Because sample size and power calculations are based on predictions of what the study results will be, they are particularly useful as tools to assist in planning. However, these predictions require some knowledge concerning the prevalence of the disease or condition of interest and its determinants. If there is a lack of knowledge on these factors in the population of interest, such as is the case for ARTI rates and its determinants in many South American indigenous populations, explorative studies are necessary. Therefore, we sincerely hope that the insights obtained by our study will be used in power calculations to assist in the planning of future clinical epidemiological studies. More studies are needed in order to create awareness for the disproportionately high morbidity associated with ARTIs in relation to demographic and nutritional characteristics of South American indigenous populations.

References

1. Verhagen LM, Gómez-Castellano K, Snelders E, Rivera-Olivero I, Pocaterra L, Melchers WJG, et al. Respiratory infections in Eñepa Amerindians are related to malnutrition and *Streptococcus pneumoniae* carriage. *J Infect* 2013;**67**(4):273–81.
2. Goodman SN, Berlin JA. The use of predicted confidence intervals when planning experiments and the misuse of power when interpreting results. *Ann Intern Med* 1994;**121**(3):200–6.
3. Levine M, Ensom MH. Post hoc power analysis: an idea whose time has passed? *Pharmacotherapy* 2001;**21**(4):405–9.
4. Hoenig JM, Heisey DM. The abuse of power: the pervasive fallacy of power calculations for data analysis. *Am Stat* 2001; **55**(1):19–24.
5. Walters SJ. Consultants' forum: should post hoc sample size calculations be done? *Pharm Stat* 2009;**8**(2):163–9.
6. Victora CG, Adair L, Fall C, Hallal PC, Martorell R, Richter L, et al. Maternal and child undernutrition: consequences for adult health and human capital. *Lancet* 2008;**371**(9609):340–57.
7. Caulfield LE, Richard SA, Rivera JA, Musgrove P, Black RE. Stunting, wasting, and micronutrient deficiency disorders. In: Jamison DT, Breman JG, Measham AR, Alleyne G, Claeson M, Evans DB, et al., editors. *Disease control priorities in developing countries*. 2nd ed. Washington (DC): World Bank; 2006 [Chapter 28].
8. Black RE, Allen LH, Bhutta ZA, Caulfield LE, de Onis M, Ezzati M, et al. Maternal and child undernutrition: global and regional exposures and health consequences. *Lancet* 2008; **371**(9608):243–60.
9. Bakhshi E, McArdle B, Mohammad K, Seifi B, Biglarian A. Let continuous outcome variables remain continuous. *Comput Math Methods Med* 2012;**2012**:639124.
10. Dawson NV, Weiss R. Dichotomizing continuous variables in statistical analysis: a practice to avoid. *Med Decis Making* 2012; **32**(2):225–6.

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Molecular epidemiology of *Staphylococcus aureus* bacteremia in children, Spain: Low risk of methicillin resistance

Dear Editor,

We read with interest the paper by Menne and colleagues[1] who found relatively high ratio of methicillin-resistant *Staphylococcus aureus* (MRSA) disease amongst children in Houston with an apparently protective effect of Diabetes. In contrast, we find that MRSA infection in our hospital in Spain is relatively low. We conducted a prospective observational study of *S. aureus* bacteremia (SAB) from 2007 to 2010 in children at the Hospital Universitario 12 de Octubre; a tertiary-care 1300-bed facility (176 for children) serving 550,000 people in southern Madrid. The study was approved by the Clinical Research Ethics Committee of the hospital. Included were all children $\leq$16 years old (excluding neonates) who had an isolate of *S. aureus* (SA) recovered from blood culture. SAB was defined as community-associated (CA) if it was diagnosed with a positive blood culture $<$48 h after admission in a child with no regular contact with the hospital (no predisposing factors)

Table 1 Demographic, clinical characteristics and antimicrobial resistance patterns of 57 children with *Staphylococcus aureus* bacteremia.

Characteristics	Total ($n = 57$)	No. episodes (%)		*p* Value
		Community-associated ($n = 13$)	Healthcare-associated ($n = 44$)	
Mean ± SD age (year)	3.7 (±4.4)	5.2 (±4.9)	3.3 (±4.2)	0.16
No. (%) male	43 (75.4)	10 (77)	33 (75)	0.60
Source of bacteremia				
Vascular catheter	19 (33.3)	—	19 (43.2)	—
Surgical wound	11 (19.3)	—	11 (25)	—
Skin/soft tissue	3 (5.3)	2 (15.4)	1 (2.3)	0.12
Bone/joint infection	7 (12.3)	6 (46.2)	1 (2.3)	<0.001
No focus	17 (29.8)	5 (38.5)	12 (27.3)	0.43
No. (%) with chronic and/or underlying conditions				
Previously healthy	18 (31.6)	12 (92.3)	6 (13.6)	<0.001
CHD (congenital heart disease)	9 (15.8)	—	9 (20.4)	—
Gastrointestinal disease	7 (12.3)	—	7 (15.9)	—
Genetic and/or metabolic disease	5 (8.8)	—	5 (11.4)	—
Organ solid transplant	4 (7.1)	—	4 (9.1)	—
Malignancy	4 (7.1)	—	4 (9.1)	—
Others	10 (17.5)	1 (7.7)	9 (20.5)	0.16
No. (%) with previous hospitalization	27(19.3)	—	27 (61.4)	—
Length of stay following diagnosis of SAB[a]				
Median (IQR), days	11.0 (6—20)	7.0 (6—9)	12.5 (8—24)	0.007
No. (%) with previous antimicrobial exposure	23 (40.3)	—	23 (52.3)	—
CRP[b] **level at presentation**				
Median (IQR), mg/dl	4.9 (2.3—13.8)	2.9 (1.6—4.8)	5.6 (2.9—16.0)	0.01
White blood cells at presentation[c]				
Median (IQR), cells 10^3 mm^3	11.7 (7.6—17.0)	8.9 (8.2—12.2)	12.1 (6.7—17.9)	0.27
No. (%) with empiric anti-staphylococcal therapy				
Cloxacillin or β-lactam	29 (50.9)	11 (84.6)	18 (40.9)	0.01
Vancomycin	18 (31.6)	1 (7.7)	17 (38.6)	0.01
Others	4 (7.01)	1 (7.7)	3 (6.8)	0.45
No	6 (10.5)	—	6 (13.6)	—
Outcome				
Discharge without complications	48 (84.2)	12 (92.3)	36 (81.8)	0.33
Complications	5 (8.8)	1 (7.7)	4 (9.1)	0.68
Death[d]	4 (7)	—	4 (9.1)	—
Antimicrobial resistance[e]				
Penicillin	57 (100)	13 (100)	44 (100)	—
Erythromycin	13 (22.8)	1 (7.7)	12 (21)	0.13
Clindamycin[f]	11 (19.3)	1 (7.7)	10 (22.7)	0.21
Levofloxacin	1 (1.7)	—	1 (2.3)	—
Gentamycin	2 (3.5)	—	2 (4.6)	—
Trimethoprim/sulfamethoxazole	3 (5.2)	—	3 (6.9)	—
Rifampicin	1 (1.7)	—	1 (2.3)	—

[a] *Staphylococcus aureus* bacteremia.
[b] C-reactive protein.
[c] The values of white blood cells at presentation (median and IQR) were calculated without considering oncologic/hematologic patients.
[d] 4 children died, but only two cases could be associated to *Staphylococcus aureus* bacteremia.
[e] All isolates tested were also susceptible to vancomycin, linezolid, mupirocin, and fusidic acid.
[f] Clindamycin resistance (include constitutive [$n = 1$] and inducible resistance [$n = 10$]).

and as community-onset — healthcare-associated (CO-HA) if there were predisposing factors (underlying disease, previous hospitalization, surgical procedures within the last year, or the presence of an indwelling catheter or percutaneous medical device). Hospital-onset (HO)-SAB was defined as infection diagnosed >48 h after admission. Identification and susceptibility testing were performed using conventional methods. Breakpoints for susceptibility were applied according to Clinical Laboratory Standards Institute guidelines. Accessory gene regulator (*agr*) typing and PVL detection were performed as previously described.[2,3] Multilocus sequence typing (MLST) was