

# Report of the 4th External Quality Assurance System on Isolation, Identification and Typing of Methicillin resistant *Staphylococcus aureus* (MRSA) from Swab Samples, year 2012



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**Report of the 4th External Quality Assurance System on Isolation, Identification and Typing of Methicillin resistant *Staphylococcus aureus* (MRSA) from Swab Samples, year 2012**

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## Index

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1. Introduction.....	3
2. Materials and Methods.....	4
2.1 Participants in EQAS 2012 .....	4
2.2 Preparation of samples .....	4
2.3 Isolation and identification of MRSA from swab samples.....	5
2.4 Typing.....	5
2.5 Distribution .....	5
3. Results.....	6
3.1 Methods used by EQAS-participants.....	7
3.2 MRSA isolation and identification.....	8
3.3 <i>spa</i> typing of the MRSA strains.....	9
4. Discussion .....	11
4.1 MRSA isolation and identification.....	11
4.2 <i>spa</i> typing .....	11
5. Conclusion.....	12
6. References .....	12
Appendix 1. Pre-notification EURL-AR MRSA EQAS 2012	
Appendix 2. List of participants	
Appendix 3. Expected results	
Appendix 4. Protocol MRSA EQAS 2012	
Appendix 5. Examples of Test forms MRSA EQAS 2012	



## 1. Introduction

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Methicillin resistant *Staphylococcus aureus* (MRSA) have recently emerged in food producing animals. The emergence of this potential zoonotic pathogen in animals has raised the concerns of potential transmission to humans from the animal reservoirs and consequences on Public Health. In 2008, the European Commission (EC) took a decision of screening the population of pig farms in Europe for this new emerging pathogen, taking this screening into the framework of the baseline screening for *Salmonella* in pig farms (European Commission Decision 2008/55/EC). This screening has been performed in most European Countries by laboratories appointed by the national authorities and according to a common protocol defined by the EC.

The European Union Reference Laboratory for Antimicrobial Resistance (EURL-AR) took part in the development and support of the laboratories for this task by providing assistance in setting up the methods for isolation, identification, and typing of MRSA. Additionally, the EURL-AR provided training in the specific methods on individual basis as well as in an MRSA training course that was organized in April 2009.

In June 2009, the EURL-AR in addition to the External Quality Assurance System (EQAS) already performed, launched an MRSA specific EQAS, to enhance the capacity of the laboratories in MRSA isolation, identification and typing. This EQAS aimed at the identification of potential problems and identification of focus areas for training/education that might improve data quality in future European studies focusing on MRSA epidemiology.

In June 2010, a trial was prepared in October 2010, using swab samples. Since then, swab samples were used within the EQAS trial.

In 2012, we launched the fourth EQAS performed on MRSA isolation, identification and typing. As the previous EQAS, this included isolation steps besides the identification and also a molecular component; detection of methicillin resistance. The detection of the *mecA* and *mecC* gene were included as a mandatory part for confirmation of MRSA. An optional sequence based typing module based on *spa* typing was also offered. The *spa* typing trial aimed at increasing the capacity of laboratories by performing a standard typing method which can be easily performed, and which results are comparable and useful to assess the epidemiology of MRSA in Europe.

At the starting point of this EQAS, the laboratories should have implemented the methods and enhanced its performance. Therefore, the EQAS may be used to assess the quality of data provided to EFSA, but also to prepare the laboratories for correctly performing the isolation, identification and molecular detection of MRSA.

No thresholds have been set in advance to evaluate the performance of the participating laboratories, nor classify the results of this EQAS as there were issues related to stability which have caused deviations.

The MRSA EQAS was organized by the National Food Institute (DTU Food), Kgs. Lyngby, Denmark and the verification/confirmation of the strains used in the preparation of the test samples was performed at the Statens Serum Institute (SSI) in Copenhagen, Denmark.

The data in this report are presented with laboratory codes. A laboratory code is known to the individual laboratory, whereas the entire list of laboratories and their codes is confidential and known only to the EURL-AR and the EU Commission. All conclusions are public.



The technical advisory group for the EURL-AR EQAS scheme consists of competent representatives from all National Reference

Laboratories for Antimicrobial Resistance (NRLs-AR), who meet annually at the EURL-AR workshop

## 2. Materials and Methods

### 2.1 Participants in EQAS 2012

A pre-notification (App 1), inviting the participants to the MRSA EQAS 2011 was issued by e-mail to the EURL-AR network on the 16<sup>th</sup> of July 2012 to the NRL-AR's. Additionally, the laboratories that participated in the MRSA baseline studies in 2008 and participated in the MRSA EQAS in the previous year were invited to participate using the same pre-notification.

All participants were included in a participant list (App 2) before the preparation and shipping of the samples. Participation was free of charge but each laboratory was expected to cover expenses associated with their own analysis.

### 2.2 Preparation of samples

Eight swab samples were prepared and dispatched for isolation of MRSA, identification, and typing of the obtained isolates. The samples were artificially prepared to contain either methicillin-resistant *Staphylococcus aureus* (MRSA), methicillin-susceptible *S. aureus* (MSSA) and/or coagulase negative staphylococci strains (CNS), and, for the first time, we have also included samples containing a methicillin resistant *Staphylococcus* carrying the *mecC* gene and a methicillin resistant *Staphylococcus pseudintermedius* strain. Selected strains were then used as test strains and mixed in a sample containing a background flora composed of a mix of *S. sciuri*, *Enterococcus faecalis* and *Escherichia coli* which was intended to mimic the normal flora that would be present in a nasal swab collected from an animal.

The background flora was prepared by

matching bacterial suspensions of *E. faecium* NS13 (isolate originated from a nasal swab from a pig); *Staphylococcus sciuri* NS 72 (isolate originated from a nasal swab from a pig) and *Escherichia coli* ATCC 25922 to a 0,5 Mc Farland standards suspension which were then diluted to  $10^{-3}$  in saline and mixed in equal parts. The swabs were dipped into this mixture before preparation of the samples. The expected amount of each bacterial culture in the mixture was about  $10^5$  CFU/ml. This was confirmed by performing serial dilution and colony forming unit counts in duplicate from all bacterial suspensions.

The test isolates selected for the MRSA EQAS (EURL-MRSA 4.1- EURL-MRSA 4.8) were prepared in advance and subcultured in week 38-39 and re-subcultured on the day before sample preparation. For the sample standardization, suspensions equal to McFarland 0.5 were prepared in saline tubes of the relevant isolates to contain about  $10^8$  CFU/mL. The suspensions were further diluted 1:10 or 1:100 (in the case of the inoculum for samples 4.8) to  $10^7$  CFU/ml or 10 CFU/mL of which 100  $\mu$ l were used to inoculate the transport media contained in the tubes with the swab samples. The expected inoculum was expected to be about  $10^6$  CFU per sample, for samples 4.1, 4.2, 4.3, 4.4, 4.5 and 4.6, and it was about  $10^5$  CFU per sample, for sample 4.8 confirmed by performing serial dilution and colony forming unit counts in duplicate from all isolate suspensions. The sample MRSA EQAS 4.7 contained only the background flora and no added test organism.

The strains used for the EQAS were selected from the strain collections at DTU-Food and the identification were confirmed by PCR and 16S



rDNA. Furthermore, the *spa* type of the MRSA isolates was determined by PCR and sequencing and assigned according to the *spa* server using Bionumerics (App 3). Identification and the *spa* type of the selected isolates were verified and confirmed by parallel analysis conducted at SSI, Copenhagen, Denmark. The results obtained after preparation of the contaminated swab samples were confirmed at DTU-Food, by testing (isolation, identification and typing) of three sample sets just after preparation. Stability testing was performed in one set of eight samples per week, during one month. Further tests were performed after six and eight weeks using the recommended protocol for isolation and identification of MRSA. Further stability tests revealed good stability up to week six for all the samples and up to week eight for most samples, except for samples 4.3, 4.6 and 4.8 for which we detected lack of stability eight weeks after shipping.

## 2.3 Isolation and identification of MRSA from swab samples

The protocol for isolation and identification of the MRSA isolates contained in the swab samples was made available on the EURL website (<http://www.eurl-ar.eu>) (App.4). This time, the protocol for identification of methicillin resistance has been modified by recommending a new multiplex PCR able to detect both *mecA* and *mecC* genes and to simultaneously amplify fragments of the *spa* and *pvl* genes (Stegger *et al.*, 2012).

## 2.4 Typing

The isolates used for the sample preparation were typed by a single locus sequence typing method - *spa* typing (Shopsin *et al.* 1999) and in addition to verification of *spa* types at the SSI, the *spa* typing results were verified a third time in the isolates obtained from prepared samples.

The laboratories with capacity to perform *spa*

typing were invited to also include the *spa* typing results to the MRSA EQAS database, which were evaluated for accuracy against the expected *spa* types.

## 2.5 Distribution

The samples were prepared a week before shipment and were kept at 4°C between the preparation and shipment process. The tubes containing the swab samples in transport media were enclosed in double pack containers (class UN 6,2) and sent to the selected laboratories according to the [International Air Transport Association](#) (IATA) regulations as “Biological Substance category B” classified UN3373. The parcels were dispatched from DTU-Food October 1<sup>st</sup>, 2012. 2.6 Procedure

The laboratories were instructed to download the protocol and test forms (App. 4 and 5), from <http://www.eurl-ar.eu>

The EQAS protocol was based on the EC baseline protocol for isolation of MRSA from dust samples, however, with slight changes in the volume of the media needed in the enrichment steps, since the samples were sent as swab samples in a tube containing transport medium in contrast to large dust swabs. The method recommended for the identification of the isolates was a new multiplex PCR which would allow identification of *S. aureus* and also identify the *mecA* and *mecC* genes, mandatory for the classification of isolates as MRSA (App 4).

After completion of the tests, the laboratories were requested to enter the obtained results into an electronic record sheet in the EURL-AR web based database through a secured individual login, or alternatively send the record sheets by fax to DTU Food (App 5). The database was activated 17th October, 2012 and closed December 22<sup>nd</sup> 2012.

The samples were categorised as positive or negative in function of the isolation and

identification of MRSA isolates and no quantitative variable was introduced. Negative samples could be subdivided into different categories (negative sample, MSSA, MRCNS, MRSP, CNS), however they would be grouped as negative. Final interpretations of the results obtained were compared to the expected results and classified as correct or incorrect, without further classification of the deviation.

Optionally, results of *spa* types were requested for typing the positive MRSA samples. In this case, the participants would be invited to choose the obtained *spa* type from a pick list, and the typing result would be evaluated against the expected *spa* type and classified into correct or incorrect.

### 3. Results

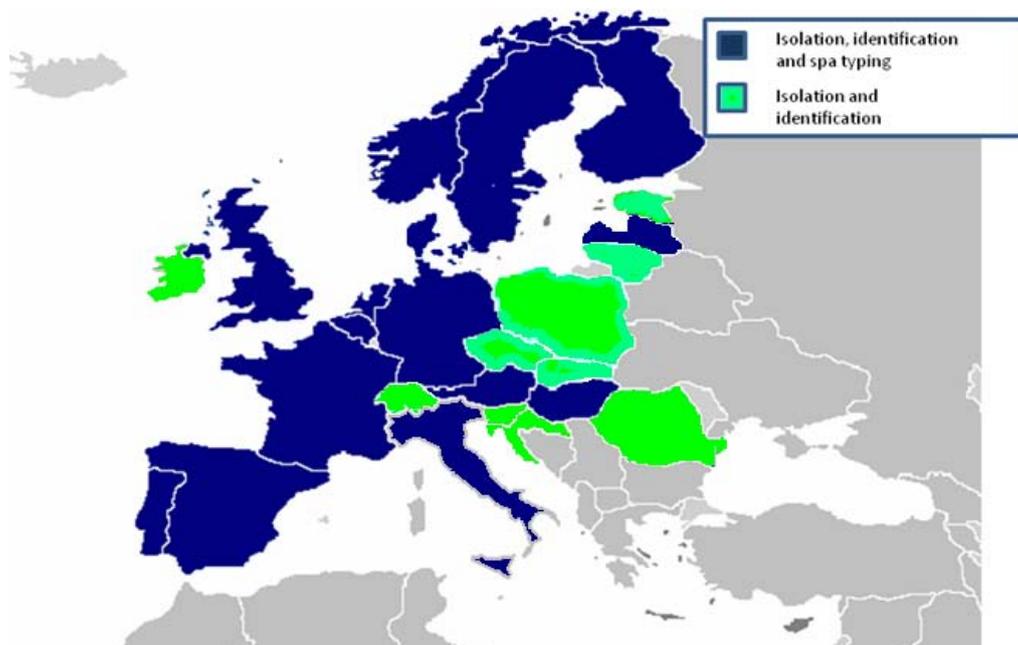
A total of 33 laboratories; including 21 NRLs, seven additional non-NRLs in EU and laboratories from Croatia, Norway, Serbia, Switzerland and Turkey responded to the pre-notification, and were enrolled in the EQAS.

When the deadline for submitting results was reached, 27 laboratories in 25 European countries (including Croatia, Switzerland and Norway) had uploaded data. One of the laboratories decided not to take part (Lab #52) and four laboratories (Labs #37, #40 and #54,

#57) did not upload results data due to technical issues.

One laboratory or more from the following countries provided results to at least one of the EQAS components (also shown below in Figure 1): Austria, Belgium, Croatia, Czech Republic, Denmark, Estonia, Finland, France, Germany, Hungary, Ireland, Italy, Latvia, Lithuania, the Netherlands, Norway, Poland, Portugal, Romania, Slovakia, Slovenia, Spain, Sweden, Switzerland, and UK.

**Figure 1.** Participating countries in MRSA EQAS 2012. Participating countries are marked in green for laboratories participating in MRSA isolation and identification. Dark blue represents countries participating in the *spa* typing.





### 3.1 Methods used by EQAS-participants

Of the 27 laboratories submitting results all (100%) of the laboratories participated in the MRSA isolation and identification module whereas only 18 laboratories (67%) participated in the optional *spa* typing module offered.

Information on the methods used for isolation, identification and typing was collected from the participants through the database.

Most laboratories (n=21) reported that isolation has been performed according to the protocol provided by the EURL-AR for this EQAS and any changes in media, concentrations of antibiotics, etc. were referred. The differences reported by some laboratories from the method described in the original protocol were: use of 6.0% salt (Lab#17), use of 5.0 µg/ml ceftazidime (Lab #55, use lower concentration of aztreonam at 50mg/L (Lab #17) of phenol red mannitol broth with 5.0 µg/ml ceftizoxime and 75 µg/ml aztreonam. In one lab (Lab #17) the selective medium was modified by using a lower concentration of aztreonam of 50 µg/ml and 6.0 % NaCl (instead of 6.5 %) was added to the MH-pre-enrichment broth which was incubated 24h and then further 24h if growth was

negative. Different selective plates for the selective isolation, included CHROMagar MRSA (Mast Diagnostica), BD MRSA Chrom Agar (BD); Chrom ID MRSA Agar (bioMérieux), ORSA (Oxoid) , MRSA Select (Bio RAD) and Baird Parker agar plates. Some laboratories indicated they use different volumes of media in the enrichment steps, and others do perform additional cultures on blood agar to observe typical growth of *Staphylococcus aureus*.

The confirmatory testing of *S. aureus* was performed using the new EURL-AR recommended PCR containing the *mecA*, *mecC*, *pvl* and *spa* gene in most laboratories uploading results (n=16) and the other referred methods for identification included the old EURL-recommended method (n=5), other published (n=1) or in-house PCR and RT-PCR methods (n=4) and one did not reply.

The species identification was mostly performed by PCR, using the EURL recommended PCR primers (n=13), however seven laboratories have still used the old protocol for this purpose. Other methods included using other published or In-house PCR methods in the remaining laboratories that reported methods (n=3) and biochemical reactions (n=2).

**Table 1.** The overall performance of MRSA isolation and identification, 2012.

Isolation of MRSA from swab samples		Correctly classified samples	
Number of performed tests		Number of correct tests N(%)	
n	%	N	%
215	100	200	93
Number of expected negative tests		Number of correctly identified negative tests	
n	%	N	%
81	38	78	96
Number of expected positive tests		Number of correctly identified positive tests	
N	%	N	%
134	62	122	91

### 3.2 MRSA isolation and identification

A total of 215 tests (most laboratories have reported results for all the eight samples and only Lab #23 uploaded results for all samples except for sample nr 4.3) have been performed and the overall result indicate that 200 tests were correct, corresponding to 93%. From the 81 samples expected to be negative 96% (n=78) were correctly assigned, and the remaining three were found false positive. Regarding the samples expected to be found positive, there were 91% of these found positive (n=122) (Table 1).

As described above, most deviations were caused by a lack of sensitivity of the methods used, leading to false negative results in 12 samples in total whereas the results deviating due to false positives were only three. Among the laboratories with two deviations, one participant (Lab # 21) reported that the deviations were due to mistakes occurred in the transcription of the results and reporting phase for one sample and /or cross contamination of one of the samples.

The results per sample show that most deviations were observed for samples EURL-MRSA 4.3 (n=6) and EURL-MRSA 4.8 (n=5) which both contained an MRSA (Graph 1). Four laboratories of the laboratories obtaining deviation for sample 4.3 have obtained deviations by considering it an MSSA. One probable explanation for this is that the EURL-MRSA 4.3 contained an MRSA which carried the new *mecC* gene, and some of the laboratories might not have optimized the methods for its confirmation as methicillin resistant. The two remaining laboratories have not found any isolate in this sample, which might be related to lack of sensitivity in the method used. Three participants did not find any *Staphylococci* strains in sample 4.8 (Labs #2, 22 and 35) and further two have either reported MSSA or CNS as a result for this

sample (Labs #20 and 56), respectively. This might have been partially caused by this sample having been inoculated with a lower inoculum, at circa  $10^5$  cfu per sample. In the stability testing of these samples, Both samples 4.3 and 4.8 showed good stability until the sixth week after preparation (5<sup>th</sup> November 2012) but both could not be retrieved on the eight week (19<sup>th</sup> November 2012). As part of the EQAS instructions, the laboratories had received indications to process the samples as soon as possible after reception, thus we expect the samples would have been processed early after reception and therefore do not consider this late stability loss as cause of deviations. However, the data collected from the laboratories did not contain the date of isolation and therefore we cannot be totally sure if the stability could have interfered in some results. Moreover, there was only one more false negative result for sample 4.1 and all samples had been prepared in the same way and on the same day, following equivalent procedures (except for the lower inoculum in sample 4.8). Regarding sample 4.5 and 4.7, two and one deviations were observed, respectively, meaning that MRSA was found in these samples which were expected to be negative for MRSA. These results must have been caused by either cross contamination or switch between samples or data. (Graph 1).

As for the sample 4.6 containing the methicillin resistant *Staphylococcus pseudointermedius* (MRSP) strain, no deviations were reported, meaning that this strain was not reported wrongly as a MRSA. However, the negative results reported vary between the most correct classification as MRSP (n=14), *mecA* positive but coagulase negative (n=7), *mecA* and *mecC* negative and not *S.aureus* (CNS) (n=1), and no isolate found (n=1).

An internal control was prepared in order to have one strain in common to both MRSA EQAS 2009 and 2010 trials. The internal control was shipped within sample EURL-MRSA 4.1, which contained the same MRSA *spa* t075



strain sent in 2009 as CRL-MRSA 1.3 and in 2010 as EURL-MRSA 2B.7. Only one deviation was found for this sample. Furthermore, unlike last year, there were no issues regarding stability of samples containing this strain.

In general, the individual laboratory results of this MRSA EQAS on isolation and identification of MRSA from swab samples, showed a very good specificity by most laboratories. This was observed in most laboratories provided that only three false positives were observed.

However, the sensitivity was slightly lower and 12 of the samples expected to be positive were misclassified. The remaining laboratories had between one and two deviations only, among the eight samples shipped (Graph 2 and 3). One laboratory, Lab #23 has only submitted the final interpretation for seven of the positive samples (all except 4.3) and has therefore only reported seven correct results, although no deviating results were reported.

### 3.3 *spa* typing of the MRSA strains

The *spa* typing module accounted participation of 18 laboratories, which have uploaded *spa* typing data.

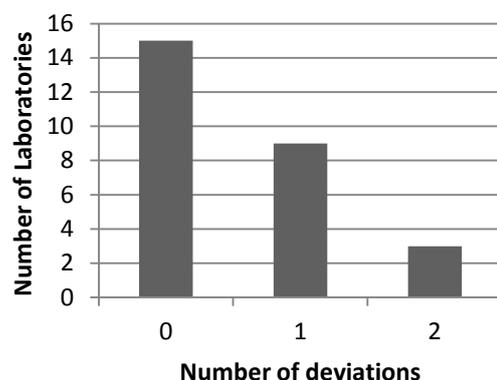
The reported results for *spa* typing included 106 tests and the general results show that 99 (93%) of results were considered correct whereas 7 (7%) deviation were observed. This time four of the participants were able to correctly assign all the eight samples, which is a clear improvement. Other nine laboratories did not have any deviations either, however, these laboratories uploaded results for two to six samples.

In this module, samples EURL-MRSA-4.1, EURL-MRSA-4.2, EURL-MRSA-4.3 and EURL-MRSA-4.4 and EURL-MRSA 4.8 were identified positive for MRSA. Therefore, optional *spa* typing was offered for the respective isolates found, whereas the remaining negative samples EURL-MRSA-4.5, EURL-MRSA-4.6 and EURL-

MRSA-4.7 would not render a positive MRSA isolate for typing and therefore be classified as N/A (not applicable) (Table 2).

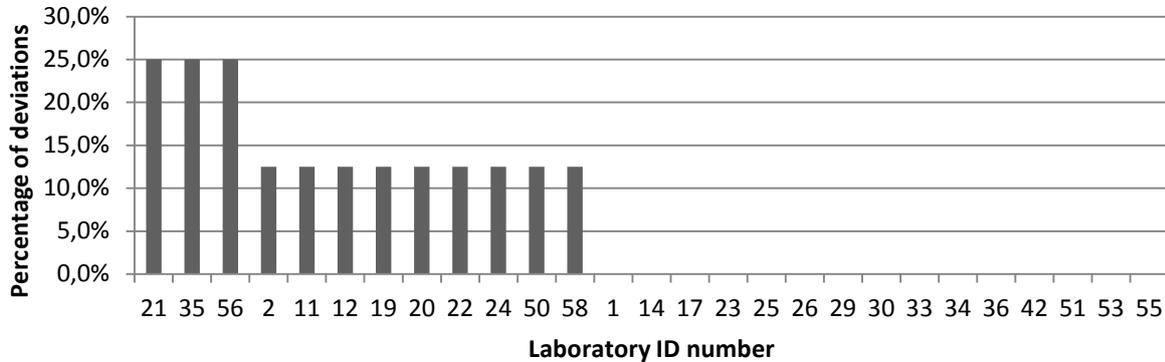
Some of the laboratories have only reported the results regarding the sample previously found positive for MRSA, whereas no more than eight have reported Not applicable results for all the samples considered MRSA negative, as required. In this way the range of uploaded *spa* types diverged from one to eight samples, uploaded by each participating lab.

By laboratory, the results show that 13 laboratories did not have any deviations. Seven participants uploading *spa* typing data have obtained some deviations (ranging from 0-2 deviations per lab), mostly related to the lack of isolation of the expected MRSA (false negatives, which were therefore not *spa* typed) (Graph 4 and 5). Lab #22 has only uploaded results for *spa* typing of EURL-MRSA 4.7 and EURL-MRSA 4.8 which was incorrectly assigned, and has therefore obtained 50% deviation, however representing one deviation only. Laboratories with deviations in the *spa* typing module were as follows Labs #12, 21, 22, 35 and 50. As for the causes of deviation,



**Graph 2:** Number of deviations per laboratory for isolation and identification of methicillin resistant *S. aureus* (MRSA)

**Graph 3:** Deviating results per laboratory. The laboratories were ranked by decreasing percentage of deviation.

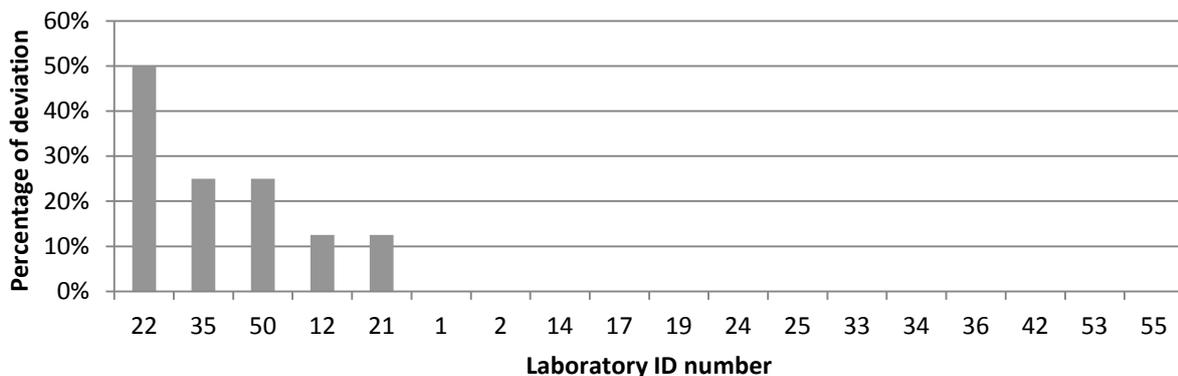


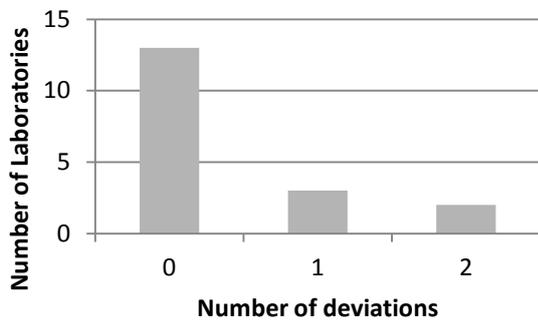
**Table 2.** Results of the *spa* typing trial per sample.

Sample number	N participating laboratories	Repeat succession	expected <i>spa</i> type	correct	Deviating results (number of deviations)
EURL-MRSA 4.1	15	11-19-21-21-12-21-17-34-24-34-22-25	t075	13	N/A (2)
EURL-MRSA 4.2	15	08-16-02-25-02-25-34-24-25	t034	15	None
EURL-MRSA 4.3	14	04-82-17-25-17-25-25-16-17	t843	12	N/A (1) t034 (1)
EURL-MRSA 4.4	15	08-16-02-25-02-25-34-24-24-25	t1793	15	None
EURL-MRSA 4.5	9	None (MSSA)	N/A	8	t127 (1)
EURL-MRSA 4.6	11	None (MRSP)	N/A	11	None
EURL-MRSA 4.7	11	None (blank)	N/A	11	None
EURL-MRSA 4.8	15	08-16-02-25-02-25-34-24-25	t034	13	N/A (2)

N/A- not applicable

**Graph 4-** Deviating results for *spa* typing, per participating laboratory. The laboratories were ranked by decreasing percentage of deviation. Note: Lab #22 has only uploaded results for two *spa* typed samples of which one was found wrong, therefore, showing a 50% deviation, even though it represents only one deviation.





**Graph 5:** Number of deviations per laboratory for *spa* typing.

four of the deviations were caused by lack of isolation of the expected MRSA isolates and uploading a *spa* typing result as Not applicable. One additional deviation was caused by considering *spa* type as Non applicable. The Opposite also happened, by one participant reporting a *spa* type for a *S. aureus* isolated as a false positive. At last one deviation was actually caused by wrong *spa* type assignment. Meaning that the *spa* type reported was different from the expected one.

## 4. Discussion

### 4.1 MRSA isolation and identification

In the 2012 EURL-AR MRSA EQAS trial, the samples were prepared with strains selected based on recent findings and the quantity inoculated was increased 10 times (inoculum of circa  $10^6$  cfu/sample) for the samples EURL-MRSA 4.1, 4.2, 4.3, 4.4, 4.5 and 4.6 and maintained at the main level used in 2011 (approximately  $10^5$  cfu/sample) for sample EURL-MRSA 4.8. This has reduced the problems experienced in the past with lack of sensitivity.

The results were overall very good and both expected negative and expected positive samples were mostly well classified, with few exceptions of 12 false negative and two false positive results. However, the level of contamination of the samples used in this EQAS iteration was rather high, therefore we believe there would be still be a need to further improve the sensitivity of the method as we have seen previously that sensitivity declined

when samples with lower inoculum were analyzed (as observed in MRSA EQAS 2011).

### 4.2 *spa* typing

For *spa* typing, 18 laboratories participated in the trial which indicates a slightly increase in participation. The results uploaded were excellent, with thirteen of the 18 laboratories showing no deviation. The range of uploaded results by the participating laboratories was very broad and most deviating results were caused by lack of isolation of the MRSA, one was caused by lack of *spa* typing, another by typing an *S. aureus* from a false positive isolation and only one deviation was actually caused by wrong *spa* type assignment. Most deviations observed do not demonstrate any problems with the *spa* typing method, but reflect only a small issue concerning possible cross contamination or sample management that might have caused the deviation observed in one of the *spa* types found incorrect (found *spa* type could be from MRSA in another sample from this EQAS).



## 5. Conclusion

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In general, the results of the fourth MRSA EQAS 2012 demonstrate that most participating labs have set up the methods and are able to isolate MRSA from swab samples in a reliable fashion. Furthermore, the identification of MRSA using molecular methods is performed successfully in most the participating laboratories, with excellent specificity, and improved test sensitivities. However the methodology itself still might call for further optimization.

The participation in the *spa* typing module has increased indicating that more laboratories have this method available among the laboratories in Europe. However, still nine laboratories participating in the MRSA EQAS 2012 did not take part in this optional module. This might indicate that these laboratories have

difficulties in performing *spa* typing and/or have not set up this methodology.

The results of this module show that *spa* typing as expected is a reproducible method which did not cause major problems relative to the execution or interpretation in the participating laboratories. Most deviations observed in this module were due to lack of isolation of the MRSA and therefore as a result of false negative results. One additional deviation was due to false positive result in isolation. The only deviation observed which were due to wrong *spa* type assignment might be due to possible switching of samples or cross contamination between samples within the EQAS samples, which again shows the need of controlling the analysis process in every step, to obtain a reliable final result.

## 6. References

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## Appendix 1-EURL-AR MRSA EQAS 2012 pre-notification

### **EXTERNAL QUALITY ASSURANCE SYSTEM (EQAS) 2012 FOR DETECTION OF METHICILLIN RESISTANT *STAPHYLOCOCCUS AUREUS* (MRSA) IN SWAB SAMPLES**

The EURL-AR is pleased to announce the launch of the fourth MRSA-EQAS trial. The EQAS provides the opportunity for proficiency testing, which is considered an important tool for the production of reliable laboratory results of consistently good quality. This EQAS offers detection, identification and typing of MRSA from eight samples which contain a background flora and of which some will contain MRSA. The samples will be swabs in tubes containing transport medium

This EQAS is specifically for designated NRL-ARs and additional designated laboratories performing the selective isolation and identification of MRSA from pig farms. These laboratories do not need to sign up to participate but are automatically regarded as participants. You may contact the EQAS-coordinator, if you wish to inform of changes. If you have not participated in the MRSA EQAS 2011, you are welcome to contact us to sign up for the participation in this EQAS. Participation is free of charge for all above-mentioned designated laboratories.

#### **TO AVOID DELAY IN SHIPPING THE ISOLATES TO YOUR LABORATORY**

Please remember to provide the EQAS coordinator with documents or other information that can simplify customs procedures (e.g. specific text that should be written on the invoice). As means of avoiding passing the deadline we ask you to send us this information already at this stage. For your information, the content of the parcel is UN3373 "Biological Substance Category B".

#### **TIMELINE FOR RESULTS TO BE RETURNED TO THE NATIONAL FOOD INSTITUTE**

Shipment of isolates and protocol: The samples will be shipped in October 2012. The protocol will be provided via our website. This year protocol, as in the previous trials will be based on the protocol used in the baseline studies for the isolation procedure and therefore we would like to ask you to have the same media referred in the baseline protocol and any materials or reagents needed for the selective isolation procedure should be readily available for processing the samples which will need to be processed right upon arrival. The confirmatory PCR method recommended will be modified this year, due to the inclusion of MRSA carrying the novel gene *mecA<sub>LGA251</sub>* (*mecC*). Therefore a new protocol for the PCR will be posted on our website and the *mecC* controls distributed within the shipments of the test samples for this EQAS.

Returning of results: Results must be returned to the National Food Institute by December 14<sup>th</sup> 2012. Upon reaching the deadline, each participating laboratory is kindly asked to enter the password-protected website once again to download an automatically generated evaluation report.

EQAS report: When the EQAS is concluded, the data will be collected in an overall report in which it is possible to see all participants' results in comparison. In the report the laboratories will be coded, thus ensuring full anonymity; only the National Food Institute and the EU Commission will be given access to un-coded results.

**Any comments regarding the EQAS, please contact me by e-mail ([licav@food.dtu.dk](mailto:licav@food.dtu.dk)) or by fax (+45 35 88 63 41).**

Sincerely,

Lina Cavaco

**MRSA EQAS-Coordinator**

## Appendix 2- Participant list

registered	Isolation MRSA	spa typing	Institute	Country
X	X	X	Austrian Agency for Health and Food Safety	Austria
X	X	X	Veterinary and Agrochemical Research Centre	Belgium
X			National Diagnostic and Research Veterinary Institute	Bulgaria
X	X		Croatian Veterinary Institute	Croatia
X	X		SVI Olomouc	Czech Republic
X	X	X	The National Food Institute	Denmark
X	X	X	Estonian Veterinary and Food Laboratory	Estonia
X	X	X	Finnish Food Safety Authority EVIRA	Finland
X	X	X	ANSES (French Agency for Food, Environmental and occupational Health & Safety).	France
X	X	X	Federal Institute for Risk Assessment	Germany
X	X	X	Central Agricultural Office, Veterinary Diagnostical Directorate	Hungary
X	X		Central Veterinary Research Laboratory	Ireland
X	X	X	Istituto Zooprofilattico Sperimentale Delli Regioni Lazio e Toscana	Italy
X	X	X	National Diagnostic Centre of Food and Veterinary Service	Latvia
X	X		National Food and Veterinary Risk Assessment Institute	Lithuania
X	X		Central Veterinary Institute of Wageningen	Netherlands
X	X	X	Faculty of Veterinary Medicine Utrecht	Netherlands
X	X		Food and Consumer Product Authority (VWA)	Netherlands
X	X	X	Veterinærinstituttet	Norway
X	X		National Veterinary Research Institute	Poland
X	X	X	Faculdade de Medicina Veterinária- UTL	Portugal
X			Laboratório Nacional de Investigação Veterinária (LNIV)	Portugal
X	X		Institute for Diagnosis and Animal Health	Romania
X			Institute of Veterinary Medicine of Serbia	Serbia
X	X		State Veterinary and Food Institute (SVFI)	Slovakia
X	X		National Veterinary Institute	Slovenia
X	X	X	Complutense University of Madrid	Spain
X	X	X	National Veterinary Institute, SVA	Sweden
X	X	X	Vetsuisse faculty Bern, Institute of Veterinary Bacteriology	Switzerland
X			National Food Reference Laboratory	Turkey
X	X	X	The Veterinary Laboratory Agency	United Kingdom

## Appendix 3 –Expected results MRSA EQAS 2012

<b>Sample</b>	<b><i>mecA</i></b>	<b><i>mecC</i></b>	<b><i>spa</i> type</b>	<b>MRSA status sample</b>
<b>MRSA EQAS- 4.1</b>	positive	negative	t075	Positive
<b>MRSA EQAS- 4.2</b>	positive	negative	t034	Positive
<b>MRSA EQAS- 4.3</b>	negative	positive	t843	Positive
<b>MRSA EQAS- 4.4</b>	positive	negative	t1793	Positive
<b>MRSA EQAS- 4.5</b>	negative	negative	N/A (t127)	Negative (MSSA)
<b>MRSA EQAS- 4.6</b>	positive	negative	N/A	Negative (MRSP)
<b>MRSA EQAS- 4.7</b>	N/A	N/A	N/A	Negative (blank)
<b>MRSA EQAS- 4.8</b>	positive	negative	t034	Positive

N/A- not applicable



## Appendix 4- Protocol for MRSA EQAS 2012

For selective isolation, detection and typing of methicillin resistant *Staphylococcus aureus* (MRSA) from swab samples.

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1	INTRODUCTION .....	1
2	OBJECTIVES .....	2
3	OUTLINE OF THE MRSA EQAS 2012.....	2
3.1	SHIPPING, RECEIPT AND STORAGE OF STRAINS .....	2
4	DETECTION AND IDENTIFICATION OF MRSA FROM SWAB SAMPLES .....	2
4.1	SELECTIVE ENRICHMENT AND ISOLATION .....	2
4.2	IDENTIFICATION OF MRSA .....	3
4.3	SPA TYPING .....	3
5	REPORTING OF RESULTS AND EVALUATION .....	3
6	HOW TO ENTER RESULTS IN THE INTERACTIVE DATABASE.....	4

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### 1 Introduction

One of the tasks as the European Union Reference Laboratory for Antimicrobial Resistance (EURL-AR) is to organise and conduct External Quality Assurance Systems (EQAS's). Usually the EQAS's have been focused on susceptibility testing, however, due to the recent concern about FA-MRSA (farm acquired methicillin resistant *Staphylococcus aureus*) detected in European farms and the recently performed baseline screening performed aiming at the detection of FA-MRSA in pig farms, we have now decided to continue the MRSA EQAS to evaluate the proficiency of the laboratories on the selective isolation procedures for detection of MRSA, including their confirmatory testing and *spa* typing.

As referred in the pre-notification, this EQAS is designed specifically for designated NRL-ARs and additional designated laboratories performing the selective isolation and identification of MRSA from pig farms.

**In this MRSA EQAS we have prepared swab samples, which should be processed according to the description found in this protocol.**



## 2 Objectives

The main objective of this EQAS is to support laboratories in assessing and if necessary improve the quality of selective isolation for detection, confirmatory testing and *spa*-typing of MRSA. Furthermore, to assess and improve the comparability of the baseline screening data reported to EFSA by different laboratories within the EU.

## 3 Outline of the MRSA EQAS 2012

### 3.1 Shipping, receipt and storage of strains

In October 2012 all EU appointed National Reference Laboratories (or the alternative laboratories that have processed the MRSA baseline sample analysis) will receive a parcel from the EURL-AR containing eight swab samples which contain a background flora and might contain MRSA (some samples will be negative, or contain other methicillin susceptible or resistant *Staphylococcus* strains).

**NOTE:** The samples should be received and processed immediately upon arrival, or as quickly as possible to assure the stability of the samples. Please take note of the day you start the isolation procedure and provide this information in our database.

## 4 Detection and identification of MRSA from swab samples

### 4.1 Selective enrichment and isolation

1. In the laboratory, open carefully the tubes containing the swab samples in transport medium (in a laminar air flow bench and using protective gloves) and inoculate each swab into a tube containing 10 ml of Mueller-Hinton broth supplemented with 6.5 % NaCl. Mix thoroughly.
2. Incubate at 37 °C for 16-20 h.
3. Take one millilitre of this first pre-enrichment culture and then inoculate into 9 ml Tryptone Soya Broth with 3.5 mg/L cefoxitin and 75 mg/L aztreonam. Mix thoroughly.
4. Incubate for 16-20 h at 37 °C.
5. Take one loop-full (10µl loop) of the latter selective enriched culture and streak onto a Brilliance MRSA Chromogenic Agar plate (Oxoid) and a blood agar plate.
6. Incubate 24-48 h at 37 °C.



7. Observe the colony morphology (size and coloration) of the colonies obtained on the Brilliance MRSA Chromogenic Agar plate, choose up to five blue colonies indicative for being MRSA and isolate them **from the MRSA selective plate** onto a new blood agar plate. The additional blood agar plate obtained from inoculation of the selective broth is used for parallel observation with the MRSA plate to double-check the colony morphology (to observe typical *S. aureus* morphology and haemolysis), but should not be used for isolation.
8. Incubate the new blood agar plates containing the isolates during 24h at 37°C.
9. Observe the colony morphology of the isolates on the blood agar plate (colour, appearance, haemolysis). Check for purity and re-isolate if necessary.
10. Presumptive isolates of methicillin resistant *Staphylococcus aureus* should at this stage either be stored under appropriate conditions (–80°C) for later identification and characterisation or processed immediately.

## 4.2 Identification of MRSA

Presumptive MRSA isolates should be confirmed as *Staphylococcus aureus* isolates carrying the *mecA* gene or the *mecC* gene (previously known by *mecA<sub>LGA251</sub>*) by PCR. There is no need to perform other screening methods (such as screening with either oxacillin or cefoxitin) if the isolates have been obtained from selective isolation, thus, the presence of the *mecA* or *mecC* gene can be directly confirmed by PCR amplification. The species identification is simultaneously confirmed by using the new EURL-AR recommended multiplex PCR protocol including the amplification of the *spa* gene (specific for *Staphylococcus aureus* species and which may be sequenced for *spa* typing), the *mecA*-gene and the *mecC* gene (encoding methicillin resistance) and the *pvl* gene (encoding the Panton Valentine Leukocidin), which should be performed according to the new EURL-AR recommended protocol (<http://www.eurl-ar.eu/233-protocols.htm>).

## 4.3 *Spa* typing

*Spa* typing of the MRSA isolates may be performed additionally if the laboratory has the capacity to perform and analyse the *spa*- typing data. In case you decide to include *spa* types in the data submitted, these will be evaluated on the accuracy of the *spa* typing.

## 5 Reporting of results and evaluation

Fill in your results in the enclosed test form. Please enter your results into the interactive web database. Please read the detailed description below before entering the web database. When you enter the results via the web, you will be guided through all steps on the screen and you will



immediately be able to view and print a submission report of your results. Please submit results by latest **December 14<sup>th</sup> 2012**. After the deadline, the database will be closed and you will be able to view and print an automatically generated report evaluating your results.

If you experience difficulties entering the data, please return results by e-mail, fax or mail to the EURL-AR.

All results will be summarized in a report which will be made available to all participants. The data in the report will be presented with laboratory codes. A laboratory code is known to the individual laboratory, whereas the entire list of laboratories and their codes is confidential and known only to the EURL-AR and the EU Commission. All conclusions are public.

If you have any questions, please do not hesitate to contact the MRSA EQAS Coordinator:

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## 6 How to enter results in the interactive database

Please read this passage before entering the web page. Before you go ahead, you need your test form.

You are able to browse back and forth by using the forward and back keys or click on the EURL logo.

You enter the EURL-AR EQAS 2012 start web page (<http://thor.dfvf.dk/eurl>) then write your username and password in low cases and press enter. Your username and password is the same as in the previous EQAS's arranged by The National Food Institute. If you have problems with the login please contact us.

Click on "[MRSA tests](#)" to start entering your data regarding the MRSA EQAS.



Please read carefully the instructions on the webpage and start by answering to the questionnaire on the work performed in your laboratory relative to MRSA by clicking on "[General MRSA questionnaire](#)".

Please choose the options that more correctly describe your work on MRSA and before you leave this page click on "[Save page](#)" which will take you back to the previous menu.

Then, we will ask you to fill in the methods used in a second page which you will reach by clicking on "[Methods for MRSA test samples.](#)"

In the next page you navigate to fields with the Tab-key and mouse.

Fill in what kind of method you have used for the selective isolation and confirmation of MRSA in this EQAS.

Click on "[Save and go to the next page](#)"

In the data entry pages for each sample "[EURL-MRSA 4.1, ...](#)", you enter the obtained results for each of the MRSA EQAS samples.

If you wish so, you will have the option to include the *spa*-typing results.

If you did not perform *spa* typing leave the field blank, in case you have obtained an isolate but it is not a methicillin resistant *Staphylococcus aureus*, choose "not applicable (N/A)", otherwise if you have performed the *spa* typing, choose the *spa* type from the list. Click on "[save and go to next page](#)" to navigate to the next sample results, until you finish to upload all your data.

From the last result sheet you get into the general menu, from where you can review the input pages, approve your input and finally see and print the evaluated results:

Browse through the pages and make corrections if necessary. Remember to save a page if you make any corrections. If you save a page without changes, you will see an error screen, and you just have to click on "[back](#)" to get back to the page and "[go to next page](#)" to continue.

At the end, approve your input. Be sure that you have filled in all the results before approval, as **YOU CAN ONLY APPROVE ONCE!** The approval blocks your data entry in the interactive database, but allows you to see the submitted results.



MRSA External Quality Assurance System (EQAS) 2012

**Appendix 5- Example of Test forms MRSA EQAS 2012**

Name:
Name of laboratory:
Name of institute:
City:
Country:
E-mail:
Fax:

How many samples did you process in 2011 for MRSA detection? (Choose only one option)

- less than 50
- 50-100
- 101- 200
- 201-400
- more than 400

Which kind of samples did you process in your laboratory for MRSA detection in 2011?

- dust swabs
- nasal swabs
- skin swabs
- faecal samples
- other matrices      Specify:

Which was the origin of the samples processed for MRSA detection in 2011?

- from humans
- environmental
- from animals if you check this answer, please answer the next question
- other .      Specify:

The samples processed from animals included samples obtained from which species:

- pigs
- cattle
- poultry
- pets
- other .      Specify:

Any other Comments:



MRSA External Quality Assurance System (EQAS) 2012

**TEST FORM – MRSA methods**

Method used for selective isolation of MRSA in this EQAS:

Selective isolation procedure using the exact protocol

different enrichment, agar plates or incubation conditions  
If you used different pre enrichment please indicate:

Salt concentration used in the Müller Hinton broth: %

Other medium:

If you used different enrichment please indicate

Cefoxitin concentration: mg/L

Aztreonam concentration: mg/L

Other modifications: medium antimicrobials or concentrations:

If you used different selective agar plates

Different agar brand:

If you used different incubation conditions

Specify: pre enrichment °C/ h;

selective enrichment °C/ h;

selective plating °C/ h

Method used for confirmatory testing of MRSA (choose only one option)

PCR using the new EURL recommended multiplex PCR protocol (*spa*, *mecA*, *mecC*, and *pvl*)

PCR using the old EURL multiplex PCR protocol (16S rDNA, *mecA* and *nuc*)

modified protocol but same multiplex PCR primers

other published PCR method

in- house PCR method

Describe if you did not use the new EURL recommended method and justify your choice:

Method used for confirmation of species identification (choose only one option)

PCR using the new EURL recommended multiplex PCR protocol (*spa*, *mecA*, *mecC*, and *pvl*)

PCR using the old EURL multiplex PCR protocol (16S rDNA, *mecA* and *nuc*)

biochemical methods

other published PCR method

in-house PCR method

Describe if you did not use the EURL recommended method and justify your choice:



## MRSA External Quality Assurance System (EQAS) 2012

**TEST FORM****Entry data Sample EURL-MRSA 4.X****Date the isolation procedure was started:****Please describe the results you have observed regarding this swab sample:**

Growth in pre-enrichment:

Yes / No 

Growth in selective enrichment:

Yes / No 

Growth in MRSA selective plates:

Yes  / No **Please describe the growth observed on MRSA selective plates?** (choose only one option)

- Mixed culture containing typical colonies
- Mixed culture without typical colonies
- Pure culture of typical colonies
- Pure culture without typical colonies
- No growth

**Results of confirmatory PCR and species identification:** (choose only one option)

- no isolates tested, sample negative
- mecA* positive, but coagulase-negative Staphylococci (MRCNS)
- mecA* positive, but *S. pseudintermedius* (MRSP)
- mecA* and *mecC* negative and not *S. aureus* (CNS)
- mecA* and *mecC* negative, *S. aureus* (MSSA)
- mecA* positive, *S. aureus* (MRSA)
- mecC* positive, *S. aureus* (MRSA)

**Spa Typing (optional): spa type** (choose only one option)

- Not performed
- Not applicable (N/A)
- t011
- t021
- t034
- t075
- t108
- t127
- t337
- t524
- t571
- t843
- t899
- t1333
- t1430
- t1730
- t1793
- t2510
- t2922

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