

Differential Proteomic Analysis of the Reactivated p53 via Nutlin-3A, in 3 Different Types of Human Lymphomas



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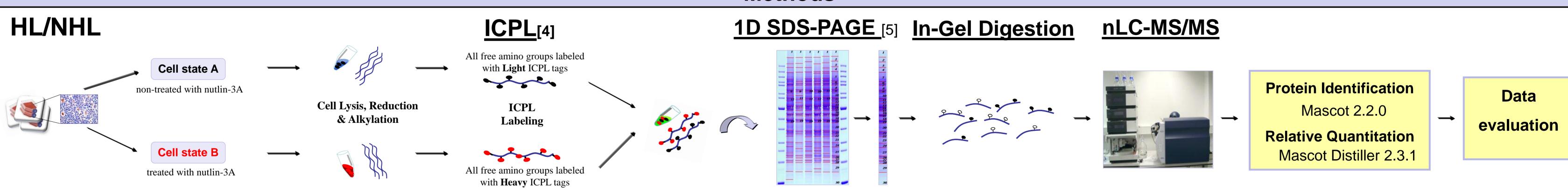
Overview

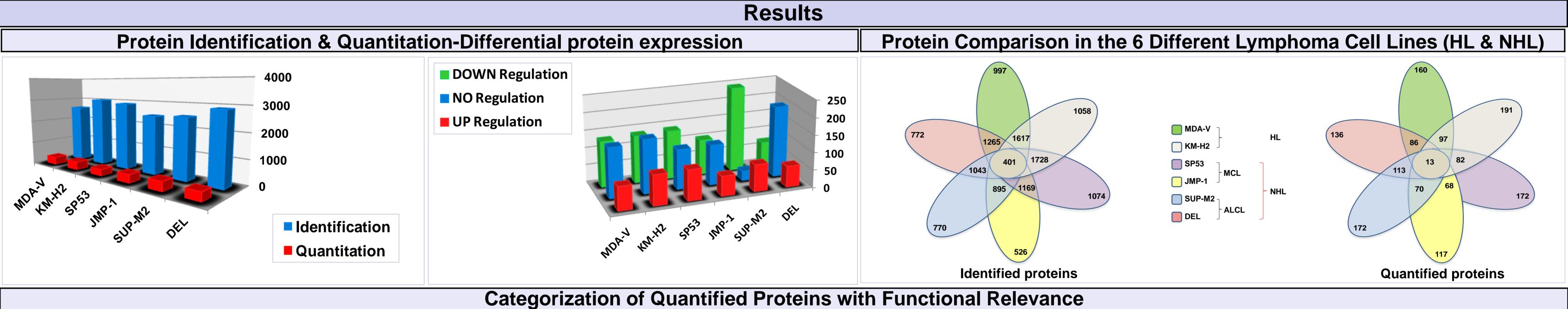
- > Purpose: The identification and quantification of protein expression levels of nutlin-3A-induced p53 stabilization and activation in human lymphoma.
- > Methods: The Isotope Coded Protein Label (ICPL) technique was followed by nano-Liquid Chromatography coupled on-line with Mass Spectrometry (nLC-MS/MS).
- > Results: Reliable identification & differential quantitative determination of human lymphoma proteome profile, revealing alterations in the HSPs relative expression levels.

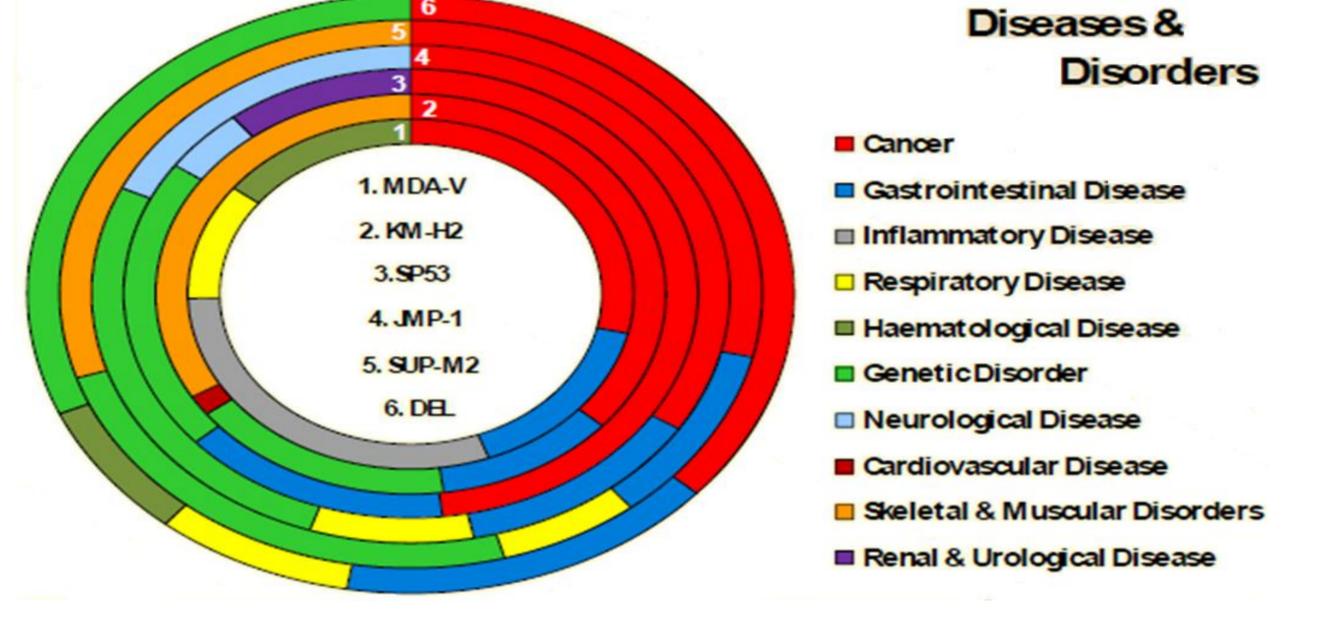
Introduction

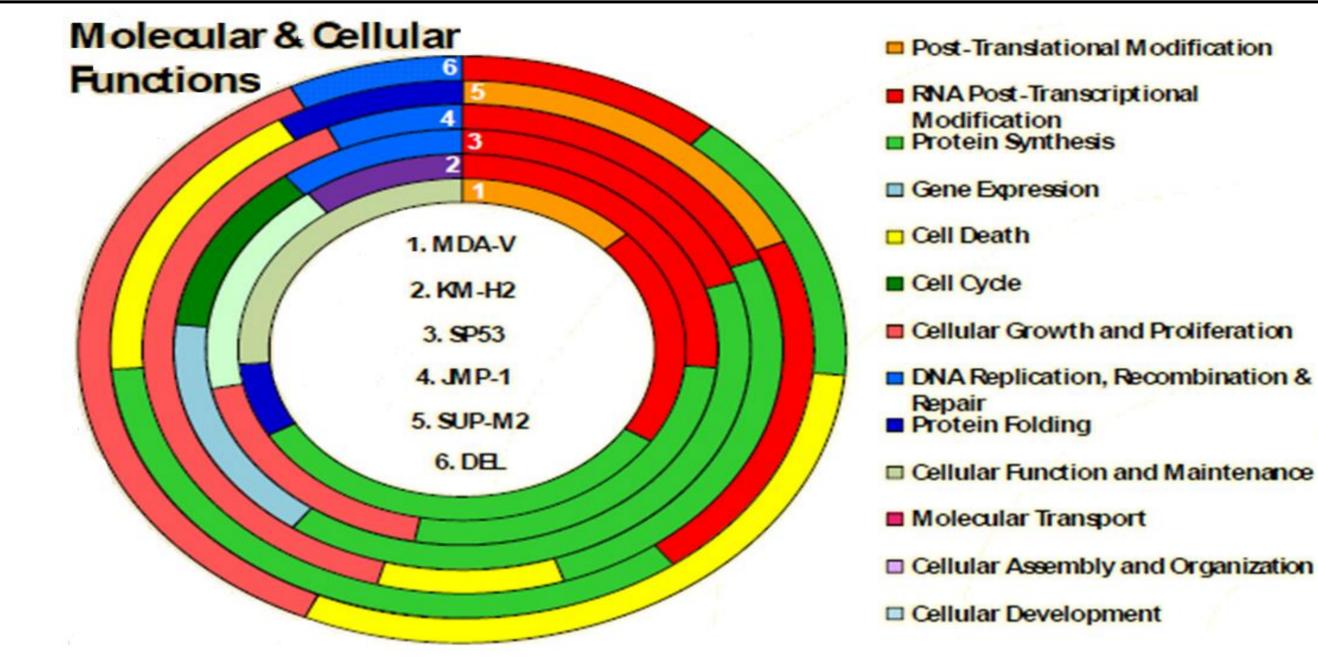
- > p53, a master tumor suppressor gene is impaired in >50% of all human cancers [1]. However, >80% of haematological malignancies including Hodgkin's (HL) and Non-Hodgkin's lymphomas (NHL).
- > MDM2 (HDM2 in humans) binds to wt p53 and negatively modulates its transcriptional activity and stability [2].
- ➤ Nutlin-3A, an MDM2-antagonist, induces stabilization and reactivation of the wt p53 pathway in cancer cells, followed by the infliction of cell cycle arrest and apoptosis [3].
 - > Scope of the study is the mode of action of nutlin-3A-mediated wt p53 stabilization and reactivation, in human cell lines of HL (2) and NHL, Anaplastic Large Cell Lymphoma (ALCL, 2) and Mantle Cell Lymphoma (MCL, 2).

Methods

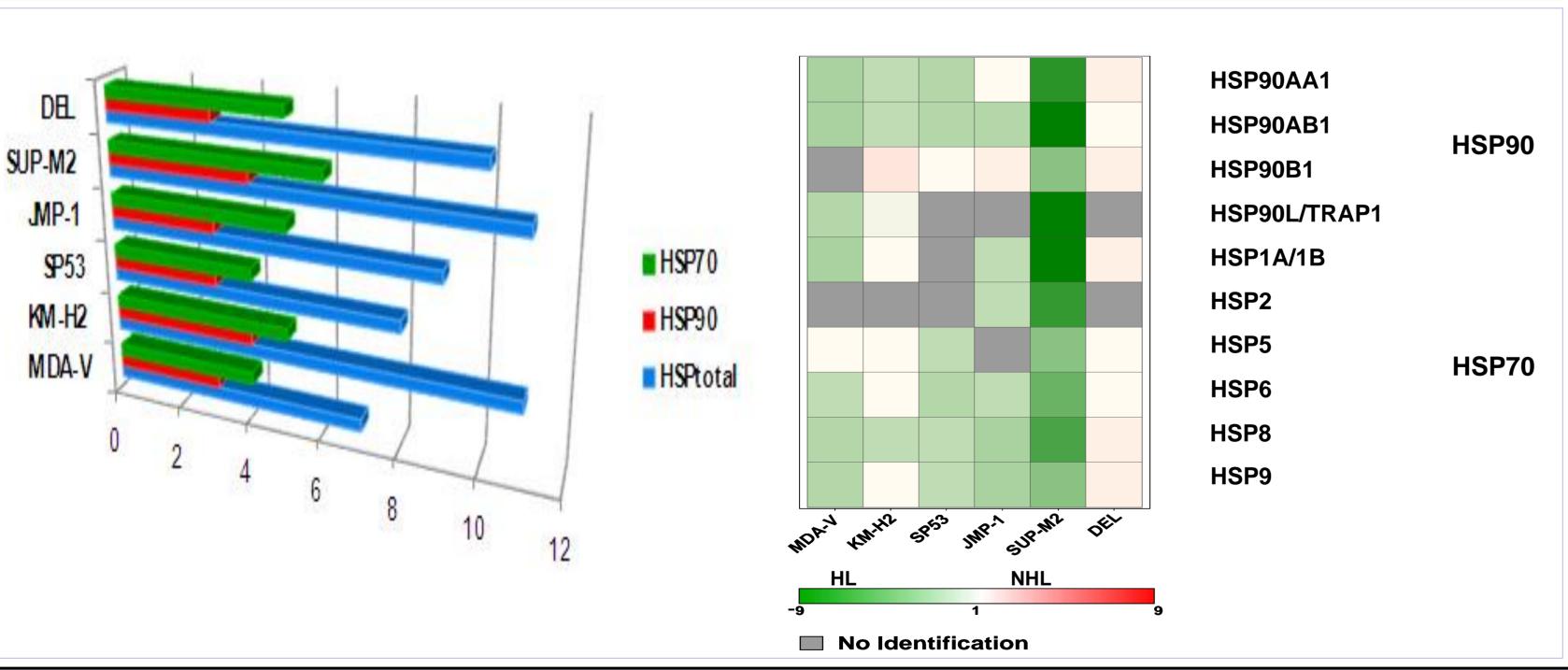








HSP90 & HSP70 Identification & Relative Expression Levels



12 10 ■ MDA-V FOLD CHANGE □KM-H2 □ SP53 JMP-1 ■SUP-M2 DEL -6 -10 -12

Distribution of HSP90 & HSP70 Regulation

Conclusions – Future Plans

- > ICPL approach coupled with 1D-SDS-PAGE & nLC-MS/MS was applied for a large-scale proteomics analysis of 3 types of human lymphoma, providing successful identification & relative quantitation of differentially expressed proteins.
- > Our findings provide important advances in understanding the biology of nutlin-3A treatment in wt p53 lymphoma cells, demonstrating substantial decrease in HSPs levels.
- > This study stresses out the biological similarities as well as differences between HL, MCL & ALCL. Further data processing will uncover far more comprehensive & thorough information on the participating pathways in haematological malignancies.
- > Validation studies using genetic approaches are being performed, confirming a selection of abundantly expressed proteins of interest.

References

- 1. Hollstein et al. Science 1991;253:49–53.
- 2. Moll UM et al. Mol Cancer Res. 2003;1: 1001-1008

2. ProFI lab & Prof. Anastassios Economou, Institute of Moleculal Biology &

- 3. Vassilev et al. Science. 2004;303: 844-848.
- 4. Schmidt A et al. A novel strategy for quantitative proteomics using isotope-coded protein labels. Proteomics 2005, 5:4-15
- 5. Shevchenko et al. (1996) Mass spectrometric sequencing of proteins from silver stained polyacrylamide gels. Anal. Chem. 68, 850-858.

Acknowledgements

1. Prof. Dieter Oesterhelt, Dr. Frank Siedler, Dr Matthias Schlesner, Max-Planck-Institute of Biochemistry, Department of Membrane Biochemistry, Martinsried, Germany

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