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Circulating levels of Resokine, a soluble modulator of the immune system, are upregulated in both experimental cancer models and in patients across multiple tumor types

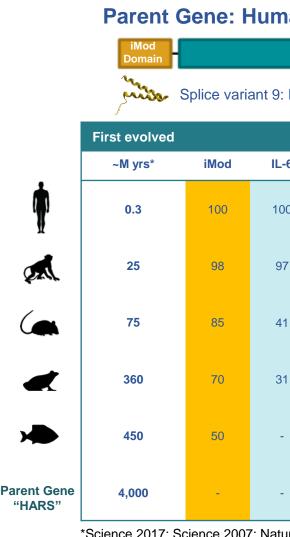
Ryan Adams, Elisabeth Mertsching, Leslie Nangle, Kathy Ogilvie, Steven Crampton, John Bruner, Samantha Tyler, Sanna Rosengren, Andrea Cubitt, David King, John Mendlein

aTyr Pharma, San Diego, CA

Abstract

The Resokine family of proteins are derived from the histidyl tRNA synthetase gene (HARS) via proteolysis or alternative splicing and appear to be important as extracellular modulators of cellular activity. Resokine is a newly identified regulator of immune cell activity, and circulating levels of Resokine in normal individuals may represent a soluble set-point control to modulate T cell activity. Resokine activity is a non-canonical function arising from the tRNA synthetase gene family, and the activity is effected by a 60 amino acid N-terminal domain arising from the gene for histidyl-tRNA synthetase. This domain is present in the full-length protein as well as multiple splice variants that have lost their original tRNA synthetase functionality. Resokine is secreted from cells, including tumor cell lines, and *in vitro* studies have demonstrated that Resokine can inhibit the activation of immune cells. *In vitro*, for example, Resokine addition during T cell activation induced by antibodies to CD3 and CD28, can result in reduced levels of inflammatory cytokines, such as IL-2, interferon gamma, and TNF alpha; inhibition of the up-regulation of cell-surface activation markers, such as CD69, CD40L, and 4-1BB; and inhibition of release of the cytotoxic mediator granzyme B. We have tested levels of circulating Resokine in both mice with syngeneic tumors as well as >300 cancer patients across multiple tumor types. In normal C57BL/6 mice serum levels of Resokine ranged from 70-250pM (n=10) whereas in mice bearing B16F10 tumors, levels were significantly higher (450-3000pM, p<0.001) and correlated with tumor size. Resokine levels in normal human volunteers exhibit a more variable range, from 8pM to >2333pM (n=148), with 18% of individuals having levels <30pM, which was set as the active threshold level based on the concentration required to inhibit T cell activation *in vitro*. In contrast, samples across >300 cancer patients with different tumor types exhibited higher circulating levels with only 4% of individuals having levels below the activity threshold of 30pM. This data is consistent with the hypothesis that tumors secrete Resokine as an additional mechanism to down-regulate immune activity, and suggests further investigation of the utility of Resokine levels as a new biomarker of immune activity in patients.

iMod Domain: Conservation Among Orthologs



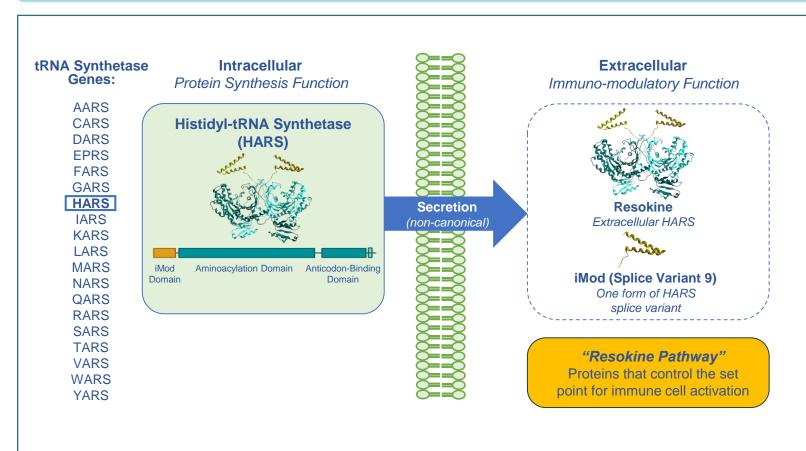
Comparison of sequence alignments between iMod domains in multiple species has shown a high level of evolutionary conservation spanning many millions of years. This type of species conservation is similar or greater to that observed with notable cytokines, growth factors, and checkpoint modulators.

Resokine Absent PI3K PIK3IP AKT DACT1 TRIM2 Th1/Tc1 Larger circles represent higher expression level

Cartoon compiled from RNAseq, flow cytometry, and ELISA data (publication submitted)

treated with picomolar amounts of Resokine.

Resokine: Extracellular Proteins Derived From HARS Gene

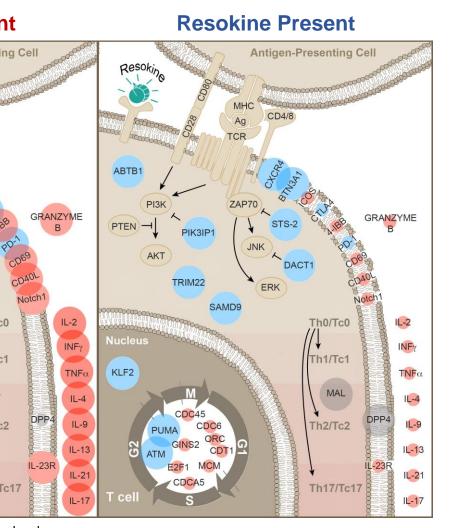


Resokine (the extracellular proteins derived from the HARS gene) is secreted from cells via a non-canonical pathway and circulates naturally in all individuals tested. The N-terminal "iMod" domain consists of amino acids 2-60 from HARS and has structural similarity to 4 alpha–helical bundle cytokines.

Parent Gene: Human HARS (Histidyl-tRNA Synthetase) Catalytic Domain Splice variant 9: Resokine iMod (immuno-modulatory) domain Percent identity to human protein IL-12 IL-13 TGF-β PD-1 CTLA-4

*Science 2017; Science 2007; Nature 2002; Nature 2010; Genome Research 2000

Resokine Sets Level for T Cell Activation at pM Concentrations



• The presence of Resokine attenuates the activation of T cells stimulated with antibodies against CD3/CD28. Analysis of gene expression profiles from stimulated T cells revealed lowered levels of many immune activation markers of inflammation when

Cancer Models

