2004 TE Calibration for COMPASS Polarized Target

Isabel Llorente Garcia

INTRODUCTION

- Thermal equilibrium (TE) calibration of the Nuclear Magnetic Resonant (NMR) system for the polarized target in COMPASS experiment. May and June 2004.
- The polarization of the target is proportional to the area of the NMR signal:

 $\begin{aligned} Pol &= B \times Area; \\ B &= \frac{Pol_{TE}}{Area_{TE}} \\ Pol_{enhanced} &= \frac{Pol_{TE}}{Area_{TE}} \times Area_{enhanced} \end{aligned}$

- **B** is obtained measuring the TE-Area, and calculating the TE-Polarization analytically from the Brillouin function at a known temperature.
- The TE-Area also depends on the temperature used.
- To avoid repeating the process each time the temperature changes, Curie Law is used:

$$Area_{TE} = \frac{C}{T}$$

 Five different temperatures for measuring the TE-Area were used to obtain *C*.

GENERAL PROCEDURE

- Data for 5 different TE temperatures.
- For each file corresponding to one TE temperature:
 - Subtract background from signal
 - Find baseline: fit the off-resonance points to a straight line
 - Subtract baseline
 - Calculate TE area by integration of the remaining signal
- All the areas from all files corresponding to one temperature were plotted against time and fitted to a constant to obtain the final TE area for that temperature.
- The 5 values of the final TE areas for each temperature were plotted against the inverse of temperature and fitted to a Curie law to perform the calibration.

FILES	No. of signals	TE temperat.
TE1K5 → 5-7May 2004	201	1.5065 ± 0.0037
TE1K2 → 8-9 May 2004	162	1.2802 ± 0.0011
TE1K → 10-12 May 2004	249	1.1713 ± 0.0020
TE2_1K → 10-12 June 2004	216	0.9994 ± 0.0023
TE2_1K3 → 13-14 June 2004	131	1.3157 ± 0.0018





Signal minus background

Signal and background





Baseline subtracted

Baseline fit

- Files corresponding to 15 hours after each reset of the TE temperature were not considered (not at equilibrium).
- At thermal equilibrium (<u>TE</u>) the <u>signal is small</u>, and its integration to obtain the <u>TE area</u> <u>depends</u> a lot <u>on the baseline</u> calculation.
- <u>100 baseline fits</u> were calculated for each signal.
 <u>Each</u> fit had a <u>different</u> width of the <u>region</u> selected for the baseline fit.
- <u>Several methods</u> were studied: the <u>'Average</u> <u>method</u>', the <u>'Histogram method</u>'.

Example of 8 different baseline fits for one coil.

Signal minus background. Selected region for baseline fit.

The region selected for the baseline fit gets narrower from the first to the last fit.



The 'Average Method'

- 100 baselines calculated for <u>each signal file</u>:
 - Fit no. 1 → widest fitting region, close to resonant peak.
 - Fit no. 100 \rightarrow narrowest fitting region, far from peak.
- For each baseline \rightarrow calculate area.
- Average all those areas to obtain the final TE area for that file. (Error is the standard deviation).
- Plot all the final TE areas from <u>all files</u> corresponding to one TE temperature against time.
- Plot the histogram of all these values and select only those between certain probability quantiles.

- The quantile, q(p), with $0 \le p \le 1$, of our normalized distribution of areas, *f(area)*, is the value of the area such that the integral of the distribution: $\int_{area}^{q(p)} f(area)d(area) = p$
- For example, the median would be the q(0.5) quantile.
- Next step: select only the area values within the 0.09 and the 0.91 probability quantiles. This eliminates data points which are too high or too low.



• In the plots of the TE area values against time:



- Finally the **median** of all the selected area values is calculated because it is the value that minimizes the sum of the absolute deviations in the fit of these values to a constant. This is the area for one given temperature.
- The error of the median is calculated as the half width of the area interval containing 68% probability inside it (region between the 0.16 and 0.84 probability quantiles in the of all areas).

The 'Average method'...

Different fitting regions:

Comparison between Case 1 and Case 2:

- For single files → average of the 100 areas calculated from the 100 different baseline fits → difference of 1% to 16% approx. between Case 1 and Case 2.
- For grouped files → median of the selected average areas from all files → difference of 0.1% to 4% between both cases.
- → Different ranges of fitting regions certainly produce different <u>average</u> values of the TE area.

The 'Average method': Curie Fits

- Using the widest range of fitting regions (Case 1).
- So far we obtained one final value of the TE area for each of the 5 temperatures.
- Curie Law:

$$Area_{TE} = \frac{C}{T}$$

- The values of the areas were plotted against the inverse of temperature and fitted to a line, area = A + C.(1/T), where A was forced to zero and C is the Curie constant.
- Error in fit parameter *C* was between 2.0% and 4.2% for this method.
- 8 NMR coils inside the target → each step of the method was carried out for each coil.

Curie fits \rightarrow 'Average method'

Curie fits \rightarrow 'Average method'

Curie Fits for the 'Average method'					
Coil number	χ 2 / ndf	А	С	% error in C	
1	0.0817 / 4	0 ± 0	-8746 ± 285	3.3	
2	0.1602 / 4	0 ± 0	-8663 ± 235	2.7	
3	0.1009 / 4	0 ± 0	-6593 ± 275	4.2	
4	0.2031 / 4	0 ± 0	-10210 ± 286	2.8	
7	0.3241 / 4	0 ± 0	-9752 ± 196	2.0	
8	0.3368 / 4	0 ± 0	-7812 ± 171	2.2	
9	0.2963 / 4	0 ± 0	-7803 ± 167	2.1	
10	0.1014 / 4	0 ± 0	-9004 ± 239	2.7	

Area = **A** + **C**.(1/T)

The 'Histogram Method'

1. Histograms of all areas.

- 100 baseline fits calculated for <u>each</u> signal <u>file</u>.
- For each baseline \rightarrow calculate TE area.
- Enter those areas into a histogram.
- Find the most probable area (highest bar).
 Error estimated as the width of the bar.
- For <u>all files</u> corresponding to one temperature: plot all those most probable areas against time.
- Enter them into a histogram and select only those between the 0.09 and 0.91 probability quantiles.
- Find the median of those selected areas. This is the final area for the given temperature. (As in the 'Average method').

Area for each file obtained from the highest bar in the histogram. Error is width of highest bar.

- Five different ranges of fitting regions were used and the results were compared for single files: the values of the calculated areas could differ a lot, up to 27%.
- Therefore, this method was quite sensitive to the choice of fitting regions for the 100 fits that were done.
- It was seen that there was nearly no difference between calculating 100 fits and 500 fits.

2. Histograms of selected areas: X² selection.

- For each of the 100 baseline fits: calculate *X*²/*ndf*.
- *ndf*: no. of degrees of freedom, no. of fitted points minus one.
- X²/ndf indicates how good the linear fit is. For a perfect fit it would be zero.
- Find the lowest X²/ndf value and accept only those fits that have a value within the range [(X²/ndf)_{min} ± α].
- This eliminates the worse fits from the analysis.
- After this, only the areas coming from those selected fits are entered into the histograms to calculate the most probable values.
- From here: same procedure as before...

- Several values of *a* were tested on single files.
- Areas obtained from α = 4,7,9,11, were quite similar (4% difference at the most).
- Always a higher number of accepted areas for coils 7 to 10.
- For one file, accepted areas were very close to each other and came from baselines with a small number of fitted points (fit no. close to 100).

		α = 4	= 4 α = 7 α = 9		α = 11			
coil	Ν	TE area	Ν	TE area	Ν	TE area	Ν	TE area
1	5	-9087.5	6	-9087.5	13	-9087.5	16	-9087.5
2	5	-5187.5	7	-5187.5	9	-5187.5	10	-5187.5
3	4	-6812.5	6	-6812.5	8	-6812.5	12	-6812.5
4	3	-7787.5	8	-7462.5	8	-7462.5	11	-7462.5
7	10	-8112.5	41	-8112.5	58	-7787.5	99	-7787.5
8	29	-5837.5	79	-5837.5	99	-5837.5	100	-5837.5
9	49	-6162.5	100	-6162.5	100	-6162.5	100	-6162.5
10	9	-6162.5	58	-6812.5	96	-7137.5	100	-7137.5

Study of the X²/ndf parameter:

The values of the <u>X²/ndf</u> were plotted against the fit number. It was clear that <u>X²/ndf</u> decreased from fit no. 1 to fit no. 100 (less fitted points).

The histograms of the X^2/ndf values from each of the 100 fits were plotted for each coil.

For **coils 1 to 4**, the range of X^2/ndf values was wider than for **7 to 10**. For **coils 1 to 4**, the values of X^2/ndf were higher than for **coils 7 to 10**.

- Due to the small dependence of X²/ndf on the fit number, this way of selecting baseline fits was not clearly valid, since the lowest values of X²/ndf would systematically come from baseline fits calculated from a small number of points, far from the resonant peak.
- This X² selection compared fits of different regions and different points. The fit with the lowest X²/ndf did not necessarily give the best possible baseline.
- It was also seen that this selection method did not help to get rid of "bad points" in the plots of TE areas vs time.
- X² selection could be used with a large value of α, to try and eliminate "very bad" fits only.

The 'Histogram method': Curie Fits

- The widest range of fitting regions was used.
- X^2 selection with $\alpha = 85$ was used to control "bad fits".
- One final value of the TE area was obtained for each of the 5 temperatures.
- Curie Law:

$$Area_{TE} = \frac{C}{T}$$

- The values of the areas were plotted against the inverse of temperature and fitted to a line, area = A + C.(1/T), where A was forced to zero and C is the Curie constant.
- Error in fit parameter C was between 2.0% and 3.5% for this method.
- 8 NMR coils inside the target → each step of the method was carried out for each coil.

Curie fits \rightarrow 'Histogram method'

Curie fits \rightarrow 'Histogram method'

Curie Fits for the 'Histogram method'					
Coil number	χ 2 / ndf	А	С	% error in C	
1	0.2419 / 4	0 ± 0	-8669 ± 283	3.3	
2	0.3129 / 4	0 ± 0	-8632 ± 250	2.7	
3	0.3483 / 4	0 ± 0	-6536 ± 227	4.2	
4	0.3161 / 4	0 ± 0	-10190 ± 280	2.8	
7	0.6411 / 4	0 ± 0	-9813 ± 192	2.0	
8	1.7490 / 4	0 ± 0	-7879 ± 167	2.2	
9	0.4314 / 4	0 ± 0	-7879 ± 168	2.1	
10	0.3775 / 4	0 ± 0	-9027 ± 224	2.7	

Area = **A** + **C**.(1/*T*)

Comparison between the 'Average method' and the 'Histogram method'

The differences in the value of **C** between both methods ranged between 0.2% and 1.0%.

The values agree within their errors.

Comparison for Curie fit parameter C					
coil	Average method	Histogram method	% difference		
1	-8746	-8669	0.9		
2	-8663	-8632	0.4		
3	-6593	-6536	0.9		
4	-10210	-10190	0.2		
7	-9752	-9813	0.6		
8	-7812	-7879	0.9		
9	-7803	-7879	1.0		
10	-9004	-9027	0.3		

One last method

• From the Curie Law:

Area
$$_{TE} = \frac{C}{T_{TE}} \Rightarrow Area _{TE} \times T_{TE} = C$$

- C is the Curie constant that should not depend on temperature.
- The products *Area_xT* could be plotted against time for all files and for all times. Values coming from different temperatures were plotted one after the other on the same graph.
- Two ways of obtaining the final Curie constant **C**:
 - a) All values of $Area_{x}T$ entered in a histogram \rightarrow select those between 9% and 91% quantiles \rightarrow find the median of those selected values of $Area_{x}T$.
 - b) Fit all values (no quantile selection) to a gaussian. Obtain the mean and sigma from the fitted gaussian function.

The last method

Selected values of Area. T between quantiles

'Average method'

'Histogram method'

The last method: results for the Curie parameter **C**.

	The 'Avera	ge method'	The 'Histogram method'	
coil	Median of selected values of Area.T	Mean±Sigma from gaussian fit of all values	Median of selected values of Area.T	Mean±Sigma from gaussian fit of all values
1	-8730 ± 662	-8688 ± 846	-8668 ± 646	-8787 ± 801
2	-8651 ± 561	-8655 ± 756	-8644 ± 507	-8722 ± 704
3	-6573 ± 617	-6575 ± 790	-6542 ± 550	-6663 ± 631
4	-10196 ± 647	-10171 ± 826	-10233 ± 570	-10198 ± 564
7	-9721 ± 467	-9738 ± 592	-9776 ± 500	-9895 ± 494
8	7776 ± 401	-7785 ± 503	-7796 ± 402	-7794 ± 536
9	7796 ± 383	-7799 ± 488	-7806 ± 390	-7850 ± 476
10	9020 ± 522	-9030 ± 653	-9046 ± 502	-9194 ± 667

For the 'Average method':

- Error between 4.8% and 9.4% in the median of selected values of <u>Area.T</u> (a).
- Error between 6.1% and 12.0% in the mean of the gaussian fit of all <u>Area.T</u> (b).
- Difference between a) and b) is between 0.03% and 0.49%.
- Error between 2.0% and 4.2% in C obtained from the <u>Curie fit</u>.
- Difference between using <u>Curie fits</u> and using the median of selected values of <u>AreaxTemperature</u>, (a), is between 0.09% and 0.45%.
- Difference between using <u>Curie fits</u> and using the mean of the gaussian fit of all values of <u>AreaxTemperature</u>, (b), is between 0.04% and 0.67%.

For the 'Histogram method':

- Error between 5.0% and 8.4% in the median of selected values of <u>Area.T</u> (a).
- Error between 5.0% and 9.5% in the mean of the gaussian fit of all <u>Area.T values</u> (b).
- Difference between a) and b) is between 0.04% and 1.82%.
- Error between 2.0% and 3.5% in C obtained from the <u>Curie fit</u>.
- Difference between using <u>Curie fits</u> and using the median of selected values of <u>AreaxTemperature</u>, (a), is between 0.01% and 1.05%.
- Difference between using <u>Curie fits</u> and using the mean of the gaussian fit of all values of <u>AreaxTemperature</u>, (b), is between 0.08% and 1.95%.

• <u>Difference between the 'Average method' and the 'Histogram</u> method':

-For the median of selected values of <u>AreaxTemperature</u> (a), between 0.08% and 0.71%.

-For the mean of the gaussian fit of all values of <u>AreaxTemperature</u> (b), between 0.11% and 1.78%.

or the <u>Curie fits,</u> the difference between both methods is between 0.2% an