

# New molecular approach in the diagnosis of bloodstream infections

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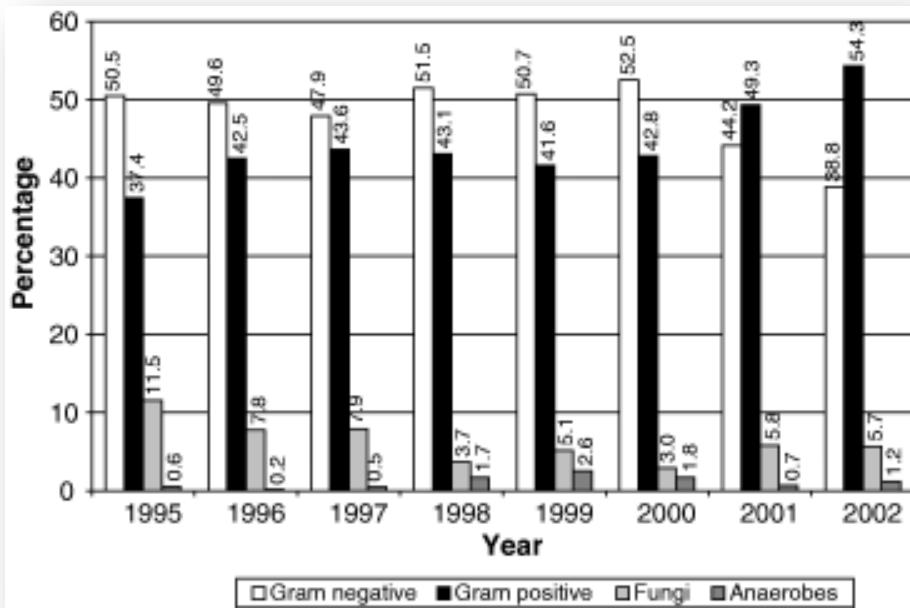
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# The most frequent causative agents of sepsis

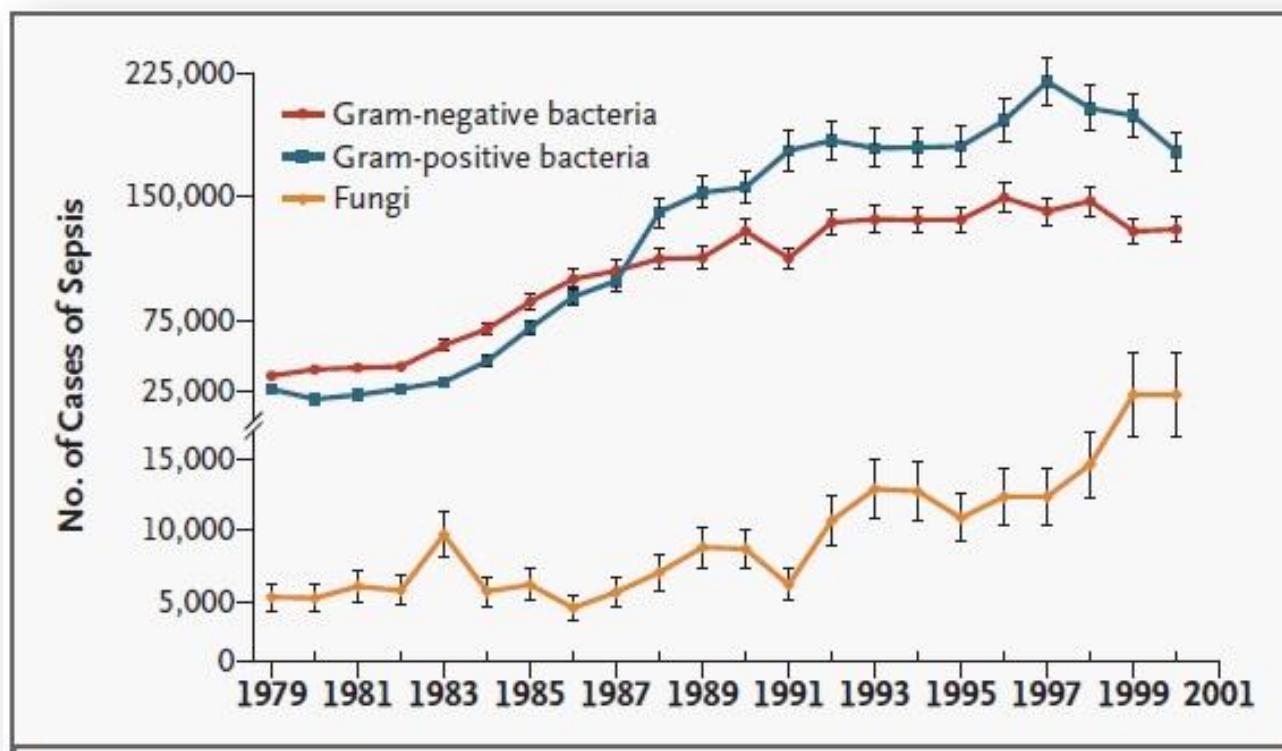


A. S. Hadziyannis et al., 2003

Pathogenicity	Incidence
Candida	<i>C. albicans</i>
	<i>C. glabrata</i>
	<i>C. tropicalis</i>
	<i>C. parapsilosis</i>
	<i>C. krusei</i>
	<i>C. lusitaniae</i>
Aspergillus	29%
Other mold	14%
Non identified	6%
<i>Cryptococcus</i>	4%
Endemic fungi	3%
<i>Pneumocystis jiroveci</i>	2%

J. Loeffler et al., 2000

# Numbers of cases of sepsis in the United States, according to the causative organisms

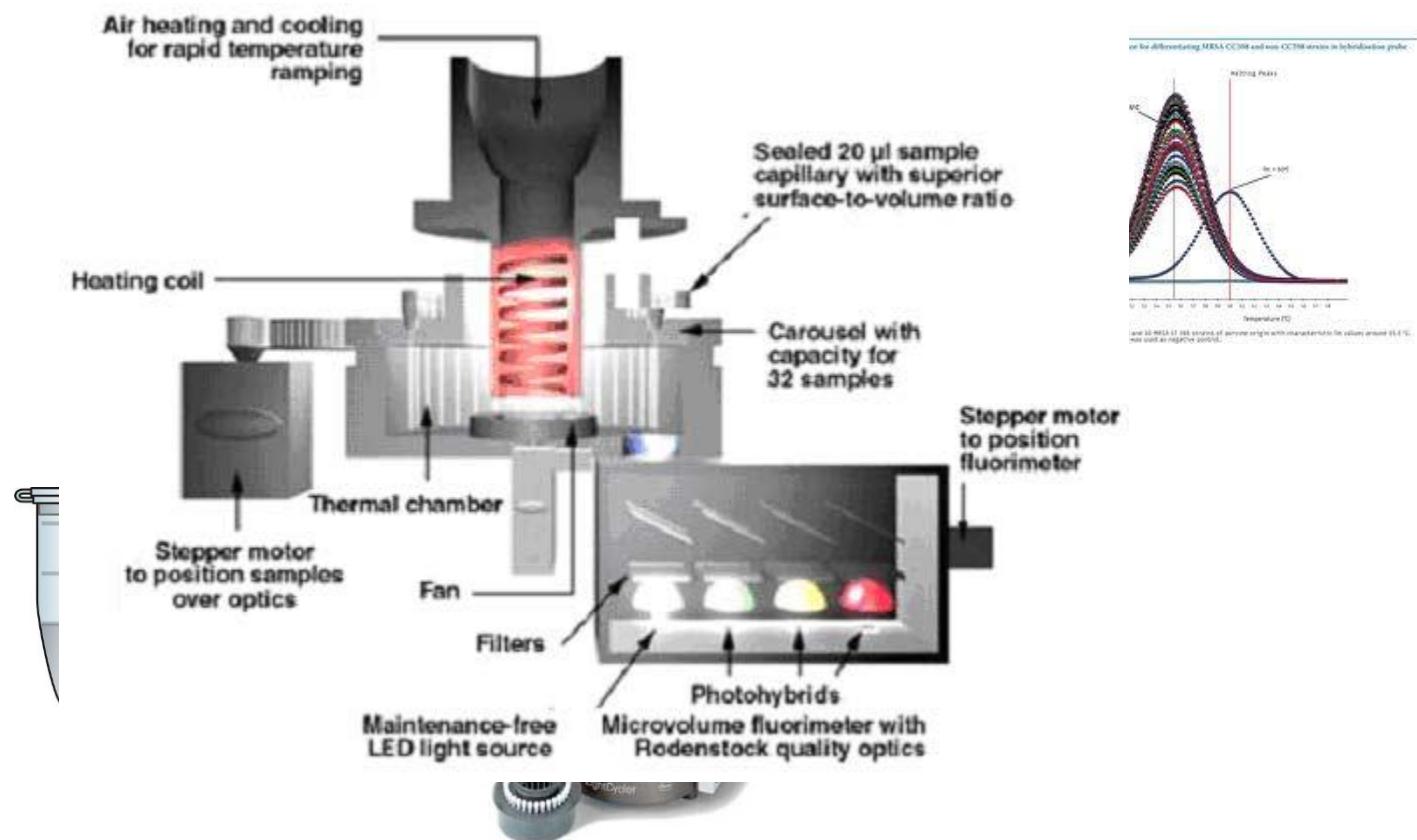
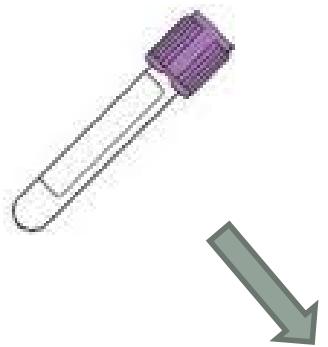


Greg S. Martin et al., 2003

# Recent approaches in the diagnosis of sepsis

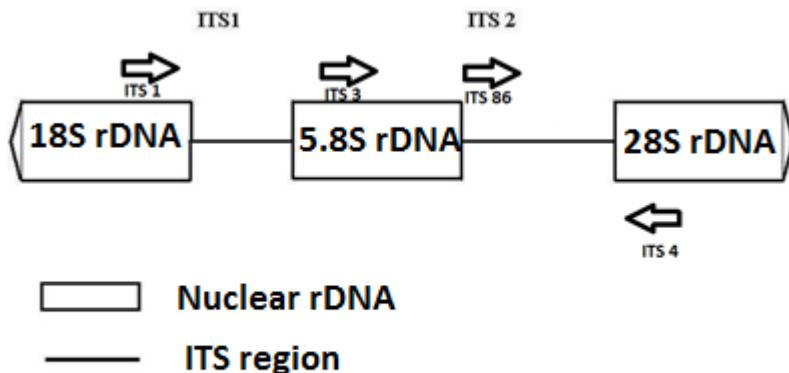
Method	Time (h)	Instrumentation	Cost	Adaptability
Blood culture	32-48	+	+	+++
Molecular techniques from blood				
1. FISH	2-3	++	++	+
2. PCR/LCR/NASBA	28-34	++	++	+
3. Real Time PCR	1-3	++	++	+
Molecular from blood				
1. PCR+sequencing	8	+++	+++	+
2. Real Time PCR	1-3	++	++	+++

# Real Time PCR + Fluorescence Resonance Energy Transfer



# Differentiation of the fungal and bacterial pathogens

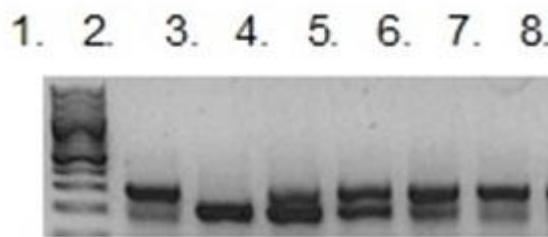
- Fungal primer



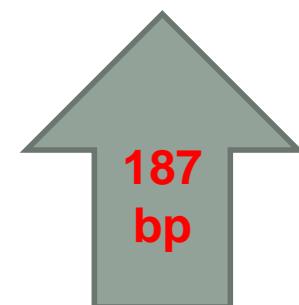
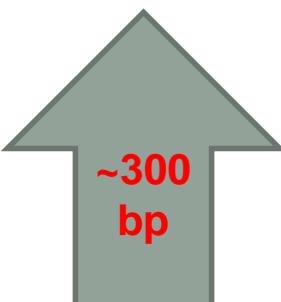
Somogyvári et al. 2005

- Bacterial primer

- Primers PLK1 PLK2 are highly conserved in different groups of eubacteria.
- The primers amplify conserved regions of the bacterial 16S rRNA gene.

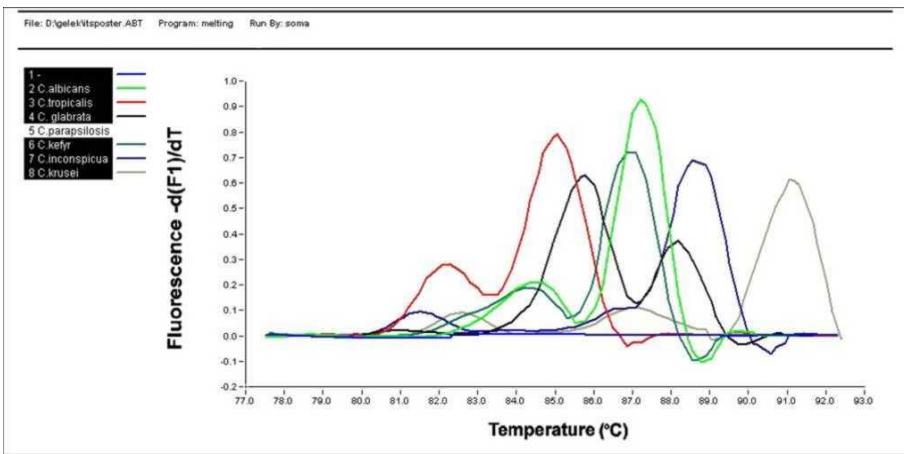


1. 100 bp ladder; 2. *C. alb.*; 3. *S. aur*; 4. *S. aur+C. alb.*; 5. *S. aur* 10x+C. alb.; 6. *S. aur* 100+C. alb.; 7. *S. aur* 1000+C. alb.; 8. *S. aur* 10000+C. alb.,



# Melting peaks of the fungal pathogens

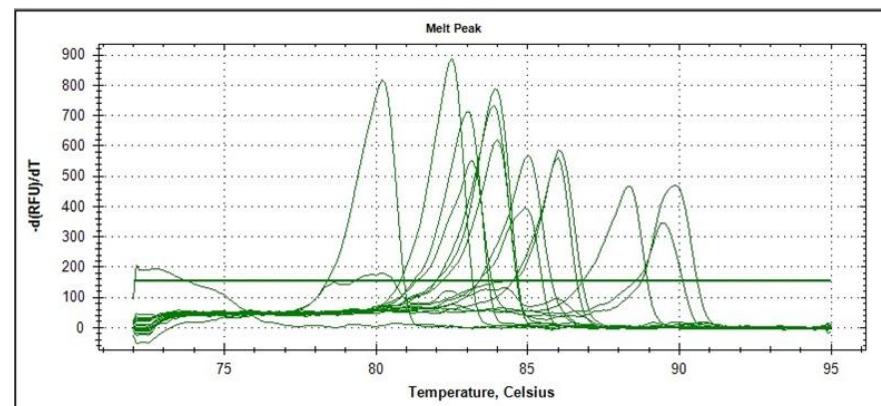
## Melting Point Analysis



Amplification with ITS86; ITS4 primer pair.

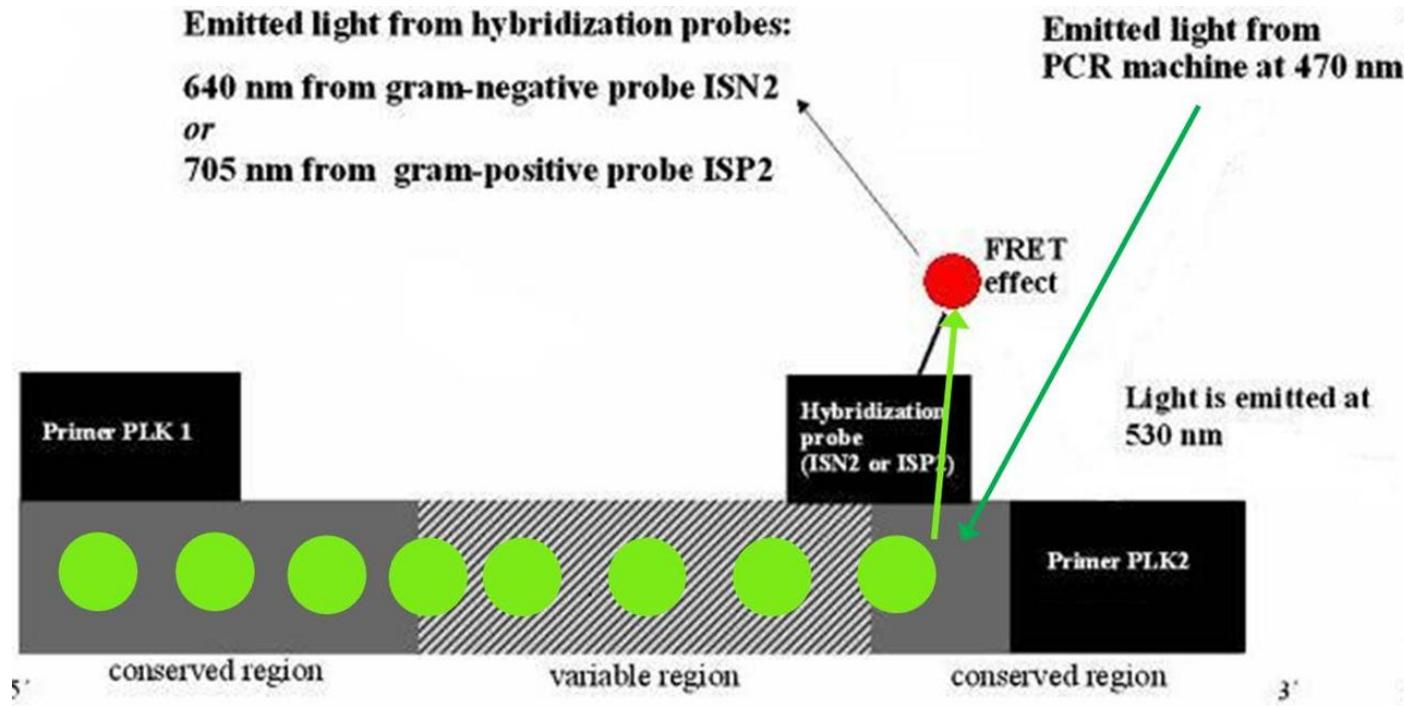
**Ctrl blue;** *C. albicans* **green;** *C. tropicalis* **red;** *C. glabrata* **black;** *C. kefyr* **dark green;** *C. inconspicua* **purple;** *C. krusei* **grey.**

## High Resolution Melting Point Analysis (HRM)

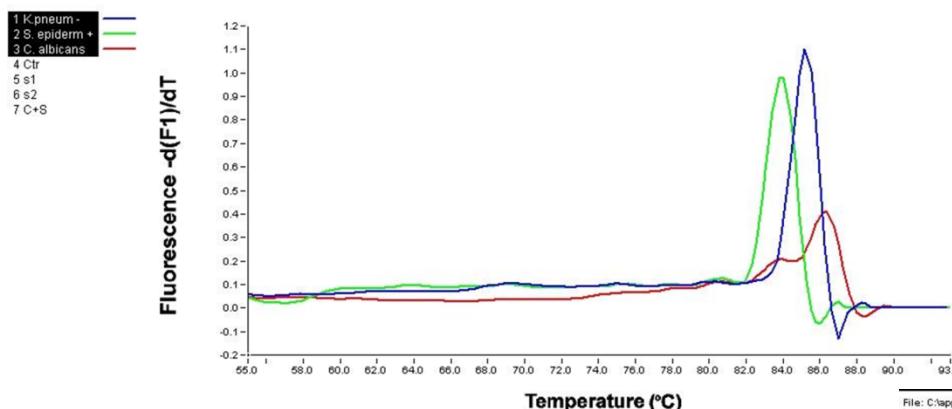


Fugal strains	Melting Point of the amplicon (°C) ± 0.05 °C
<i>Mucor mucedo</i>	80,7
<i>Candida tropicalis</i>	81,8
<i>C. parapsilosis</i>	82,6
<i>C. guilliermondii</i>	82,8
<i>C. glabrata</i>	83,2
<i>C. dubliniensis</i>	83,5
<i>Cryptococcus neoformans</i>	84,1
<i>C. albicans</i>	84,5
<i>C. lusitaniae</i>	85,4
<i>Fusarium oxysporum</i>	85,4
<i>C. norvegensis</i>	86,2
<i>C. inconspicua</i>	86,4
<i>C. krusei</i>	88,6
<i>Aspergillus niger</i>	89,6
<i>A. flavus</i>	90,4
<i>A. fumigatus</i>	90,9
<i>A. terreus</i>	ND

# Gram strain classification with FRET



File: C:\apps\LightCycler3\Users\Soma\EFRET\110110.ABT Program: melt Run By: tritec  
Run Date: Jan 10, 2011 15:42 Print Date: July 18, 2011

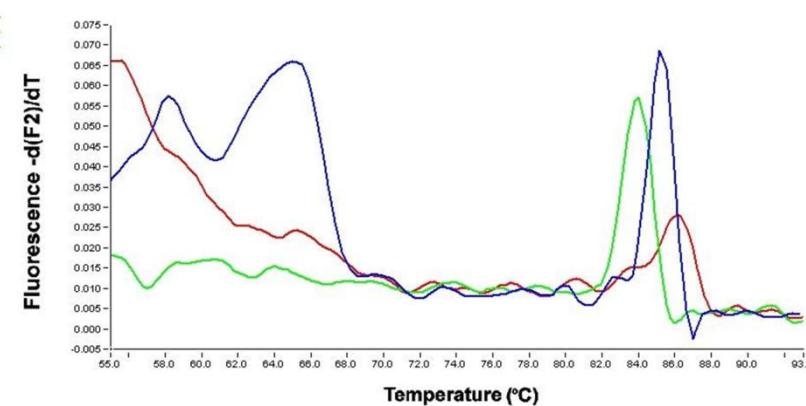
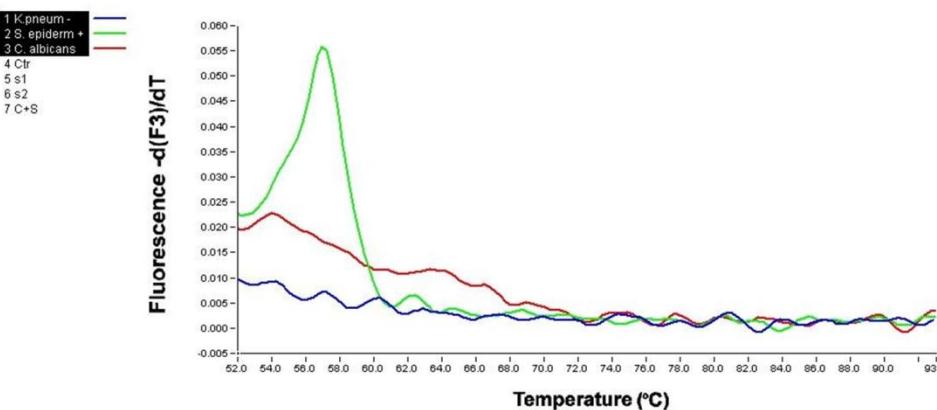


File: C:\apps\LightCycler3\Users\Soma\EFRET\110110.ABT Program: melt Run By: tritec  
Run Date: Jan 10, 2011 15:42 Print Date: July 18, 2011

1 K.pneum -  
2 S. epiderm +  
3 C. albicans  
4 Ctr  
5 s1  
6 s2  
7 C+S



File: C:\apps\LightCycler3\Users\Soma\EFRET\110110.ABT Program: melt Run By: tritec  
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# Summary

- We applied the fungal PCR for the detection of the bacterias.
- The sensitivity of the PCR was less than 5 CFU/ml. The multiplex reaction is working with extrem dilution of the templates.
- The Melting Point Analysis and High Resolution Melting Point Analysis were approriate to discriminate the most common pathogen fungus.
- All bacteria tested were correctly classified as gram positive or gram negative with FRET

# Further aims:

- Identification of all bacterial pathogens
- We would like to perform a Real Time PCR without DNA purification from whole blood or serum - and save more time
- Grow up the reliability of the method with internal control.

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THANK YOU FOR YOUR ATTENTION!

DZIĘKUJĘ ZA UWAGĘ!

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