RAD51 nuclear foci.* Oncogene, 2003. **22**(8): p. 1115-23.
8. Powell, S.N., H. Willers, and F. Xia, *BRCA2 keeps Rad51 in line. High-fidelity homologous recombination prevents breast and ovarian cancer?* Mol Cell, 2002. **10**(6): p. 1262-3.
9. Davies, A.A., et al., *Role of BRCA2 in control of the RAD51 recombination and DNA repair protein.* Mol Cell, 2001. **7**(2): p. 273-82.
10. Osipovich, O., et al., *Defining functional domains of Ku80: DNA end binding and survival after radiation.* Biochem Biophys Res Commun, 1999. **261**(3): p. 802-7.
11. Osipovich, O., S.K. Durum, and K. Muegge, *Defining the minimal domain of Ku80 for interaction with Ku70.* J Biol Chem, 1997. **272**(43): p. 27259-65.
12. Omori, S., et al., *Suppression of a DNA double-strand break repair gene, Ku70, increases radio- and chemosensitivity in a human lung carcinoma cell line.* DNA Repair (Amst), 2002. **1**(4): p. 299-310.
13. Walker, J.R., R.A. Corpina, and J. Goldberg, *Structure of the Ku heterodimer bound to DNA and its implications for double-strand break repair.* Nature, 2001. **412**(6847): p. 607-14.
14. Vidal, M., et al., *Reverse two-hybrid and one-hybrid systems to detect dissociation of protein-protein and DNA-protein interactions.* Proc Natl Acad Sci U S A, 1996. **93**(19): p. 10315-20.
15. Pierce, A.J., et al., *XRCC3 promotes homology-directed repair of DNA damage in mammalian cells.* Genes Dev, 1999. **13**(20): p. 2633-8.
16. Ewing, T.J., et al., *DOCK 4.0: search strategies for automated molecular docking of flexible molecule databases.* J Comput Aided Mol Des, 2001. **15**(5): p. 411-28.
17. Brooijmans, N. and I.D. Kuntz, *Molecular Recognition and Docking Algorithms.* Annu Rev Biophys Biomol Struct, 2003.
18. Krumrine, J., et al., *Principles and methods of docking and ligand design.* Methods Biochem Anal, 2003. **44**: p. 443-76.