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Introduction:

To date, the m echanisms underlying de novo and acquired ER+/PR- breast cancer remain poorly defined (1). Thus, elucidation of the molecular basis of ER+/PR- breast tumor developm ent has the po tential to rev eal new therapeutic targets in the treatment, or even prevention, of the resist ance to anti-estrogen therapy in patients with breast cancer(2, 3). TIP30 is a human cellular 30kDa protein that was purified as a HIV-1 Tat interacting protein (4) and is e xpressed in various tissues in hum ans and mice(4, 5). Using genetically-engineered m ouse models generated in our laboratory, we have demonstrated that *Tip30* deletion results in developm ent of ducta 1 hyperplasia and tum ors in m ouse several ti ssues (6, 7). Recently, we made novel observations that *Tip30* deletion accelerates m ammary t umorigenesis induced by MMTV-Neu oncogene and m ammary tum ors consisting of ER-positive and PRnegative (ER+/PR-) lu minal epithelial cells. This project is to study the m olecular mechanism(s) underlying ER+/PR- breast tumorigenesis. Specifically, we will determine genetic and epigenetic a lterations in the initiation and progression of ER+/PR- mammary tumors aris ing in Ti p30-/-/MMTV-neu mice; and we will als o evaluate IGF-I and W isp-2 as potential therapeutic targets for ER+/PR- m ammary tumors developed in *Tip30-/-* MMTV-neu m ice. Results generated during the first year indicate that Tip30 loss accelerate s ER+/PR- mammary tumors in MMTV-Neu mice through EGF and IGF-1 mediated pathways.

Body:

Task 1. Determine specific genetic and epigenetic alterations in the initiation and progression of ER+/PR- mammary tumors arising in Tip30-/-/MMTV-neu and **Tip30+/-/MMTV-neu mice.** We have com pleted the proposed experim ents in Task 1; a and b, and m ost of experiments in Task1 d, which were proposed to com plete in the first y ear. W e have dem onstrated that Tip30 loss accelerated m ammary tumorigenesis in MMTV-Neu mice (unpubli shed data). In order to further characterize m ammary tum ors developed form these m ice, we have generated a cohort of MMTV-neu/ Tip30+/+, MMTV-neu/ Tip30+/- and MMTV-neu/ Tip30-/mice. We have been monitoring these mice for the development of mammary tumors and collected mammary tumors that developed in these mice for pathological analysis and further investigations. In order to determine expression pattern of ER α , PR-A and PR-B proteins in these m ammary tumors and their adjacen t m ammary tissues, the tumors were subjected to immunofl uorescence staining with an tibodies specific for ER, PR-A and PR-B. The tu mor cells in a ll se ven $Neu + /Tip30^{-/-}$ tumors examined were ER α positive and PR (PR-A and PR-B) ne gative (ER+/PR-) (table 1). The tumor cells from six of seven $Neu + /Tip30^{+/+}$ tumors examined were b oth ER α and PR negative (ER-/PR-) (Table 1). In additio n, we observed that the adjacen t mammary glands con tained ER-p ositive and PR-A-positive du ctal cells in both $Neu+/Tip30^{-/-}$ and $Neu+/Tip30^{+/+}$ tum ors while no PR-B-positiv e duc tal epithelial cells were detected. The antibodies for PR used in immunofl uorescence analysis are able to detect both PR-A and PR-B. This data suggests that $Neu + /Tip30^{-/-}$ female mice spontaneously develop ER+/PR- m ammary t umors and $Tip30^{-2}$ spontaneously develop ER+/PR+ or ER+/PR- m ammary tu mors. Moreover, som e of these tum or tissues were used for m aking RNA pr obes for m icroarray analysis and the establishment of tumor cell lines in Task1d and Task2.

Animal No.	Ν	Tip30	ER a	PgRA	PgRB
648	+	-/-	+	-	-
942	+	-/-	+	-	-
924	+	-/-	+	-	-
923	+	-/-	+	-	-
1281	+	-/-	+	-	-
1288	+	-/-	+	-	-
1278	+	-/-	+	-	-
634	+	+/-	-	-	-
736	+	+/-	+	-	-
743	+	+/-	-	-	-
747	+	+/-	+	-	-
906	+	+/-	+	-	-
933	+	+/-	-	-	-
951	+	+/-	+	-	-
961	+	+/-	-	-	-
1131	+	+/-	-	-	-
1764	+	+/-	-	-	-
733	+	+/+	-	-	-
762	+	+/+	+	-	-
1047	+	+/+	-	-	-
1760	+	+/+	-	-	-
2-8-08-1	+	+/+	-	-	-
2-8-08-2	+	+/+	-	-	-
2-8-08-3	+	+/+	-	-	-
2-8-08-4	+	+/+	-	-	-

Table 1. ER and PR (A,B) expressions in murine mammary tumor

To identify genetic alterations in regulatory pathways and gene expression that would explain the observed phenotypes, we perform ed an unbiased microarray analysis to identify the genes differentially expressed between $Neu+/Tip30^{-/-}$ and $Neu+/Tip30^{+/+}$ tumors using the GeneChip® Mouse Gene 1.0 ST Array (Affym etrix) that contains 28,863 mouse genes and offers whole-transcript coverage. We found that 538 genes were changed more than 2-fold, which include s 181 genes were upregulated and 357 genes were downregulated. T hese genes are involved in ion and protein transportation, cell adhesion, cell proliferation and apoptosis signaling pathway. Ingenuity pathway analysis of altered gene profiles revealed that the top cancer-associated pathways affected by Tip30 deletion in Neu+ mammary tumors are cAMP-mediated signaling, EGF signaling, IGF signaling and PI3K/AKT signaling and G-protein coupled receptor signaling. These results are consistent with our previous findings that Tip30 loss increases expression of two growth factors, IG F-1 and W sip2, in m ammary epithelial cells. In addition, these results also implicate that Ti p30 loss may accelerates an increased activation of Akt that is a common downstream target in these grow factor mediated signaling pathways.

Task 2. Evaluate IGF-I and Wisp-2 as potential therapeutic targets for ER+/PRmammary tumors developed in *Tip30-/-* MMTV-Neu mice. We have completed Task2 a and b and potions of Task2 c. Given our previous observation that expression of IGF-1 and W isp-2 was elevated in $Tip30^{-/-}$ mammary epithelial c ells (8), we exam ined IGF-1 and W isp-2 expression in the tum ors from $Neu+/Tip30^{-/-}$, $Neu+/Tip30^{+/-}$, and $Neu+/Tip30^{+/+}$ mice with IHC analy sis. Figure 1 s hows in a rep resentative comparison that the lev el of IGF-1 prote in in $Neu+/Tip30^{-/-}$ tum ors (scored as ++) appears to be higher than that in $Neu+/Tip30^{+/+}$ tumors (scored as +); IHC staining of IGF-1 and Wisp2 in the tumors are summarized in Table 2. We also used qRT-PCR to measure the mRNA levels of IG F-1 and W isp2 in four m ammary tum ors (data not shown). These results indicate that IGF-1 and Wisp2 expression are increased in $Neu+/Tip30^{-/-}$ tumors

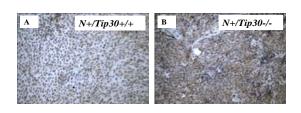


Fig.1. IGF-1 expression in mammary tumors. Paraffin sections of tumors from mice with the indicated genotypes were stained with anti-IGF-1. Brown stain indicates IGF-1 protein. Panel A: +; Panel B: ++.

Animal No.	Tip30	ERα	PR(A+B)	IGF-1	WISP-2
648	-/-	+	-	++	+
942	-/-	+	-	++	++
924	-/-	+	-	++	++
923	-/-	+	-	++	++
634	+/-	-	-	+	+
736	+/-	+	-	++	++
743	+/-	-	-	-	-
747	+/-	+	-	+	-
906	+/-	+	-	+	+
933	+/-	-	-	+	-
951	+/-	+	-	+	++
961	+/-	-	-	+	+
1131	+/-	-	-	+	+
1764	+/-	-	-	+	+
733	+/+	-	-	+	-
762	+/+	+	-	+	+
1047	+/+	-	-	-	+
1760	+/+	-	-	+	+

Table 2. Immunohistochemical analysis of IGF-1 and Wisp2

Key research Accomplishments:

- 1. Our data demonstrates that Tip30 loss accelerates ER +/PR- mammary tumors in MMTV-Neu mice.
- 2. Our data suggests that ER+/PR- mammary tumors arising in *Tip30*-null/MMTV- neu mice exhibit increased activation of EGF and IGF-1 pathways.

Reportable outcomes:

1. Part of this work was presented as a short talk at "Midwest Breas t Cancer Research Symposium" held at the University of Iowa from July 17 - 19, 2009.

2. Chengliang Zhang, Isam u Hoshino, Mikito Mori, Jill Pecha and Hua Xiao., The mechanism and role of TIP30 in m ammary tum origenesis. Midwest Breast Cancer Research Symposium. 2009. Abstract 32; pg 43.

3. A NIH RO1 grant application entitled "the role of a tumor suppressor in mammary tumorigenesis" is submitted partly based on work supported by this award

Conclusions: Our data suggest that Tip30 loss accel erates ER+/PR- mammary tumors in MMTV-Neu mice through EGF and IGF-1 mediated pathways.

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