

# Evaluation of a Semiquantitative Real-Time PCR in the Workup for PCP

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## Background

*Pneumocystis jirovecii* pneumonia (PCP) can be diagnosed by a positive immunofluorescence microscopy (IFM) in patients with a high fungal burden, e.g. HIV-positive patients.

However, a negative IFM does not exclude PCP in other patient groups that often have a lower fungal burden, e.g. patients with haematologic malignancies.

While PCR is a more sensitive method for detecting the organism, a positive PCR result does not differentiate between PCP and colonization.

We evaluate here the utility of cycle threshold (CT) values of a real-time PCR to distinguish between PCP and colonization, by comparing CT values with IFM results and patient clinical outcome.

## Conclusion

A CT value below 27 in BAL and sputum samples had good positive predictive value for PCP, and a CT value above 33 in BAL samples a good negative predictive value. Thus, the CT values of real-time PCR have utility in the workup for PCP.

## Method

Retrospective analysis of samples submitted to Karolinska University Laboratory from 2013-03-18 to 2015-12-31 for analysis of *Pneumocystis jirovecii*.

Medical chart review of symptoms, laboratory results, radiology, and response to specific treatment was used to differentiate PCP from colonization.

Selection criteria for medical chart review were:

- positive PCR of the large-subunit (LSU) rRNA gene
- BAL or sputum as sample material.

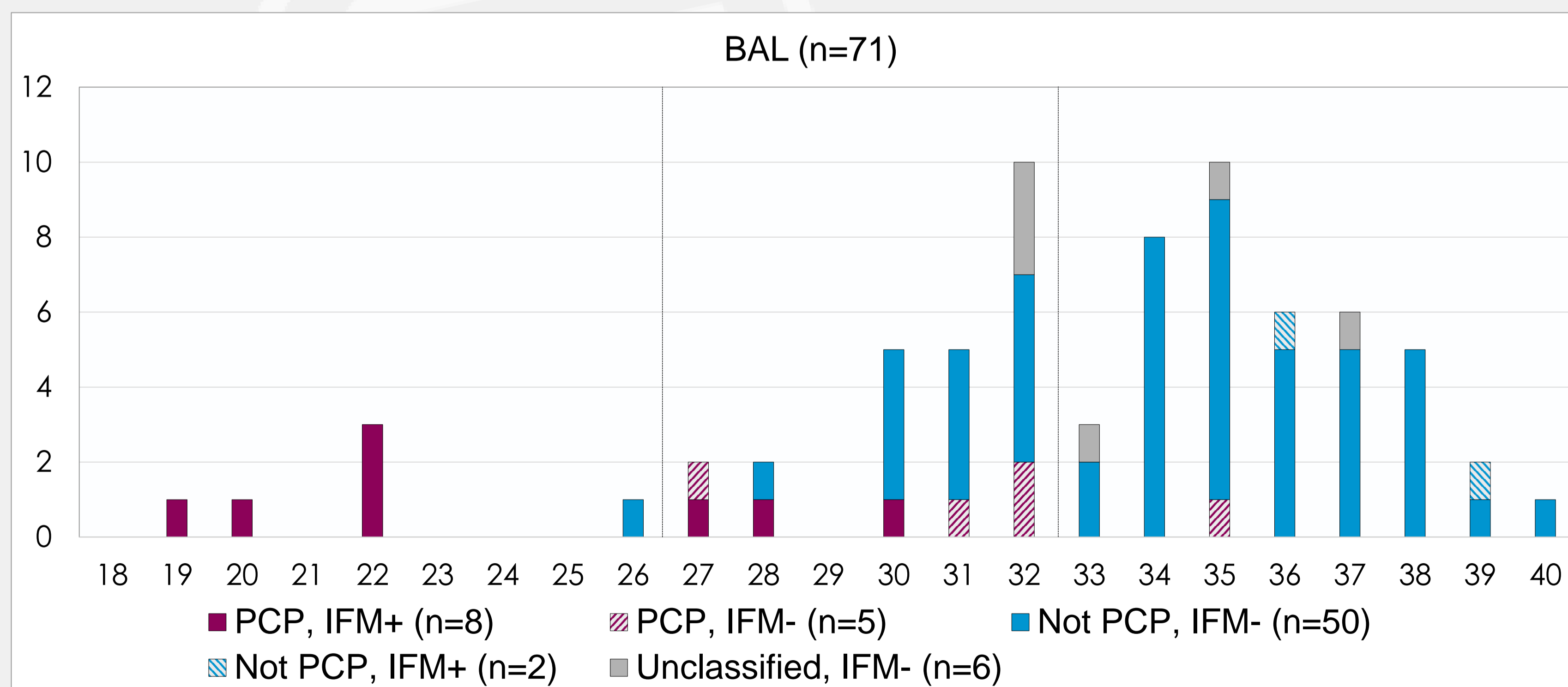
## Results

156 samples corresponding to 139 patients were reviewed. Most samples were from infectious disease (n=40), haematology (n=40), and pulmonology (n=32) clinics.

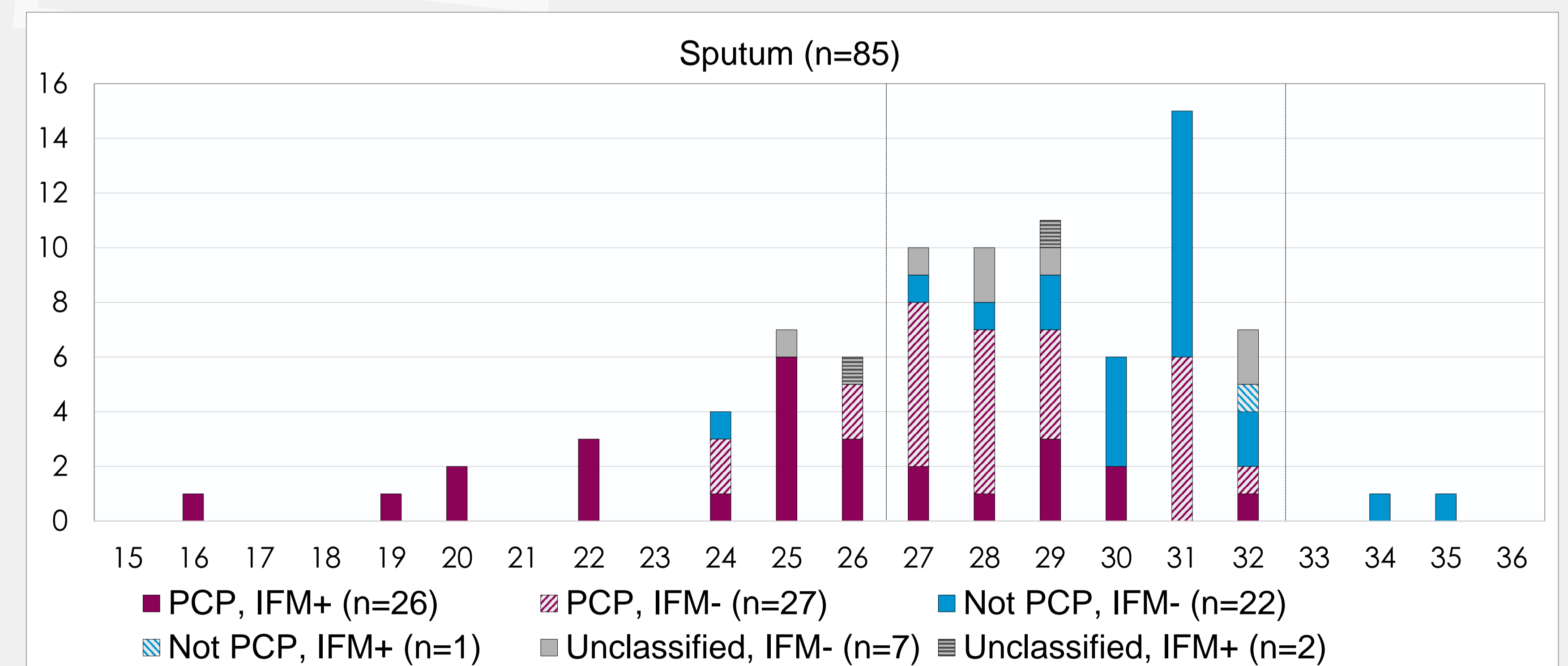
Medical chart review	IFM	BAL (n=71)	Sputum (n=85)
PCP	Positive	8	26
	Negative	5	27
Not PCP	Negative	50	22
	Positive	2	1
Unclassified	Positive	0	2
	Negative	6	7

Excluding the unclassified samples;

- for CT values below 27: in BAL samples 5/6 patients had PCP, and in sputum samples 21/22 patients
- for CT values above 33: in BAL samples 1/38 patients had PCP



X-axis: CT-value, Y-axis: number of samples



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