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CBC Corrections-RO

Document Type: Procedure

I. PURPOSE AND OBJECTIVE:

This procedure explains how to correct for various factors that may cause spurious values on automated Hematology cell counters.

II. PRINCIPLE:

A. A number of unusual factors present in patient samples may produce erroneous results on automated cell counters. This procedure explains how to correct for various factors that cause spurious values (e.g., high WBC counts, cold agglutinins, lipemia, icteria, cryoglobulins, nucleated RBCs, clumped platelets, platelet satellitosis, giant platelets, microcytic RBCs, RBC fragments, hemolysis, and lyse resistant RBCs).

B. Unknown interferences may also adversely affect results obtained from the instruments. It may be necessary to use a combination of correction procedures to obtain valid results.

III. ACRONYMS:

A. Laboratory Information System (LIS)

B. Work Area Manager (WAM)

C. White Blood Cell (WBC)

D. Red Blood Cell (RBC)

E. Hemoglobin (HGB)

F. Hematocrit (HCT)

G. Mean Corpuscular Hemoglobin Concentration (MCHC)

H. Platelet (PLT)

I. Mean Cell Volume (MCV)

J. Mean Corpuscular Hemoglobin (MCH)

K. Nucleated Red blood Cell (NRBC)

IV. SPECIMEN COLLECTION AND HANDLING:

Type	Whole blood collected in a 4 mL vacutainer. This is the preferred sample. OR Capillary blood collected in a microtainer.	
Anticoagulant:	K_2EDTA	
Amount	Whole blood	Minimum sample size is 2.0 mL. Optimum sample size is 4.0 mL.
	Capillary blood	Minimum sample size is 300 mcL. Optimum sample size is 500 mcL.
Special Handling	Specimen must be well mixed for minimum of 2 minutes before being analyzed. Rim all microtainer specimens with wooden applicator sticks for clots.	
Timing	Specimen is stable for 8 hours at room temperature (72 hours at 4^{o}C).	
Criteria for Unacceptable specimens	Specimens containing clots or inappropriate volumes are unacceptable and must be redrawn.	

V. SUPPLIES:

A. Heat block: 37^{o}C.

B. HemataStat II microhematocrit centrifuge.

C. **CellPack:** Diluent used to make 1:5 dilution due to numerical results or interpretive messages. A 1:5 dilution is made by adding 100 mcL whole blood to 400 mcL of Sysmex CellPack. Run dilution in capillary mode within 30 minutes. Results will automatically be multiplied by 5. Verify that the RBC count matches original RBC +/- 0.10. Store CellPack between 15-30^{o}C. Opened, CellPack is stable for 60 days.

VI. CALIBRATION:

Most corrections are performed via visual, temperature, or mathematical means. See Microhematocrit procedure for respective calibration directions.

VII. QUALITY CONTROL (QC):

Since most corrections are performed via visual, temperature or mathematical means, no control materials are available. The manual microhematocrit is the only procedure where a control is run. (See Microhematocrit-RO procedure).

VIII. PROCEDURE:

A. **HIGH WBC COUNTS - 485.0 x 10^9/L or higher:**

1. High numbers of WBCs can cause a false decrease in the WBC reported.To correct a

high WBC count:

a. WAM holds results.

b. Perform a 1:5 dilution of the specimen (Add 100 mcL of specimen to 400 mcL of CellPack diluent.)

c. Run on capillary mode of instrument within 20 minutes of setup. (See CBCD and Reticulocyte procedure). As a QC check, verify that the RBC count agrees within +/- 0.1 of undiluted sample. If not, rerun sample. If still not acceptable, remake dilution. Notify supervisor if unable to resolve.

d. When run in the capillary mode, the instrument automatically multiplies the results by 5 and sends them to WAM.

e. Accept the WBC count if the RBC count agrees +/- 0.1 of original RBC count.

f. In WAM, add internal comment *"By dilution"*.

i. **NOTE:** The HGB and WBC are measured in different chambers on Sysmex analyzers, so there is no WBC interference with the HGB result.

ii. **NOTE**: Do not use differential results from run on diluted specimen.

B. **COLD AGGLUTININS:**

1. Cold agglutinins cause the spontaneous agglutination of RBCs at temperatures lower than 37^{o}C. The degree of agglutination is dependent on the cold agglutinin titer.

2. Due to the fact that the Sample Rotor Valve (SRV) on the Sysmex analyzers is warmed to 37^{o}C, only strong cold agglutinins will be apparent. The strong cold agglutinins will cause spurious low RBC counts due to counting micro-agglutinates as single cells. Also, the MCV will be falsely elevated due to micro-agglutinates being sized as a single large cell. The hemoglobin reading is usually correct. Also, with a correct hemoglobin value and low hematocrit, the MCHC (Hgb/HCT x 100 = MCHC) and the MCH (MCV x MCHC/ 100 = MCH) will be spuriously elevated.

3. Check for cold agglutination on all bloods with:

a. "MCHC" greater than 38%;

b. smear and hematology analyzer MCV do not agree (**NOTE:** MCV does not necessarily have to be macrocytic to be suspicious of a cold agglutinin);

c. smears with RBC agglutinates; or

d. any blood you are suspicious of because of a "lacy" appearance in the tube or on the slide. If b, c, or d is present, follow cold agglutinin procedure, regardless of MCHC value.

4. To correct for the effect of a cold agglutinin:

a. Place the blood in a 37^{o}C incubator (e.g., heating block or coagulation water bath) for **at least 15 minutes.**

b. Mix specimen thoroughly and rerun the blood through the open mode of the hematology analyzer. (So specimen doesn't cool down).

c. Report the 37^{o}C results (for all parameters) if the MCHC is feasible. (See Figures 1 and 2 below.)

d. In WAM, add *"Possible Cold Agglutinin"* comment by double clicking on COM field next to MCHC result and selecting HE03, then SAVE.

e. For a cold agglutinin specimen that has instrument flags/lab values requiring microscopic review: If RBC agglutinates are present, make warmed smears to see if the agglutinates go away upon warming. Regardless of which smears (room temp or warmed) exhibit agglutinates, report *"RBC agglutinates present"*. If case needs further review by a pathologist, submit both sets of clearly marked slides to the pathologist.

i. **NOTE:** Cold agglutinins must **always** be incubated at 37°C before being reporting as such.

Figure 1 - Room Temperature Specimen

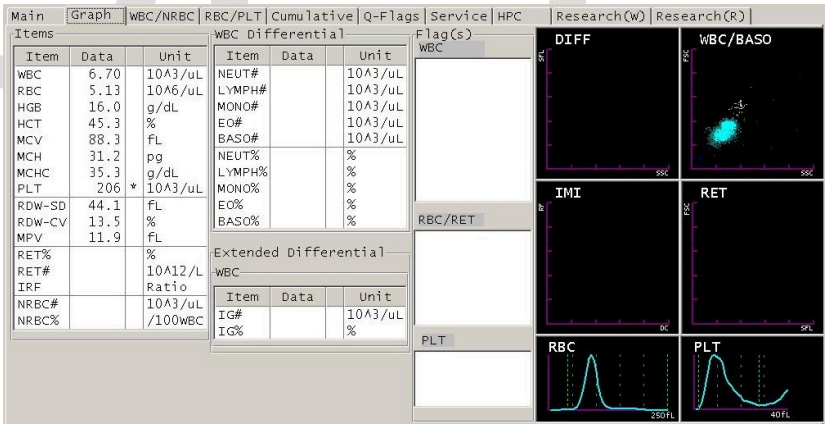


Figure 2 - 37°C Warmed Specimen

5. If a cold agglutinin does not resolve using these measures, some parameters may be reported:

a. If it is determined there is **no optical interference with the HGB** (no interference due to lipemia, icteria, or hemolysis)**,** the HGB may be reported out from the **warmed** sample. A **spun HCT** must be performed, and the **recalculated MCHC must be less than or equal to 38** to check the reliability of

these parameters. **Ensure that the HGB and HCT correlate and review for consistency with patient history.** The HGB, spun HCT and MCHC may then be reported.

b. WBC, PLT, and differential may be reported. **Verify the WBC, PLT, and differential on smear for the first occurrence** and on future occurrences if any delta checks or flags pertaining to these parameters are present.

C. **LIPEMIA**

1. Lipemic plasma can cause a falsely elevated hemoglobin due to a cloudy SLS-hemoglobin solution which decreases the amount of transmitted light through the solution to the photocell. (Lipemia usually occurs in patients with hyperchylomicronemia whose triglycerides are greater than 1,000 mg/dL.)
2. Lipemia should be suspected on all bloods with: (a) a lacy appearance of blood smear or (b) an MCHC over 36.5. Action must be taken on MCHCs greater than 38%.
3. To check for lipemia, spin blood for approximately 5 minutes (or let settle for approximately 10-15 minutes) and visually check plasma layer for characteristic milky appearance.
4. To correct for lipemia perform either of the following procedures:
    a. **Plasma Replacement:**
        i. Spin down a **PORTION** of the blood specimen at **2000** rpm for 5 minutes.
        ii. Mark the top (meniscus) of the plasma level.
        iii. Carefully remove **most, but not all,** of the plasma.
        iv. Replace the plasma with the same amount of Cell Pack diluent (add diluent up to the mark).
        v. Mix the sample and cycle through the instrument.
        vi. Use the RBC result as a guide to verify proper re-dilution of the specimen.
        vii. If the RBC result is within +/- 0.10 of the original RBC, report the HGB from the re-diluted sample.
        viii. Recalculate the MCH and MCHC using the **new** HGB and **original** RBC and HCT.
        ix. In WAM, add *"Corrected for Lipemia"* comment by double clicking on COM field next to MCHC result field and selecting HE02, then SAVE. (See Note below.)
            a. **NOTE:** To avoid any math errors, have second technologist verify calculations.
    b. **Plasma Blank:**
        i. Spin a portion of the blood.
        ii. Perform a hemoglobin on the **PLASMA** using the hematology analyzer open mode.
        iii. Use the following formula to calculate the correct hemoglobin:

a. **Corrected HGB = Original HGB - [(1-{Original HCT/100}) x Plasma HGB]**

b. **Example:**

Results on Original Run

WBC	5.1
RBC	4.03
HGB	16.1
HCT	39.3
MCV	97.5
MCH	40.0
MCHC	41.3
PLT	250

Calculation for Corrected Hemoglobin (HGB)

Plasma HGB	4.5
Corrected HGB	= 16.1 - [(1-[39.3/100]) x 4.5] = 16.1 - [(1-0.393) x 4.5] = 16.1 - [0.607 x 4.5] = 16.1 - 2.7315 = 13.4

iv. Recalculate the MCH and MCHC using **new** HGB and **original** RBC and HCT.

a. **Example**:

Corrected Report

WBC	5.1
RBC	4.03
HGB	13.4
HCT	39.3
MCV	97.5
MCH	33.3
MCHC	34.1
PLT	250

v. In WAM, add *"Corrected for Lipemia"* comment by double clicking on COM field next to MCHC result field and selecting HE02, then SAVE.

(See Note below.)

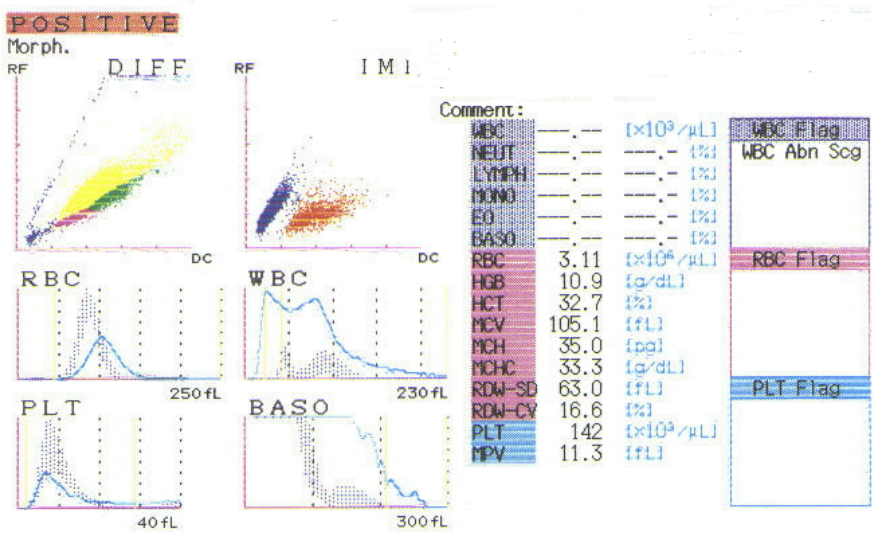
a. **NOTE:** To avoid any math errors, have second technologist verify calculations.

D. **ICTERIA (HYPERBILIRUBINEMIA):**

1. If interference from bilirubin is suspected, a correct hemoglobin value may be obtained by performing one of the correction procedures described on the previous page for LIPEMIA and free-texting *"Corrected for ICTERIA"* as an internal comment.

E. **CRYOGLOBULINS:**

1. Cold-precipitated plasma immunoglobulins (cryoglobulin) or fibrinogen (cryofibrinogen) in a blood sample can cause a falsely increased WBC count with excessively high takeoff at 35 fL resulting in a voteout (-----) and/or * code for the WBC parameter. Also, the RBC count, hemoglobin, hematocrit and platelet count may be slightly increased along with a slightly decreased MCV. (See results in Figures 3 and 4 below.)
2. Aggregates of blue staining amorphous material may be seen on Wright stained smears. Increased levels of cryoglobulin may be associated with myeloma, macroglobulinemia, lymphoproliferative disorders (e.g. CLL), metatastic tumors, autoimmune disorders, infection, and as an idiopathic disease. Cryofibrinogen has been observed in association with many disorders including myeloma, carcinoma, leukemia, aneurysm, pregnancy, the use of oral contraceptives, thromboembolic phenomena, diabetes, and as an essential disease.
3. To correct for the effects of a cryoglobulin:
    a. Warm specimen to 37°C for a **minimum** of 15 minutes.
    b. Rerun through the hematology analyzer open mode.
    c. Report the 37°C results (for all parameters) if the results are feasible **and** no parameter flags are present.
    d. In WAM, free-text internal comment *"Possible cryoglobulin"*.



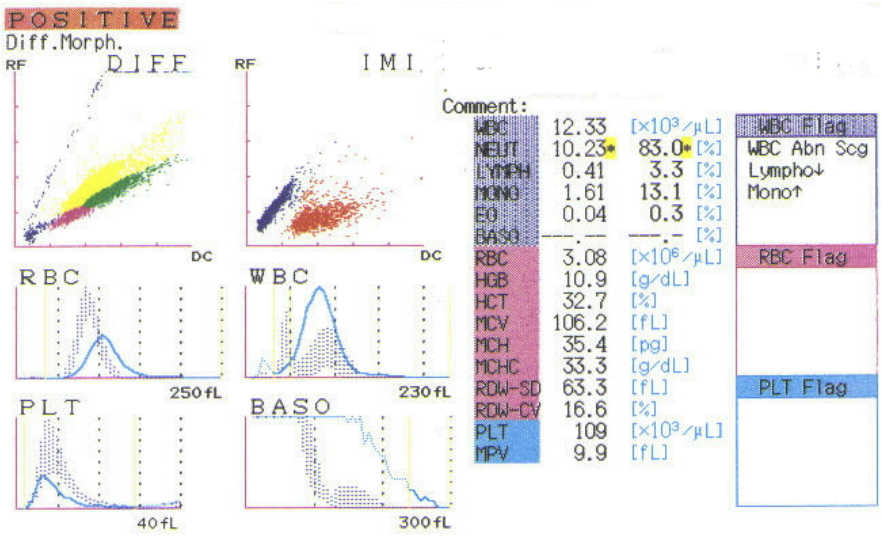
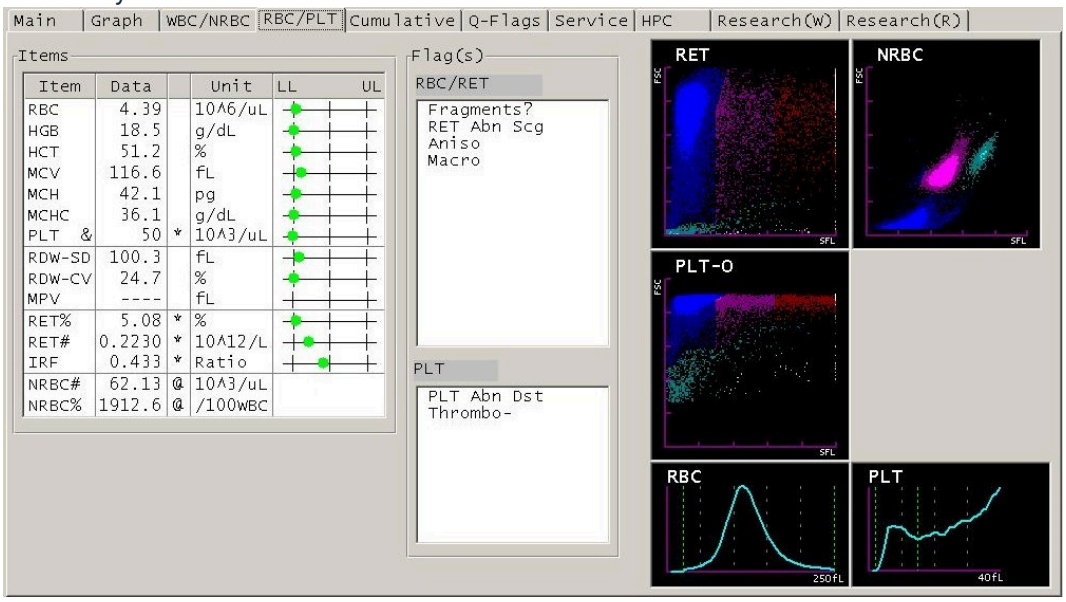


Figure 4 - Warmed Specimen

F. **NUCLEATED RBCS:**

1. NRBCs are a reportable parameter from the Sysmex XE-Series analyzers. If an "NRBC?" flag is triggered, the specimen will reflex for a numerical value and corrected WBC count and corrected lymphocyte. The comment *"WBC corrected for NRBCs"* will automatically be added to the WBC field by WAM. WBH XE-Series (2100 and 5000) NRBC counts are linear to 464 per 100 WBC. Figure 5 is an example of an NRBC outside of linearity.



2. If performing a scan and greater than 5 NRBCs are seen that were not reported by the hematology analyzer, report corrected WBC as follows:
    a. If sufficient specimen remains, order CBCWD and Retic in WAM or on hematology analyzer then run specimen to obtain corrected WBC and NRBC value. Correct report in Beaker. Add comment *"WBC corrected for NRBC"* to WBC field. Call corrected WBC to physician or nursing unit as applicable.
    b. If insufficient specimen remains, perform differential using Downtime Cell Counter software loaded onto the computers at the morphology bench. The software program will automatically correct WBC count and correct the differential absolutes. (Make sure you enter the WBC count in the cell counter so that the NRBCs will calculate. Correct report in Beaker.) Add comment *"Corrected for NRBCS"* to the WBC field. (See calculations below.)
    c. Calculations:

Calculations

Original absolute # x $\frac{\text{Corrected WBC}}{\text{Original WBC}}$ = New absolute #
$\frac{\text{Original absolute \#}}{\text{100 + NRBC}}$ x 100 = New absolute #

G. **PLATELET CLUMPING:**
1. Platelet clumping can result in **spurious low** and **widely fluctuating platelet counts** on hematology instruments.
2. Platelet clumping may occur because of poor collection technique resulting in the presence of micro clots, delays in mixing the blood and anticoagulant, the presence of platelet agglutinins, or EDTA-induced clumping.
3. Check for platelet clumping by first checking for a clot. Document as internal comment in WAM. Then examine a peripheral smear on all bloods with the following instrument flags or results:
    a. platelet count less than 75 bill/L
    b. platelet clump(s) flag
    c. platelet clumps flag
    d. platelet delta check (decrease only)
4. The WAM holds results.
5. To correct for platelet clumping:
    a. Examine Wright stained smear for clumping - particularly at the **feathered** and **side (lateral) edges**.
    b. If platelet clumps are seen:
        i. Scan peripheral smear to determine if WBC estimate matches instrument count.
        ii. If estimate does not match instrument count, add comment *"WBC may be inaccurate due to WBC/PLT interference"* to **WBC comment**

field.

iii. Note approximate platelet estimate from stained smear (e.g., ADQ, INC, DEC); and

iv. In WAM Result Validation tab, remove platelet result by clicking on Platelet Result field, then clicking Delete. Double click on the Platelet Result field. A window opens. Select the appropriate clumped platelet comment that correlates with the platelet estimate:

   a. *"Platelets clumped in EDTA, appear adequate on smear."*

   b. *"Platelets clumped in EDTA, appear decreased on smear."*

   c. *"Platelets clumped in EDTA, appear increased on smear."*

v. Click STORE and Validate All.

vi. See example below (Figure 6 and Figure 7).

vii. **Note:** If platelet clumps are present but are insignificant, report instrument count and add internal WAM comment: *"Insignificant platelet clumps present."*

c. **See Section X, Note C for another technique for handling platelet clumping.**

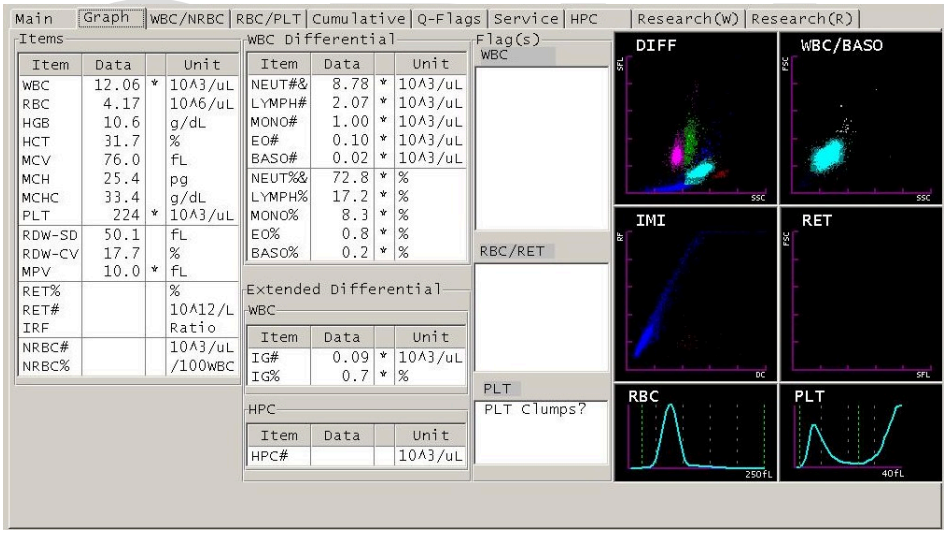


Figure 6 - Instrument Count with Platelet Clumps Flag

Complete Blood Count (CBC) W Diff

Complete Blood Count w/ Diff (Final result)

Test Name	Result		Ref. Range	Units	Resulting Lab:
WBC	**12.1**	**(H)**	3.5-10.1	bil/L	BLRYO
RBC	**4.17**	**(L)**	4.31-5.48	tril/L	BLRYO
Hemoglobin	**10.6**	**(L)**	13.5-17.0	g/dL	BLRYO
Hematocrit	**31.7**	**(L)**	40.1-50.1	%	BLRYO
MCV	**76**	**(L)**	80-100	fL	BLRYO
MCH	**25**	**(L)**	28-33	pg	BLRYO
MCHC	33		32-36	g/dL	BLRYO
RDW-CV	**18**	**(H)**	12-15	%	BLRYO
Platelets					BLRYO
Platelets Clumped in EDTA, appear adequate on smear					
Neutrophils	**8.8**	**(H)**	1.6-7.2	bil/L	BLRYO
Lymphocytes	2.1		1.1-4.0	bil/L	BLRYO
Monocytes	**1.0**	**(H)**	0.0-0.9	bil/L	BLRYO
Eosinophils	0.1		0.0-0.4	bil/L	BLRYO
Basophils	0.0		0.0-0.1	bil/L	BLRYO
Immature Granulocytes	**0.09**	**(H)**	0.00-0.04	bil/L	BLRYO
Immature Granulocyte %	0.7			%	BLRYO

Results verified at 7/13/2021 1014.

Non-Automated Differential/Morphology (Final result)

Test Name	Result	Ref. Range	Units	Resulting Lab:
RBC Morphology	Unremarkable			BLRYO
Platelet Estimate	Adequate	Adequate		BLRYO

Figure 7 - LIS Final Report with PLT Clumping Comment

H. **PLATELET SATELLITOSIS:**

1. Platelet satellitosis is the adherence of platelets to neutrophils and is seen only in EDTA-anticoagulated blood. Platelet satellitosis can cause spurious low or fluctuating platelet counts on hematology instruments. In addition, spurious neutropenia can occur in white cell differentials performed on wedge blood smears.
2. Check for platelet satellitosis by examining **feathered edges** of a blood smear on all bloods with:
    a. platelet counts less than 75 bill/L or
    b. widely different platelet results from previously reported values.
3. To correct for platelet satellitosis:
    a. Note approximate platelet estimate (ADQ, INC, DEC) from stained smear.
    b. Delete PLT result from WAM and replace with the statement: ***"Platelet satellitosis in EDTA - Appear (platelet estimate)".***
    c. Report hematology analyzer differential if scan agrees; otherwise perform manual diff.
    d. A numerical platelet count may be attempted, if physician requests, by re-collecting in sodium citrate (blue-top tube). Multiply PLT results by 1.1 to correct for dilution effect. If sodium citrate does not correct problem, remove PLT value from WAM and add comment *"Unable to report due to xxx"*.

I. **MICROCYTIC RBC OR RBC FRAGMENTS:**

1. Scan the peripheral smear for the presence of fragmented RBCs and other RBC abnormalities.
2. If extremely microcytic RBC are present:

a. Estimate the PLT count.

b. If the Retic (RET) was not ordered, there may be an Action Message stating, “Count RET Channel”. You may reanalyze the specimen in the CBC + RET mode so that an optical PLT will be run in the Retic channel. The XE judges whether or not to switch to report the PLT-O.

J. **MCHC >38.0**: Refer to CBCD and Reticulocyte – Sysmex XE5000 procedure for MCHC procedure.

K. **GIANT PLATELETS:**

1. Per Sysmex Hematology Applications Specialist, the Sysmex hematology analyzers have floating discriminators so there should be no interferences in CBC results from giant platelets.
2. If there is instrument/ smear disagreement, add the following comment to the WBC field: *“WBC may be inaccurate due to WBC/PLT interference."*

L. **HEMOLYSIS:**

1. In vitro hemolysis of red cells after sample collection may lead to a spuriously low RBC count and hematocrit.
2. Extensive **in vivo** hemolysis may lead to a falsely elevated hemoglobin value that represents both plasma and red cell hemoglobin. Thus the MCH and MCHC may be spuriously elevated. (Measured values for red cell count and hematocrit are still correct.) If in **vivo** hemolysis is suspected:
    a. Perform the plasma replacement procedure described under "LIPEMIA" above and recalculate the MCH and MCHC with the **new** corrected hemoglobin.
    b. Verify platelet count on blood smear.
    c. Free-text the internal comment: *"Corrected for hemolysis"*.

M. **RBC LYSE RESISTANCE:**

1. Red blood cells containing large amounts of abnormal hemoglobin S or C may be more resistant to lysis. Due to RBC lyse resistance, the WBC count from the DIFF scattergram may be suspect. However, a correct count is derived from the WBC channel, which has a stronger lysing reagent.
2. To correct for the presence of RBC lyse resistance, verify the hematology analyzer WBC against a WBC estimate from the peripheral smear.

IX. EXPECTED VALUES:

The presence of elevated WBC counts, lipemia, icteria, cold agglutinins, cryoglobulins, nucleated RBCs, or platelet clumping/satellitosis, giant platelets, microcytic / fragmented / RBC lyse resistance, and hemolysis is not found in normal blood.

X. NOTES:

A. In some situations a corrected value may be unable to be obtained. If a corrected value cannot be obtained by manual methods, add the comment *“Unable to perform"* to the affected parameter in Beaker. Consult supervisor if further direction is needed.

B. Instrument voteouts will come across into WAM as “#nm”. This translates to *“Unable to perform”* in

the LIS.

C. If physician requests a platelet result on a patient with EDTA-induced platelet clumping, a platelet count may be able to be reported from a venous sample collected in **FULL** 3.2% citrate tube *(corrected x 1.1 for dilution)* as long as the citrate smear does **not** exhibit clumping and the citrate platelet count is **higher** than the EDTA platelet count.

D. Abnormal paraproteins found in Multiple Myeloma patients can falsely increase the HGB. To correct HGB, perform plasma replacement or plasma blank procedure.

XI. REFERENCES:

A. Cornbleet J. Spurious results from automated hematology cell counters. Lab Med, 1983; 14(8): 509-514.

B. Gagne C, et al. Effect of hyperchylomicronemia on the measurement of hemoglobin. Am J Clin Path, 1977; 68:584-586.

C. Nelson DA. Basic methodology. In: Davidson I, Henry JB (eds). Clinical diagnosis and management by laboratory methods. 17th ed, Philadelphia: WB Saunders, 1984: 592.

D. Koepke JA. Tips on Technology. MLO, July 1995.

E. Flagging Interpretation Guide, Sysmex, Document Number MKT-40-1010, December 2008.

F. Hematology Applications Specialist, Sysmex Diagnostics. Personal communication, 2000.

Attachments

Attachment-MCHC GREATER THAN 38 WORKFLOW.pdf

Approval Signatures

Step Description	Approver	Date
	Ann Marie Blenc: System Med Dir, Hematopath	4/7/2022
Hematology Medical Director Designee	Ann Marie Blenc: System Med Dir, Hematopath	4/7/2022
Policy and Forms Steering Committee Approval (if needed)	Michele Sedlak: Medical Technologist Lead	3/29/2022
Policy and Forms Steering Committee Approval (if needed)	Gail Juleff: Project Mgr Policy	3/9/2022
	Megan Masakowski: Mgr Laboratory	3/9/2022

	Michele Sedlak: Medical Technologist Lead	1/11/2022

History

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Last Approved by Bacarella, Rebecca: Medical Technologist on 9/23/2021, 4:18PM EDT

Draft saved by Sedlak, Michele: Medical Technologist Lead on 9/29/2021, 9:07PM EDT

Edited by Sedlak, Michele: Medical Technologist Lead on 9/29/2021, 9:08PM EDT

> Added MCHC >38 protocol from CBCWD XE-5000 procedure as an atttachment. Added Note D to Section X regarding abnormal paraproteins (sentence copied from CBCWD XE-5000) procedure.

Last Approved by Sedlak, Michele: Medical Technologist Lead on 9/29/2021, 9:08PM EDT

Last Approved by Bacarella, Rebecca: Medical Technologist on 9/30/2021, 1:10PM EDT

Draft saved by Sedlak, Michele: Medical Technologist Lead on 12/14/2021, 4:13PM EST

Edited by Sedlak, Michele: Medical Technologist Lead on 12/14/2021, 4:14PM EST

> Removed patient identifiers from screenshots.

Last Approved by Sedlak, Michele: Medical Technologist Lead on 12/14/2021, 4:14PM EST

Sent for re-approval by Sedlak, Michele: Medical Technologist Lead on 12/14/2021, 4:18PM EST

> In attachment, changed "protocol" to "workflow."

Last Approved by Sedlak, Michele: Medical Technologist Lead on 12/14/2021, 4:18PM EST

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> In attachment, changed "protocol" to "workflow."

Last Approved by Sedlak, Michele: Medical Technologist Lead on 12/14/2021, 4:19PM EST

Approval flow updated in place by Juleff, Gail: Project Mgr Policy on 1/5/2022, 9:08AM EST

Sent for re-approval by Masakowski, Megan: Mgr, Division Laboratory on 1/6/2022, 8:34AM EST

> Should we add in what parameters should be reported for plasma replacement? Should we add in what parameters should be reported for cold agglutinins if the MCHC does not correct?

Last Approved by Sedlak, Michele: Medical Technologist Lead on 1/7/2022, 11AM EST

Draft saved by Masakowski, Megan: Mgr, Division Laboratory on 1/7/2022, 2:14PM EST

Sent for re-approval by Masakowski, Megan: Mgr, Division Laboratory on 1/7/2022, 2:14PM EST

> Michele to add in cold agglutinin parameters to report.

Draft saved by Sedlak, Michele: Medical Technologist Lead on 1/11/2022, 9:53PM EST

Edited by Sedlak, Michele: Medical Technologist Lead on 1/11/2022, 9:54PM EST

> In VIII.B, added step 5 regarding which parameters may be reported if cold agglutinin does not resolve using corrective measures, and the criteria used. Also added note in VIII.A.1.f.ii: NOTE: Do not use differential results from run on diluted specimen.

Last Approved by Sedlak, Michele: Medical Technologist Lead on 1/11/2022, 9:54PM EST

Last Approved by Masakowski, Megan: Mgr, Division Laboratory on 3/9/2022, 10:55AM EST

Last Approved by Juleff, Gail: Project Mgr Policy on 3/9/2022, 10:57AM EST

Last Approved by Sedlak, Michele: Medical Technologist Lead on 3/29/2022, 5:55PM EDT

Last Approved by Blenc, Ann Marie: System Med Dir, Hematopath on 4/7/2022, 9:26AM EDT

Last Approved by Blenc, Ann Marie: System Med Dir, Hematopath on 4/7/2022, 9:28AM EDT

Activated on 4/7/2022, 9:28AM EDT