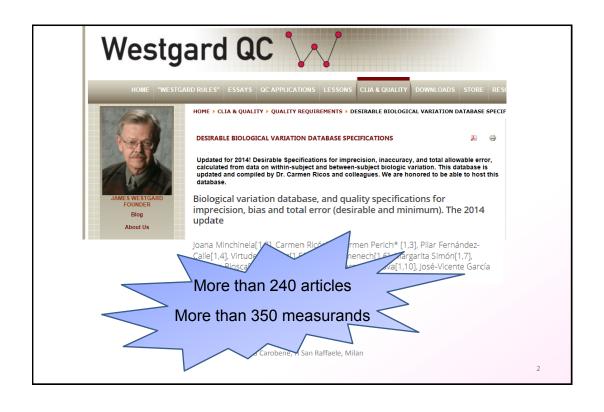
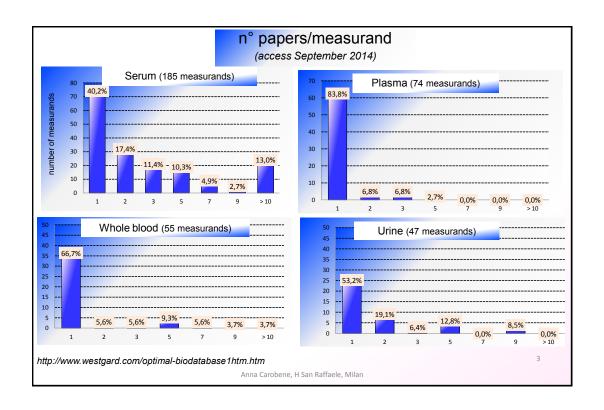
## Performance criteria based on biological variation

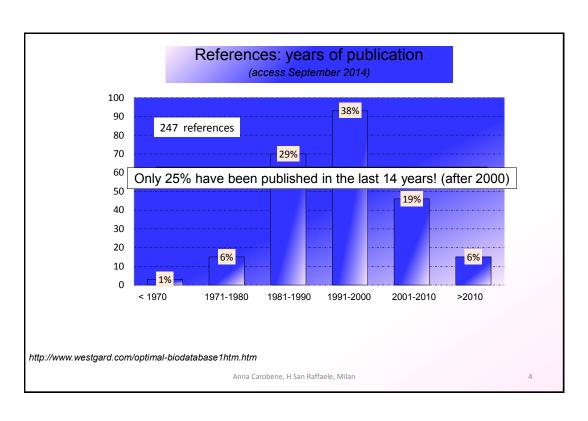
# Reliability of available biological variation information: need for improvement

Anna Carobene H San Raffaele, Milan Member of EFLM Biological Variation WG

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In 1989 Fraser and Harris published:

"Generation and application of data on biological variation in clinical chemistry"

Crit Rev Clin Lab Sci 1989;27:409-37

This review proposed a standard approach to the definition and analysis of BV:

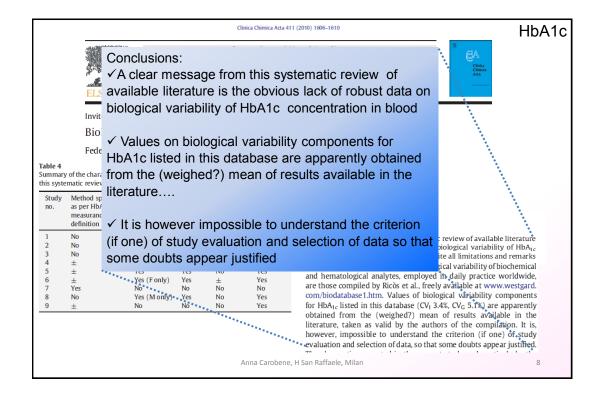
- •Selection of Subjects: They should be "reference individuals", apparently healthy (inclusion and exclusion criteria)
- •Sample collection, handling and storage: taking samples at the same time of day (usually early morning), under the same conditions, by the same phlebotomist, into tubes of the same lot number, freezing the samples to do the measurements in the same analytical run (if possible)
- •Analysis: keeping analytical variation as low as possible (one instrument, one operator, one set of calibrators, one reagent..).
- •The best experimental design: sample measurements in duplicate in a single analytical run
- •Distributional assumptions (homogeneity and normality) distribution of the data (if not normal, a transformation procedure (often logarithms) should been done;
- •Statistical treatment of raw data: detection of outliers at three different steps (set of duplicate results, results for each subject, subject in a group)
- Once we have detected and eliminated outliers, and once we have verified our distribution, we can then estimate components of Biological Variation (with ANOVA)
- √The majority of publications are very dated (1980s and 1990s), before the Fraser and Harris paper: what kind of protocol was used?
- ✓ Most BV values come from just one paper, or from very few. Was the protocol followed? Are they reliable data?
- ✓ For the BV values that come from more than one paper, was the protocol followed? Do these papers agree with each other?
- ✓ These data do not have any information about their Confidence Interval (CI). So, how can we know if they are from the same population to combine them?
- ✓ We should calculate CI around these BV data; what do we need to calculate them?
- ✓ Only after answering can we say if BV values are reliable
- ✓Some examples: HbA1c, CRP, GA, ALT, AST, γGT

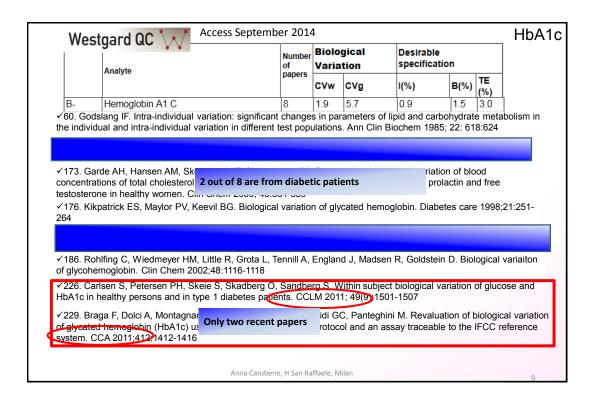
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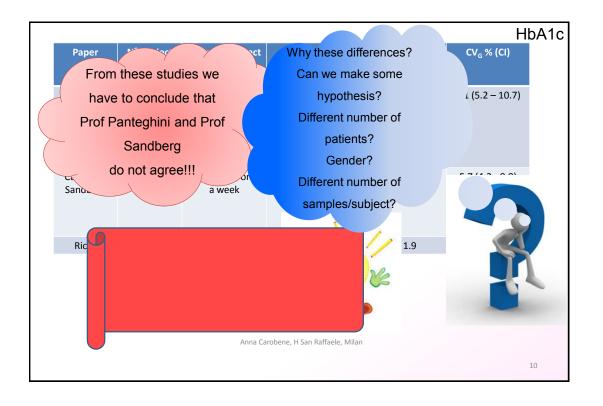
#### Glycated hemoglobin - HbA1c

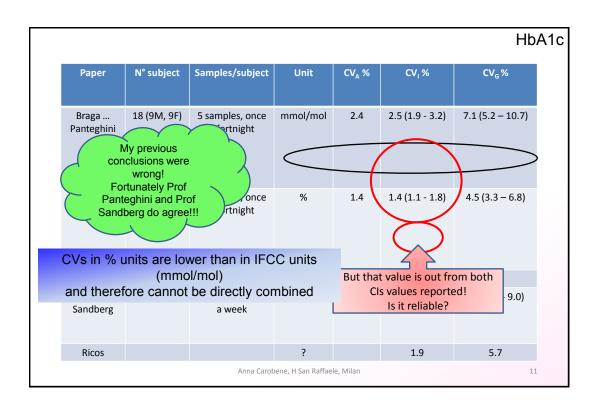


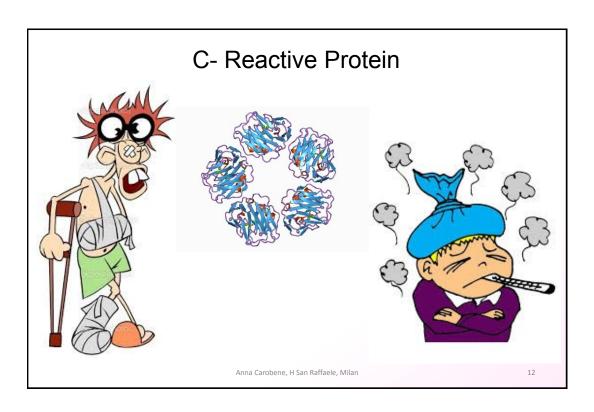
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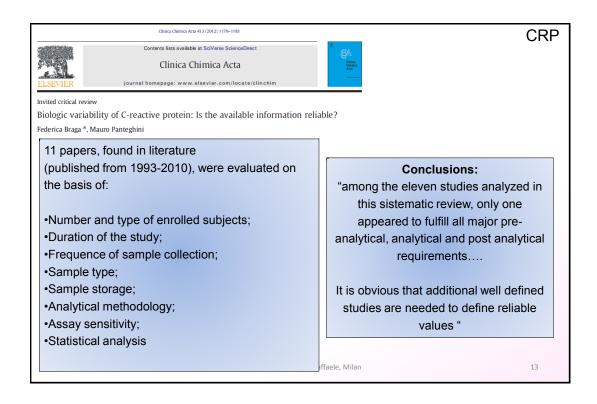


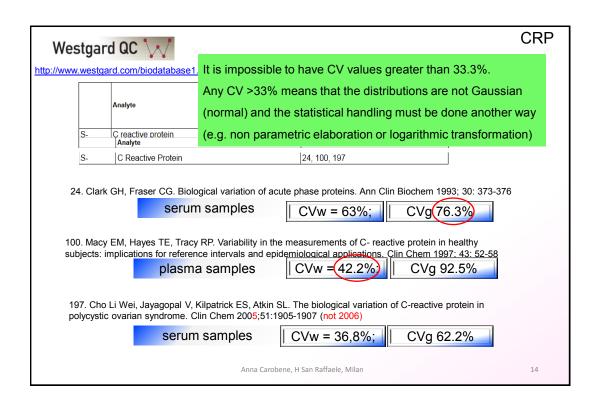












#### Glycated Albumin



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#### Westgard QC V

#### **Glycated Albumin**

	Analyte	of papers			Desirable specification		
			CVw	CVg	l(%)	B(%)	TE (%)
S-	Albumin, glycated	3	5.2	10.3	2.6	2.9	7.2

Analyte Reference 31, 60, 129 Albumin, glycated

31. Davie SJ, Whiting KL, Gould BJ. Biological variation in glycated proteins. Ann Clin Biochem 1993; 30:

Values reported are the same as in the database: CV<sub>1</sub> =5.2, CV<sub>6</sub>=10.3

They come from 10 subjects, 5 samples/sub, but just 1 replicate. It is not possible to calculate CI around the BV values obtained!!

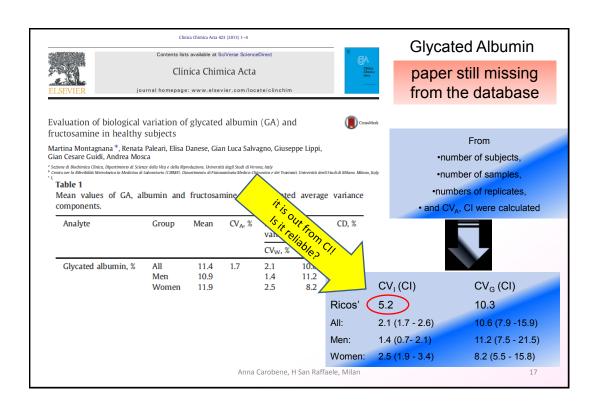
60. Godslang IF. Intra-individual variation: significant changes in parameters of lipid and carbohydrate metabolism in the individual andintra-individual variation in different test populations. Ann Clin Biochem 1985; 22: 618:624 Measurements of triglycerides, HDL Chol, Glucose, insulin and haemoglobin A1 in volunteers

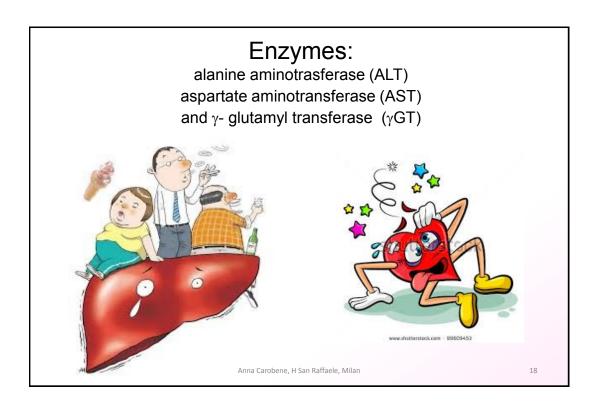
No value for glycated albumin!

129. Phillipou George, and Phillips Patrick. Intraindividual Variation of Glycohemoglobin: Implications for Interpretation and Analytical Goals. Clin Chem 1993;39:2305-2308

> Measurements of glycohemoglobin (GHb) in diabetic patients No value for glycated albumin!

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DOI 10.1515/cclm-2013-0096 — Clin Chem Lab Med 2013; aop

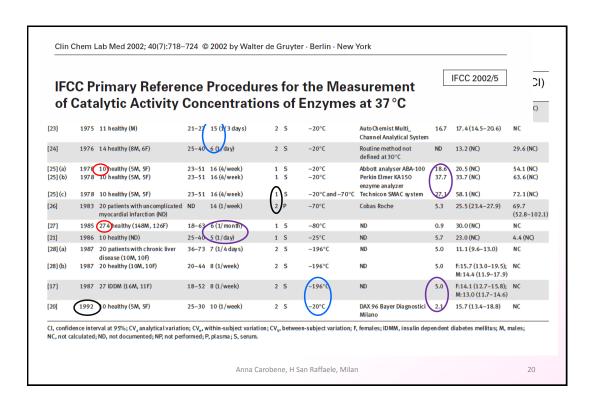
Anna Carobene\*, Federica Braga, Thomas Roraas, Sverre Sandberg and William A. Bartlett

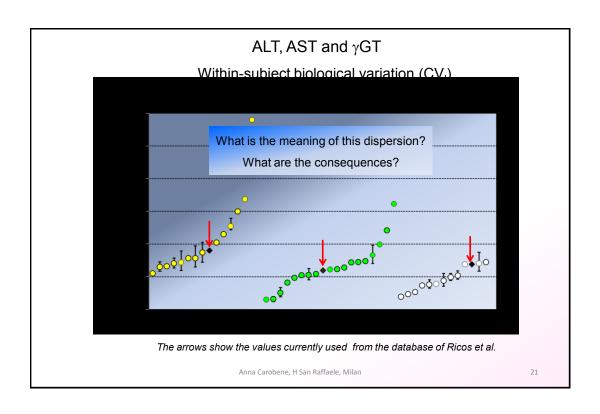
## A systematic review of data on biological variation for alanine aminotransferase, aspartate aminotransefrase and $\gamma$ -glutamyl transferase

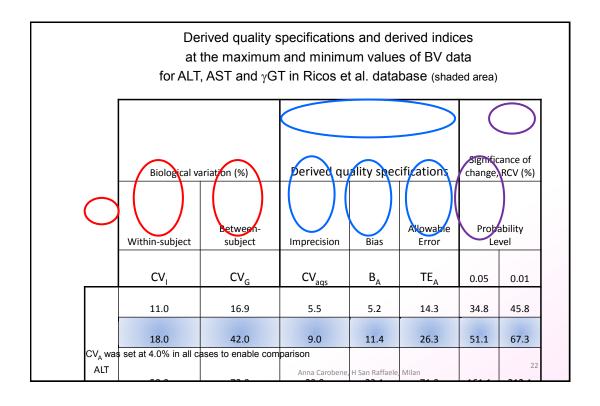
The following characteristics of studies on BV were compared:

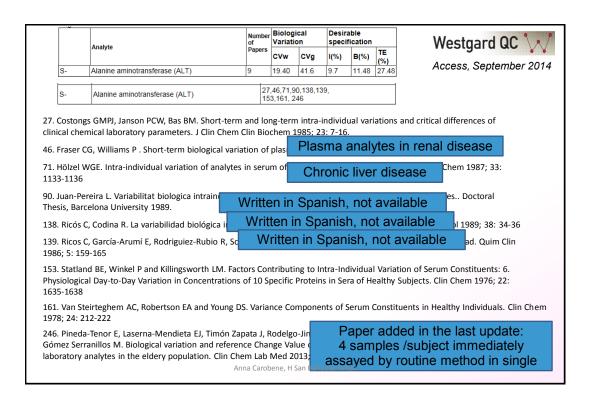
- Year of publication
- Number and type of subject (gender and health status)
- Number of samples and frequency
- Number of replicates
- Type of samples
- Sample storage
- Analytical method
- · CV<sub>A</sub>
- BV data (CV<sub>I</sub> and CV<sub>G</sub>)
- CI (if possible to calculate)

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#### On the other hand...

More than 240 articles

More than 350 measurands

An immense amount of work of a huge value!!!

And even if for some analytes the BV data are not reliable for several reasons (poor adherence to the theoretical protocol, often obsolete papers...) for many of them we have really robust BV data, both for numbers of papers and for well followed protocol!

So it is important to add the information in the database about the "quality" of the BV data published

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#### Reliability of available BV data

Since the true value cannot be absolutely determined, an estimate of the measurement uncertainty (CI) must be given.

Moreover, without CI values it is difficult to compare the estimates from different papers

## Confidence Intervals (CI): How to calculate them?

It is necessary to know:

- SD<sub>A</sub> and SD<sub>I</sub> (to calculate the ratio SD<sub>A</sub>/SD<sub>I</sub>)
  - Number of replicates (at least two)
    - Number of samples
    - · Number of individuals

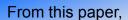
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Clinical Chemistry 58:9 1306–1313 (2012) Informatics and Statistics

Confidence Intervals and Power Calculations for Within-Person Biological Variation: Effect of Analytical Imprecision, Number of Replicates, Number of Samples, and Number of Individuals

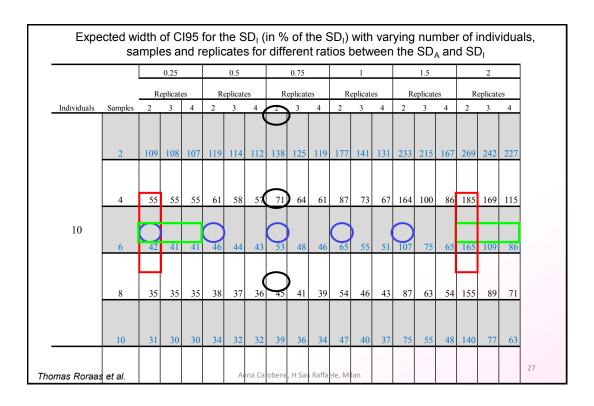
Thomas Røraas, 1\* Per H. Petersen, 1 and Sverre Sandberg 2,3



to publish BV data without their CI values is unacceptable!

(or at least without the possibility to calculate them)

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Fraser and Harris (Crit Rev Clin Lab Sci 1989;27:409-37) stated that:

"the components of variation can be obtained from a relatively small number of specimens collected from a small group of subjects ..."

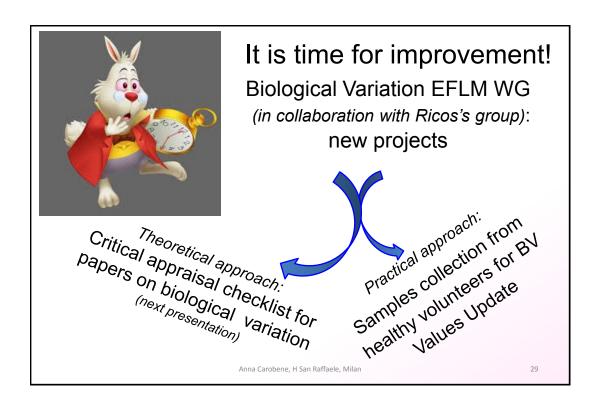
#### But now we know that:

Study design, number of replicates, number of samples, and number of subjects have a great impact on the reliability with which we can estimate the SD<sub>I</sub> of an analyte

The number of samples collected per subject is more important than the number of subjects examined when the SD<sub>1</sub> is estimated

The analytical imprecision must be taken into consideration in order to obtain good estimates

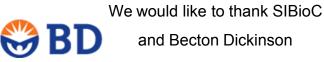
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#### Samples collection from healthy volunteers for BV Values Update

- Multicenter study involving seven European Laboratories
  - 1. S. Raffaele Hospital Milan, Italy Anna Carobene (coordinator); Ferruccio Ceriotti (promotor)
  - 2. Blood Sciences Ninewells Hospital, Dundee UK Bill Bartlett
  - 3. Haukeland University Hospital Bergen Norway Swerre Sandberg
  - 4. Hospital Universitario La Paz Madrid Spain Pilar Fernández-Calle
  - 5. Dept. of Laboratory Medicine University Hospital, Padova –Italy Mario Plebani
  - 6. Acibadem University, Gülsuyu, Maltepe Istanbul Turkey Abdurrahman Coskun
  - 7. Wilhelmina Ziekenhuis Assen Europaweg-Zuid 1, Assen, the Netherlands Niels Jonker
    - 105 healthy volunteers will be enrolled (15 subjects/lab):
      - 49 men between 18 and 50 years old (7/lab)
      - 42 women between 18 and 50 years old (6/lab)
      - 14 women > 60 years old (2/lab)
    - ➤ 10 collections /subject; once a week
      - · total of 120 aliquotes of serum/ subject,
      - total of 40 plasma EDTA / subject
      - total of 40 plasma citrate / subject
- ➤ Subject samples will be stored at -80°C, delivered and measured in a single lab

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whose fundings have made possible the kick-off of the project

### Thank you for your attention

But the best is yet to come!



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