



October 6-9, 2016 The Confidante Miami Beach, Florida

FUNCTIONAL EVALUATION OF A

CENSORED

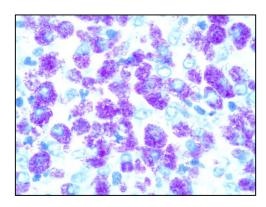
IN A

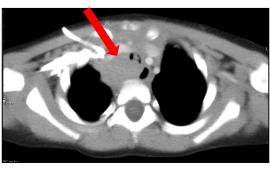
PATIENT WITH INCREASED SUSCEPTIBILITY TO VIRAL AND MYCOBACTERIAL INFECTIONS, AND DELAYED ABNORMAL DENTITION

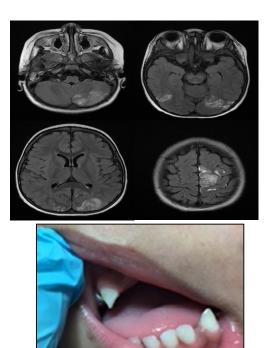
> **Cecilia Korol** National Institutes of Health Clinical Center Department of Laboratory Medicine

Patient

- Male
- African American
- Born to non-consanguineous parents



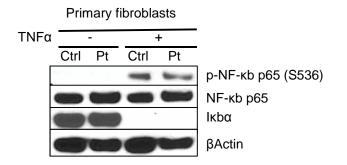




- > Infections:
 - Disseminated varicella post-VZV vaccination (17m).
 - Anterior mediastinal mass eroding the trachea. Positive for Mycobacterium avium complex (MAC).
 - CMV, HHV-6, adenovirus and enterovirus viremia.
 - Acute onset hyponatremia, seizures, and left hemiparesis. EBV DNA was found on CSF.
- Normal routine laboratories tests. Including lymphocyte phenotype/proliferation (PHA), Igs levels, protective titers to tetanus and diphtheria toxoids, 9/13 S. pneumoniae serotypes, DHR and NK cytotoxicity.
- Un-related matched cord blood transplantation (RIC 5/6) with complete engraftment (at 2y, now 1y3+ post-HSCT).
- > Post-transplantation has shown irregular dentition (e.g. conical teeth) with delayed eruption.

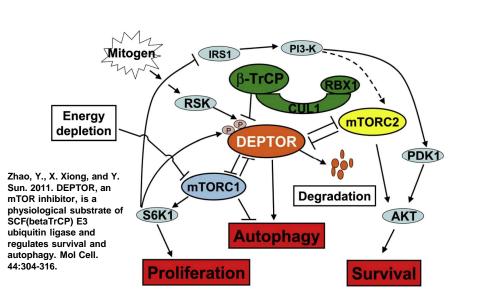
Congrats on the ones suspecting the NEMO pathway!!!!

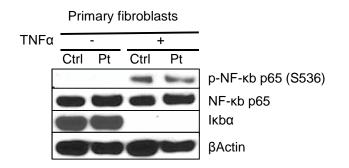
- But you were wrong: Sequencing for all known primary IDPs was normal and functional test of the pathway on patient fibroblasts gave a comparable to normal response.
- So we did whole exome sequencing searching for a possible new gene causing disease.



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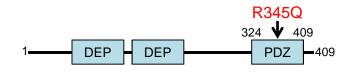
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DEP domain containing mTORinteracting protein

Predicted to be **damaging**; CADD C-score = 36 (Rockefeller Mutation Significance Cutoff MSC>11)

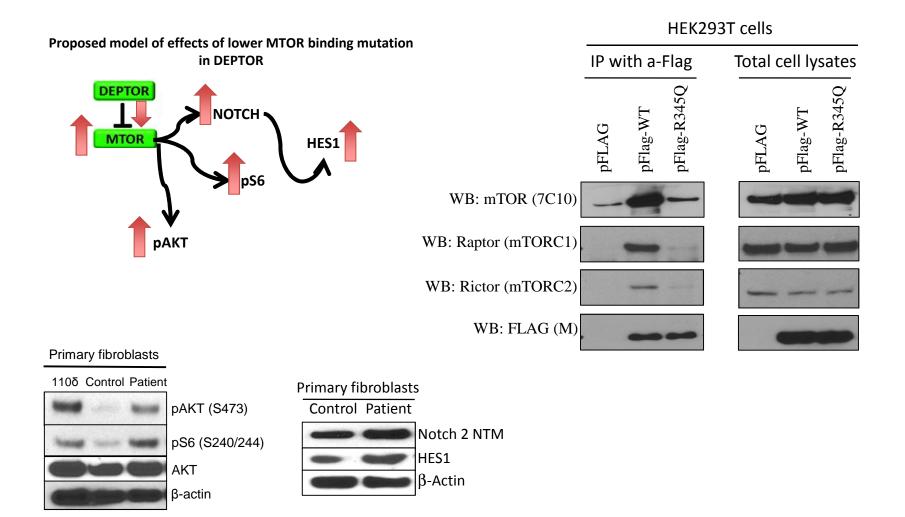


Missense mutation in the PDZ domain of DEPTOR that may affect interaction with mTOR FRAP-ATM-TRAP (FAT) domain

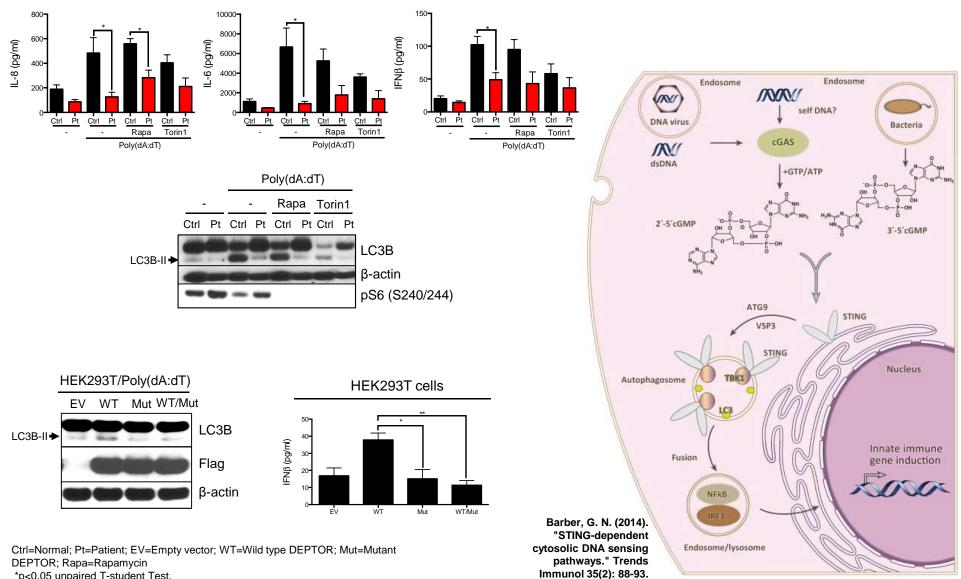
• Arg (positively charged, basic) > Gln (polar uncharged)

>Very high nucleotide position conservation scores.

Enhance mTOR signaling on patient cells/lower binding of mTORC1/2 of the mutant DEPTOR allele.



Impaired response to cytosolic DNA sensing in patient cells. Independent of mTOR signaling.



*p<0.05 unpaired T-student Test.

Summary

- > Patient with complicated infections to multiple viruses and M. avium. Post BMT he developed irregular dentition.
- > WES revealed an heterozygous mutation in DEPTOR predicted to be damaging in the MTOR binding domain.
- Both his PBMCs and primary fibroblasts revealed hyperactive MTOR, with also enhanced NOTCH2 signaling resembling NOTCH2 g-o-f patients. On transfected HEK293T cells, lower binding of the mutant DEPTOR allele to MTORC1/2 was observed.
- Patient fibroblasts were not able to mount a response comparable to controls with cytosolic DNA stimulation either by autophagy or cytokine production. This impaired response was MTOR independent. This was recapitulated on HEK293T cells transfected with mutant or WT/Mutant Deptor producing less IFNβ or LC3B-II than the cells transfected with the WT allele.
- We conclude that although further experiments are required given the nature of single patient studies, the susceptibility to infections and the abnormal dentition of the patient can be explained by a dominant negative effect on DEPTOR function by his mutation.

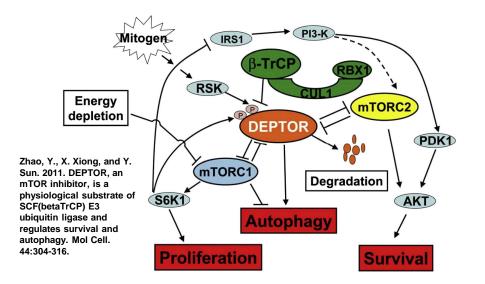
Acknowledgments

- ♦ NIH/Clinical Center:
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 - Dr. Adrian Zelazny
 - Dr. Fleisher Thomas
 - Dr. Sergio Rosenzweig

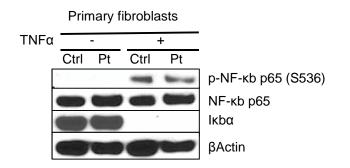
- ♦ Other centers:
 - Hana Niebur-University of Nebraska/Department of Pediatrics Division of Allergy and Immunology
 - Aleksandra Petrovic-All Children's Hospital Blood and Marrow Disorders
 - Jennifer W. Leiding-University of South Florida/Department of Pediatrics/Division of Allergy and Immunology

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DEP domain containing mTORinteracting protein

> NM_022783 c.1034G>A, p.R345Q heterozygous rare SNP MAF A=0.000615 (6/10000) Predicted to be **damaging** by SIFT, PP2, LRT, Mutation Taster

>Missense mutation in the PDZ domain of DEPTOR that may affect interaction with mTOR FRAP-ATM-TRAP (FAT) domain

- Biochemically non-conservative aminoacid substitution
 - Arg (positively charged, basic) > Gln (polar uncharged)

CADD C-score = 36 (Rockefeller Mutation Significance Cutoff MSC>11)

≻Very high nucleotide position conservation scores (GERP=5.83, PhyloP=2.77, SiPhy=20.1338)

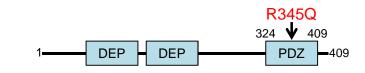
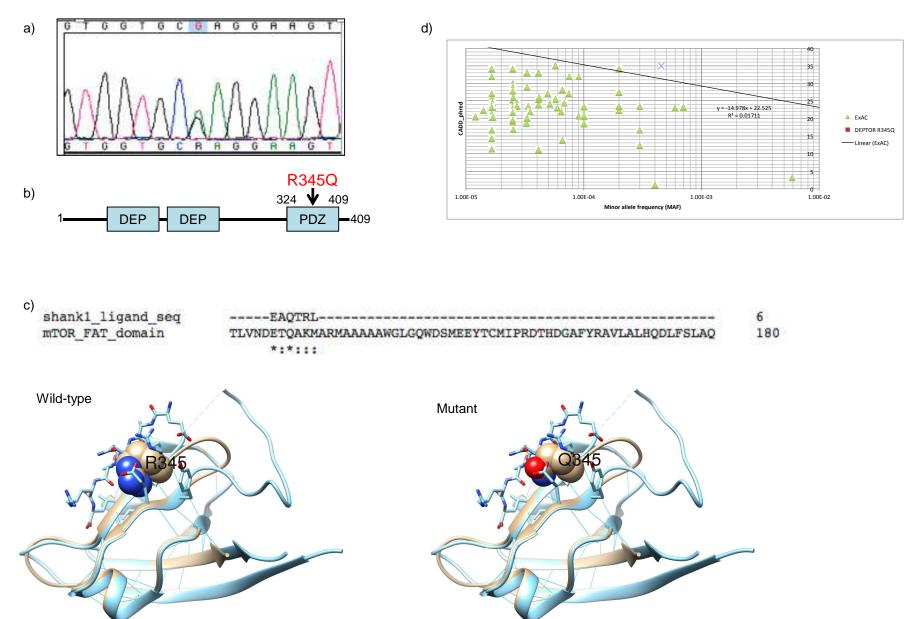


Figure 2



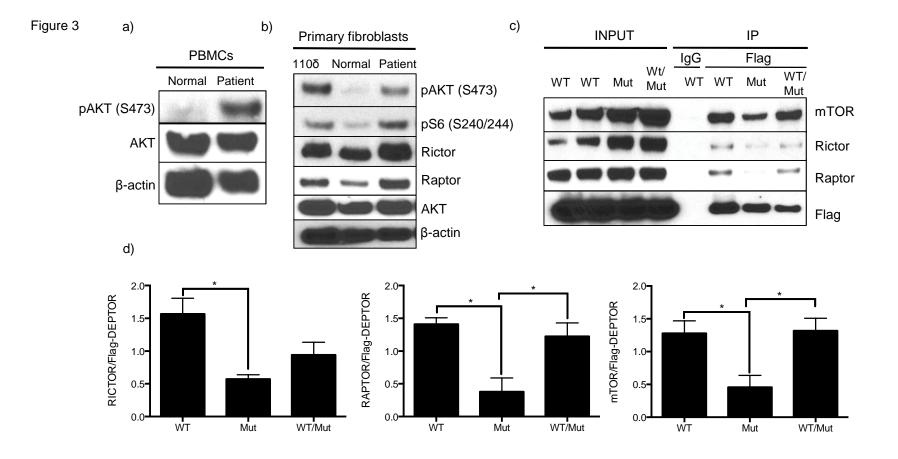
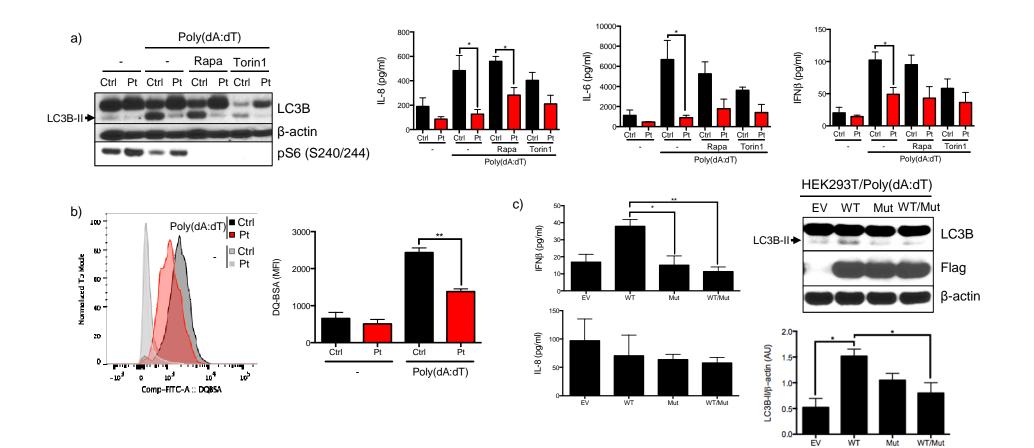
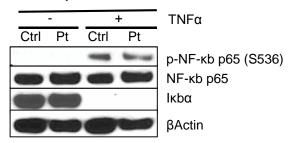


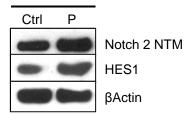
Figure 4



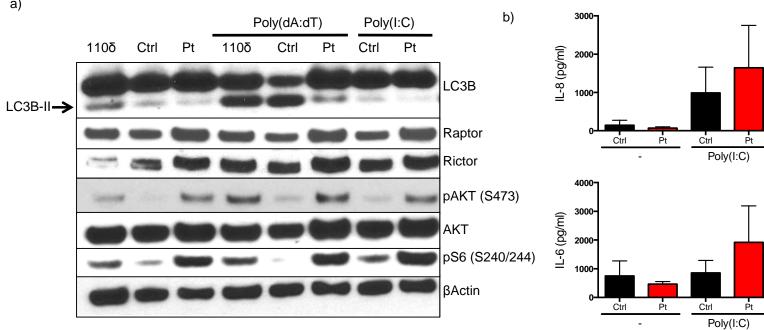
a) Primary fibroblasts



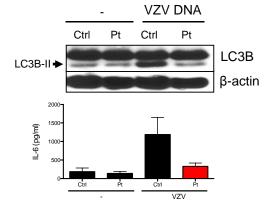
Primary fibroblasts

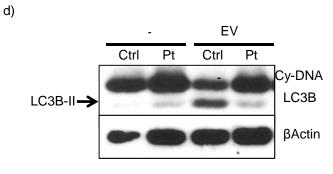


Supplemental figure



c)





a)