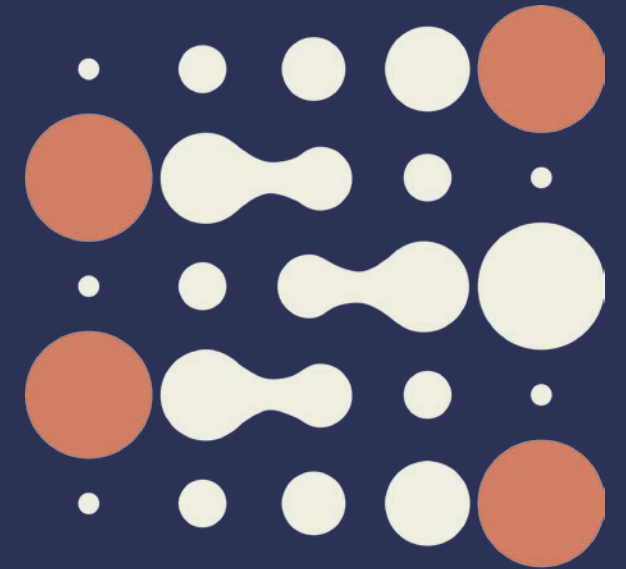


Genetic variation in SP140 in lymphomas: Results from InterLymph

Hanla Park¹ on behalf of InterLymph

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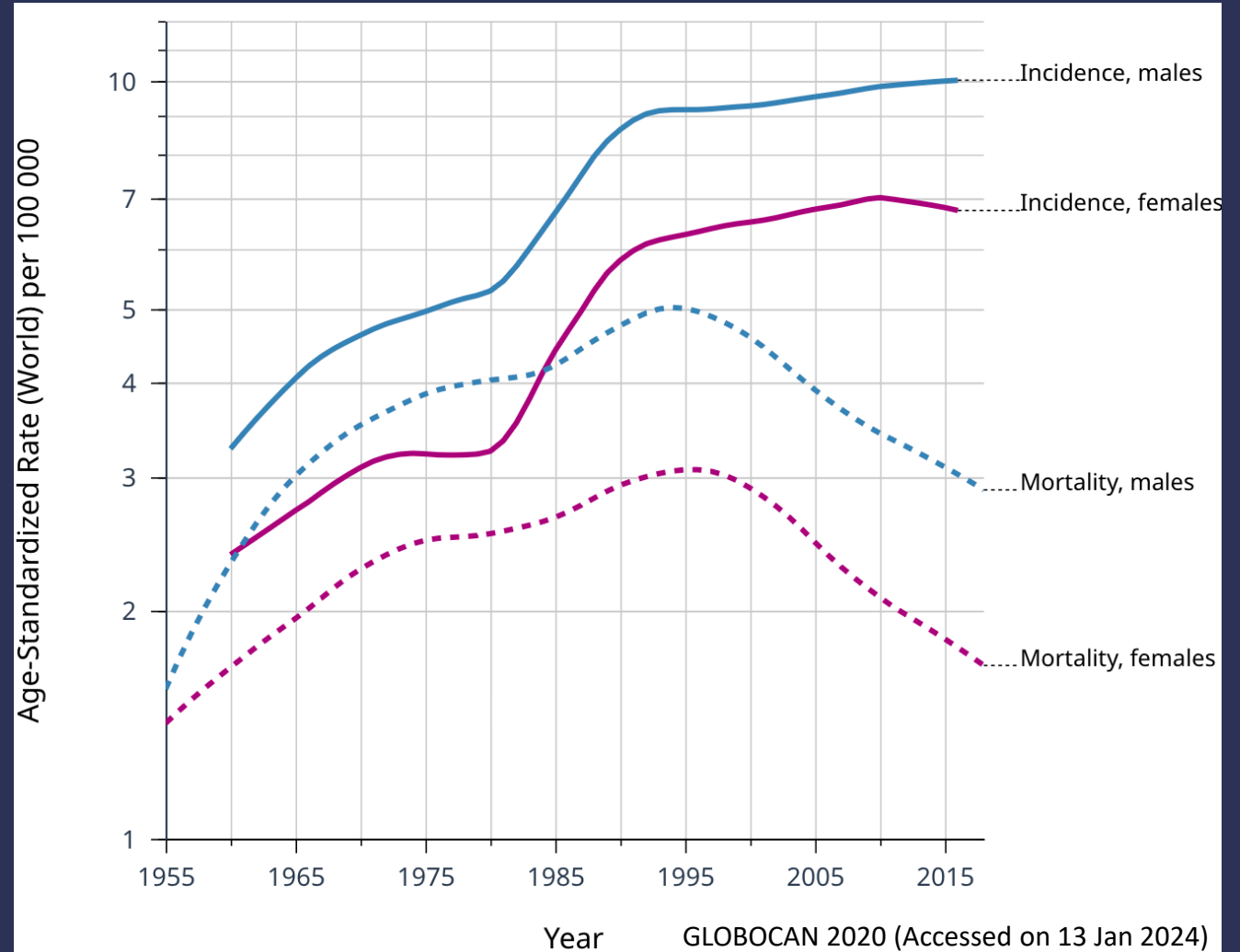
International Agency
for Research on Cancer



Lymphoma

Non-Hodgkin's lymphoma (NHL), Hodgkin's lymphoma (HL), multiple myeloma (MM)

- NHL: 10th most common cancer in North America and Europe
- Clinically heterogeneous between subtypes

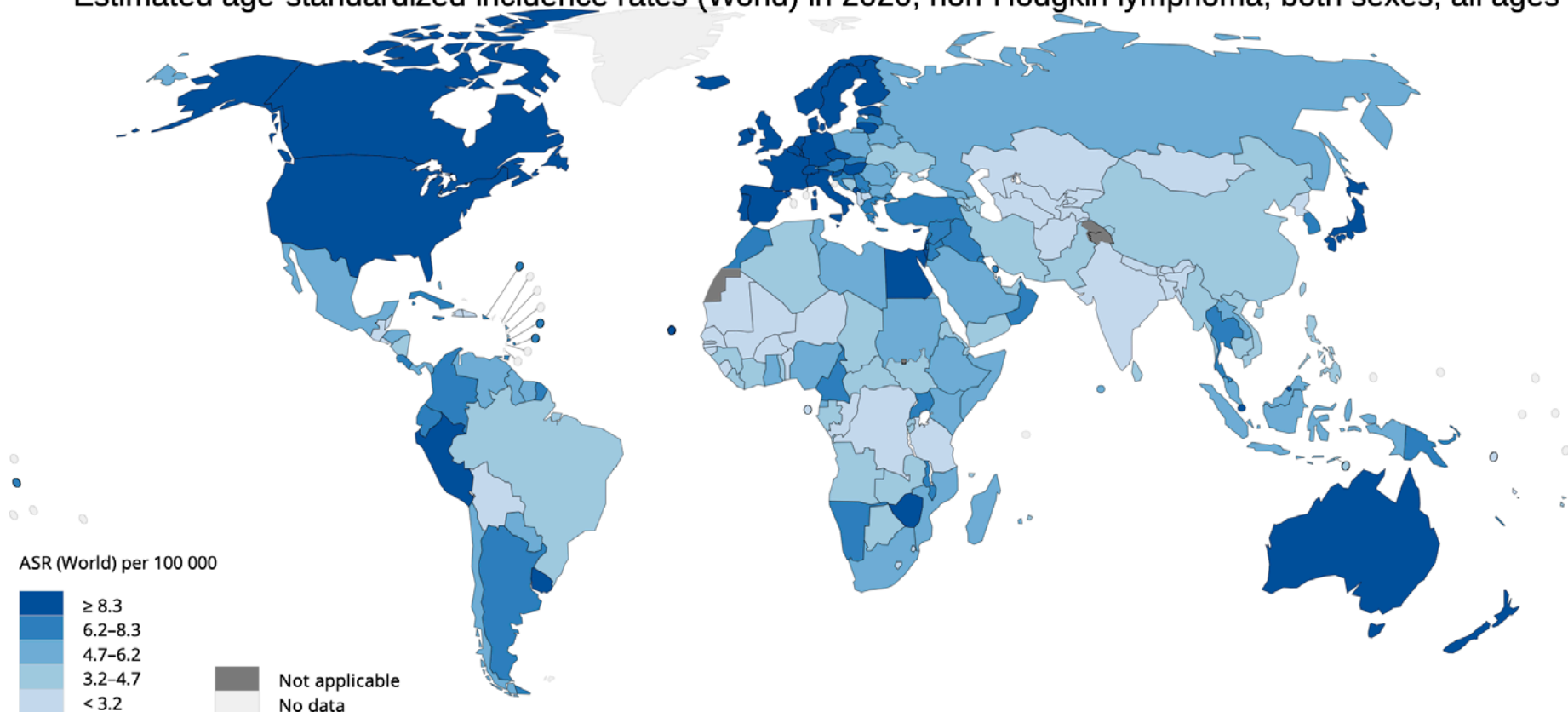


Age-standardized rate (World) per 100 000, incidence and mortality
Non-Hodgkin lymphoma in Sweden

Lymphoma

Non-Hodgkin's lymphoma (NHL), Hodgkin's lymphoma (HL), multiple myeloma (MM)

Estimated age-standardized incidence rates (World) in 2020, non-Hodgkin lymphoma, both sexes, all ages



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Data source: GLOBOCAN 2020
Map production: IARC
(<http://gco.iarc.fr/today>)
World Health Organization



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GLOBOCAN 2020 (Accessed on 13 Jan 2024)

(Aim) To better understand the environmental and genetic exposures related to lymphoma



27 different studies



60,000 lymphoma patients
137,000 controls



125 harmonized
variables

Currently, conducting the world's largest genetic studies to understand the etiology of lymphomas

IARC's role in InterLymph

- IARC acts as data coordinating center for InterLymph



James McKay (IARC)



Henrik Hjalgrim (DCSRC)



Karl Smith-Byrne (Oxford)



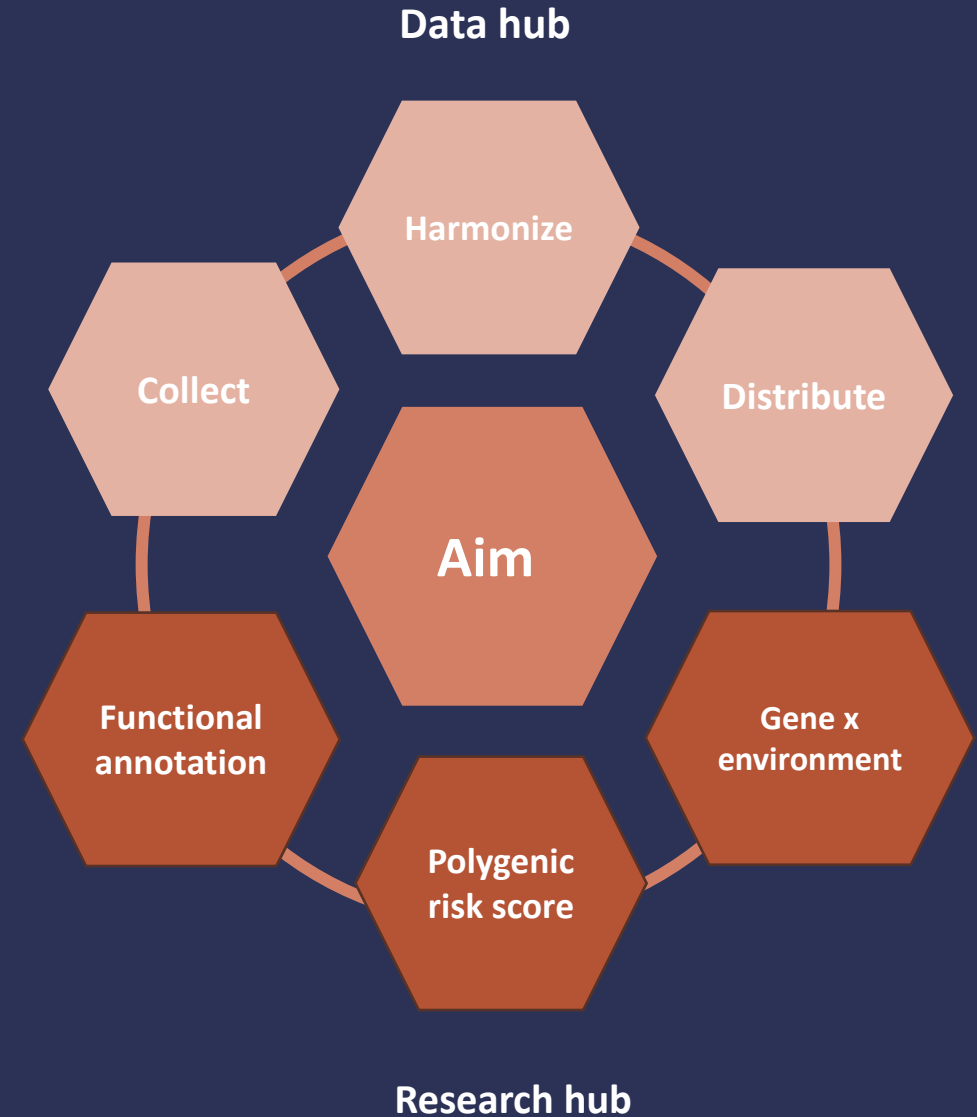
Vijai Joseph (MSKCC)



Alyssa Clay Gilmour (USC)



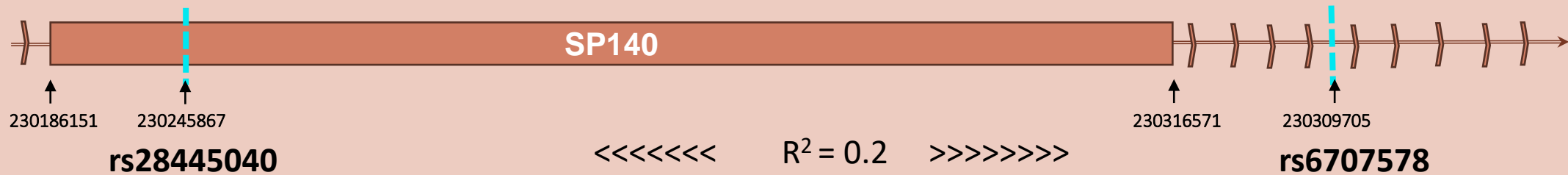
Sophia Wang (City of Hope)



InterLymph results shed light on NHL genetic loci

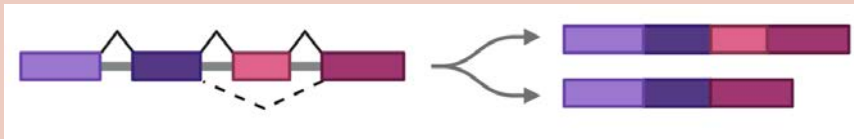
One susceptibility locus on chromosome 2 was identified in two different NHL subtypes

Genomic annotation work



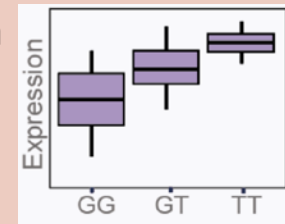
Waldenstrom macroglobulinemia (WM)

Relative abundance of SP140 alternative splicing forms



Mantle cell lymphoma (MCL)

Overall expression of SP140



- Within the *same* genetic locus, *different* genetic variants have *different* functional consequences, influence *different* lymphoma subtypes

Conclusions and take-home messages

- ❖ The InterLymph consortium is at the forefront of genetic and epidemiological research in lymphoma
- ❖ The largest GWAS of lymphomas identified over 30 novel genetic loci
- ❖ Functional annotation provides insights for disease etiology
- ❖ Next steps:
 - ✓ Ongoing GWAS on other subtypes
 - ✓ Other analyses: polygenic risk scores, gene-environment interactions

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Data coordinating center group

Waldenstrom macroglobulinemia working group

Mantle cell lymphoma working group



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