Session I: Incidence and Predispositions to WM

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Risk of lymphoproliferative disorders among first-degree relatives of lymphoplasmacytic lymphoma/Waldenström's macroglobulinemia patients: A population-based study in Sweden. Sigurdur Y Kristinsson[1], Magnus Björkholm[1], Lynn R Goldin[2], Mary L McMaster[2], Ingemar Turesson[3], and Ola Landgren[1,2] [1]Department of Medicine, Division of Hematology, Karolinska University Hospital Solna and Karolinska Institutet, Stockholm, Sweden; [2]National Cancer Institute, NIH, Bethesda, Maryland, USA; [3]Department of Medicine, Section of Hematology, Malmö University Hospital, Malmö, SWEDEN.

Background. A role for genetic factors in the etiology of lymphoplasmacytic lymphoma/ Waldenström's macroglobulinemia (LPL/WM) **is i**mplicated based on prior findings from multiply affected families and small case-control and cohort studies. Methods. We identified 2,144 LPL/WM patients (1,539 WM [72%] and 605 LPL [28%]) diagnosed in Sweden, 8,279 population-based matched controls, and linkable first-degree relatives of patients (n=6,177) and controls (n=24,609). Using a marginal survival model, we calculated relative risks and 95% confidence intervals as measures of familial aggregation. Results. We found first-degree relatives of LPL/WM patients to have a 20-fold (4.1-98.4), 3.0-fold (2.0-4.4), 3.4-fold (1.7-6.6), and 5.0-fold (1.3-18.9) increased risk of developing LPL/WM, non-Hodgkin lymphoma (NHL), chronic lymphocytic leukemia (CLL), and monoclonal gammopathy of undetermined significance (MGUS), respectively. However, there was no evidence of an increased risk of developing multiple myeloma or Hodgkin lymphoma. In analyses stratified by type of first-degree relative (parent, sibling, offspring), age at diagnosis of the probands (above/below 70 years), and sex of the first-degree relative, we did not observe the risk-estimates to be significantly different compared to the overall analyses. Conclusions. Our findings of highly increased risks of developing LPL/WM, NHL, CLL, and MGUS support the operation of shared susceptibility genes that predispose to LPL/WM and other lymphoproliferative disorders.