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9th SA
TB
Conference
8 - 11 June 2026



TB Incidence Among Household Contacts

Of individuals with **symptomatic** and **asymptomatic** TB:
A historical cohort study in the **Western Cape**

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Background & aim

Tuberculosis in South Africa

- >50% of bacteriologically confirmed TB in the 2017–18 SA national prevalence survey reported no symptoms
- Symptom-based case finding misses this reservoir entirely

The Evidence Gap

- Long-term, individual-level data on TB risk in high-burden communities are limited
- Most studies rely on cross-sectional designs

ZAMSTAR

- 2010 population-based TB prevalence survey in 8 Western Cape communities
- Collected sputum culture results, symptom status, HIV status & household data
- 30,017 adults enrolled

WC PHDC

- Integrates laboratory, pharmacy & clinical records from 1994: enables individual-level follow-up without a prospective design

Linked individuals from the ZAMSTAR survey to PHDC records up to 2020: 11 years

Objectives



1

Estimate TB incidence: over 11 years (2010–2020) among ZAMSTAR participants without prevalent TB at baseline

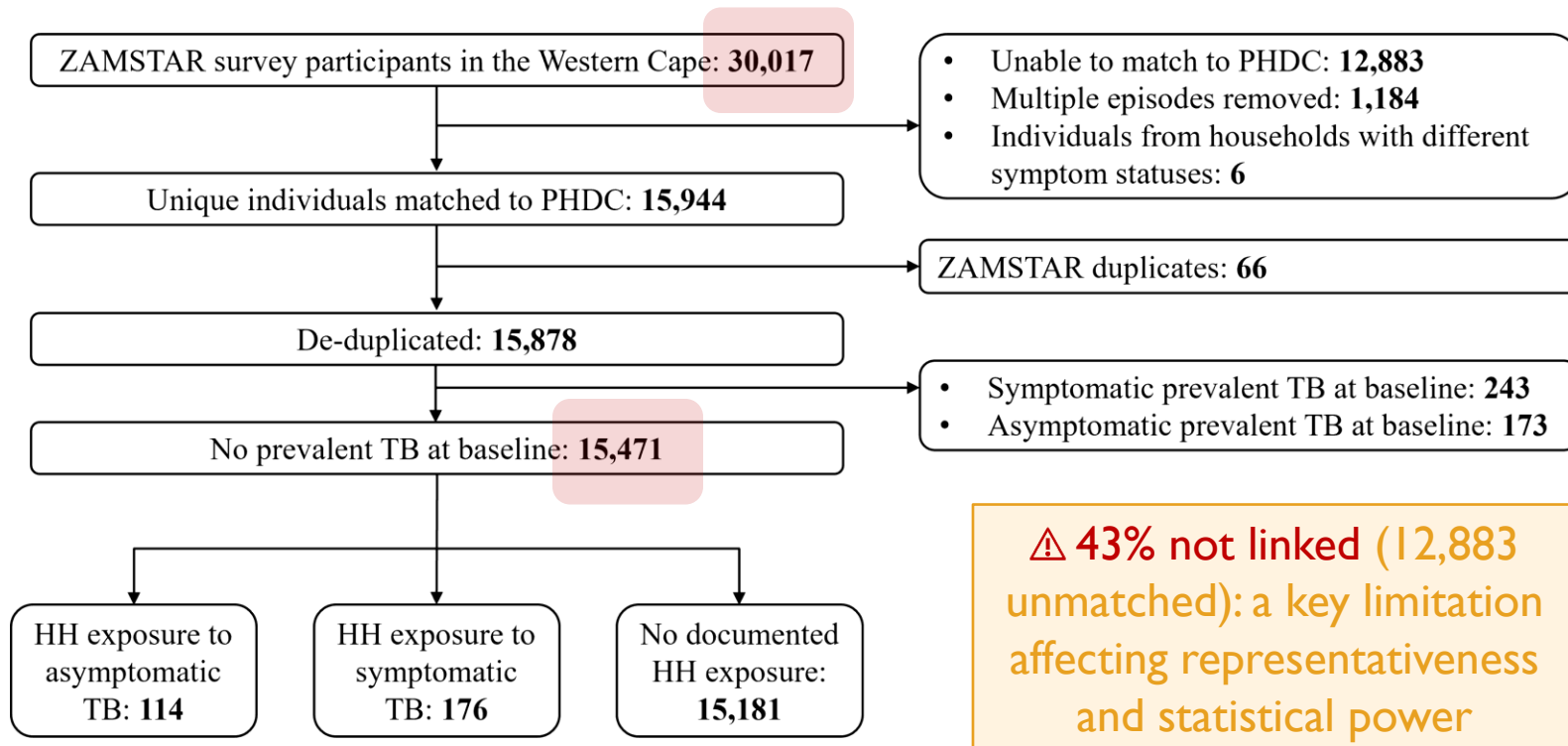
2

Assess TB risk by household exposure type and other risk factors: unexposed vs. symptomatic vs. asymptomatic index cases using Cox proportional hazards models

3

Evaluate the feasibility & limitations: of long-term follow-up via routine data linkage in a high-burden setting

Methods & cohort division



Results: Cohort Profile, Linkage & TB Incidence

30,017

Enrolled in
ZAMSTAR 2010

52.9%

Successfully
linked to PHDC

15,471

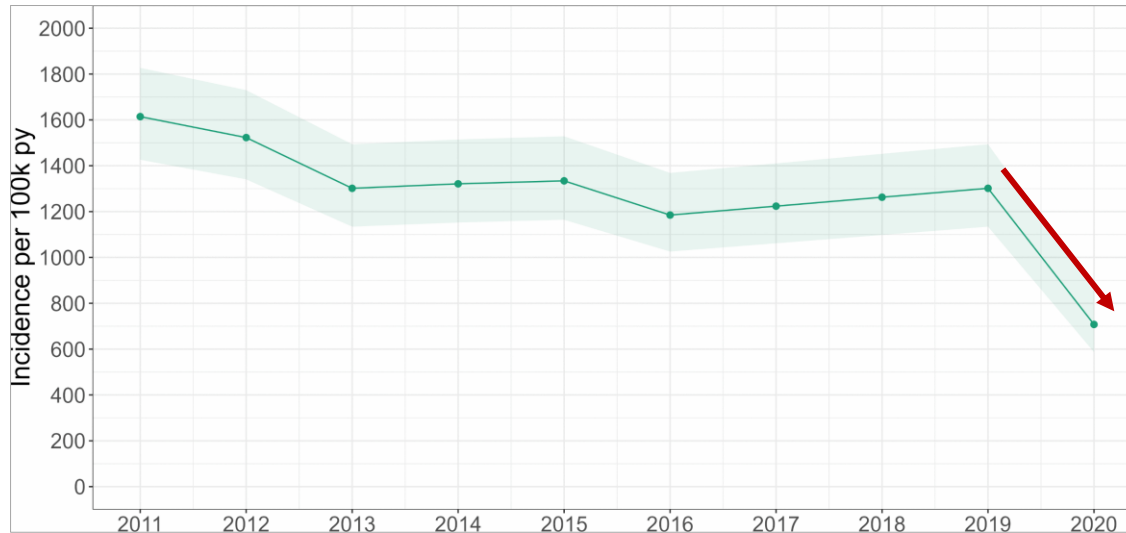
Without prevalent
TB at baseline

11.8%

Developed
incident TB

1,230

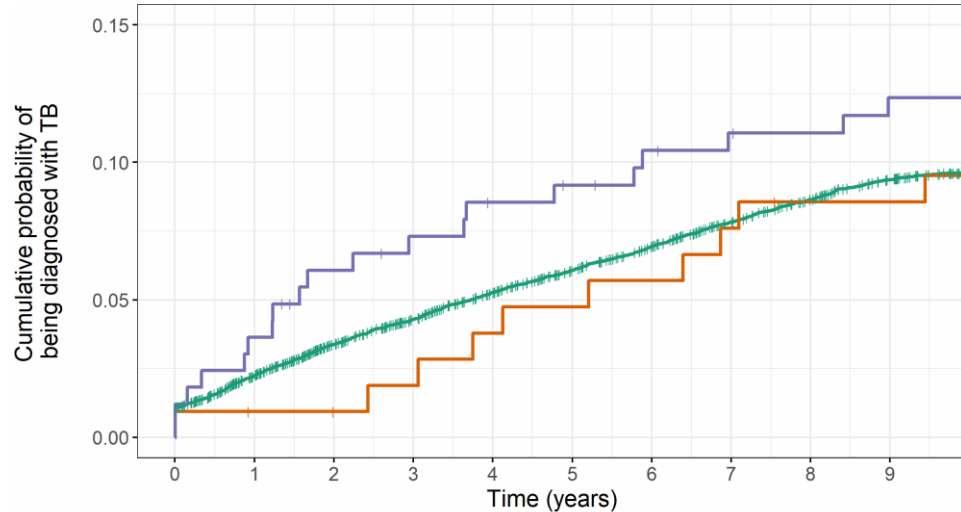
per 100k person-years
overall incidence



Results: TB Risk by Household Exposure

Strongest Predictors of TB Diagnosis	
Predictor	aHR (95% CI)
Male sex	1.85 (1.67–2.06)
PLHIV vs HIV-neg	3.32 (3.04–3.63)

Cox PH Model: Household Exposure		
Household	Events	aHR (95% CI)
Unexposed (n=15,181)	1,774	Reference
Symptomatic (n=176)	31	1.39 (0.91–2.15)
Asymptomatic (n=114)	14	1.01 (0.54–1.87)



11-year cumulative TB probability of diagnosis

Symptomatic HH (n=176):	13.0%	(7.7–18.1%)
Asymptomatic HH (n=114):	9.5%	(3.7–15.0%)
Unexposed HH (n=15,181):	~11.8%	(overall)

Interpretation



Linkage works - but coverage is the limiting factor

52.9% linkage enabled 11 years of follow-up with no prospective design. But 12,883 unmatched participants introduce selection bias and drastically reduce household exposure group sizes.



Persistently high TB incidence despite scale-up

1,230/100k PY - well above WC population-level estimates. Ongoing transmission in these communities is not adequately captured or interrupted by current case-finding strategies.



Household exposure signal exists but is underpowered

Symptomatic contacts: 13% cumulative probability vs ~11.8% unexposed. Trend is consistent with biological expectation, but CIs overlap widely - small Ns are the key constraint, not an absence of effect.



Male sex & HIV are the dominant, actionable signals

aHR 1.85 (males) and 3.32 (PLHIV) - robust findings unaffected by linkage limitations. TB/HIV integration and gender-sensitive outreach remain the most evidenced levers.

Conclusions

1

Routine data linkage can generate long-term TB cohort evidence

2

TB incidence remained high (1,230/100k PY) in this high-burden WC cohort over 11 years

3

Symptomatic HH contacts had the highest cumulative TB probability (13%), but the association was non-significant

4

Male sex (aHR 1.85) and **HIV** (aHR 3.32) were the strongest predictors of TB diagnosis

5

Strengthening routine data systems and linkage processes is necessary to improve our ability to detect important differences

Thank you!

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