

ANCA activation of such primed and adhered PMNs would then exacerbate the local inflammatory response, inducing vasculitis.

Finally, it is argued that the animal models developed are not true autoimmune models. There is no doubt that the artificial way by which the animal models are induced has its limitations, as is true for many autoimmune animal models. Nevertheless, such models are very useful because they provide us with a tool in which some of the predictions derived from in vitro studies can be investigated in an in vivo setting [3].

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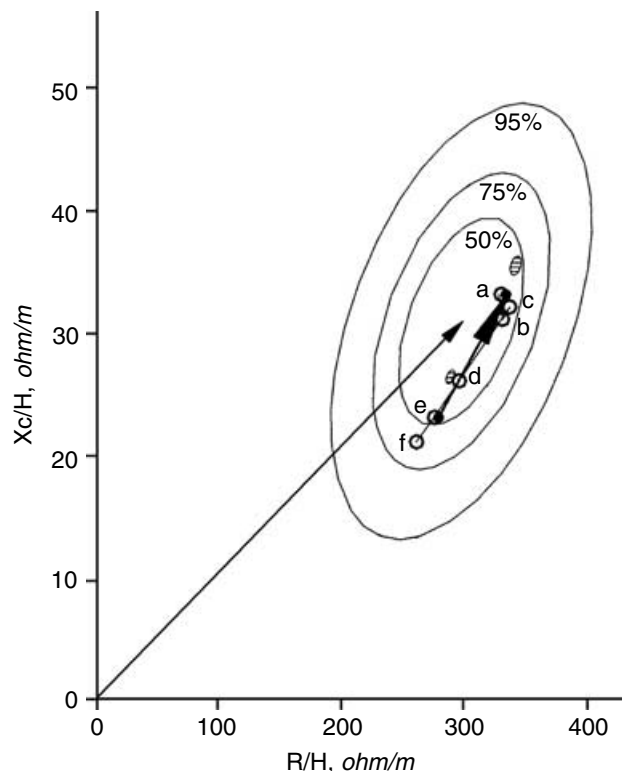
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## Bioimpedance vector migration up to three days after the hemodialysis session

**To the Editor:** Recently, Di Iorio *et al* [1] reported repeated measurements of whole-body, 50 kHz, impedance vector components, resistance (R) and reactance (Xc), performed in the last hemodialysis session of the week (27 patients, 20 males), before, at the end of the session, after 15, 30, 60, 90, 120 minutes, and in the next days, after 24, 48, and 68 hours. They focused on agreement between total body water (TBW) estimation through bioelectric impedance analysis (BIA) versus Watson equation.

We performed vector BIA (a stand-alone method using the RXc graph) [2], on data reported in Di Iorio's Table 2, and sought a pattern in impedance vector migration in the long interdialysis period.

As shown in Figure 1, mean vectors measured within 120 minutes after the session randomly fluctuated close to the end-dialysis vector (Fig. 1, labels a, b, c). Then, vectors



**Fig. 1.** The impedance vector migration associated with hemodialysis is depicted on the resistance-reactance (R-Xc) plane, normalized by the stature (R/H and Xc/H, in ohms/m). Reference values for an individual vector (thin arrow to the center of ellipses) are depicted as 50%, 75%, and 95% tolerance ellipses (male, Italian population) [2]. Solid circles represent vectors at the start and the end of the session. Open circles represent vectors after 30 (label a), 60 (label b), 120 minutes (label c), and in the next days, after 24 (label d), 48 (label e), and 68 hours (label f). The vector lengthening during the hemodialysis session is represented by the bold arrow in the direction of the major axis. The trajectory followed by vector shortening after dialysis is represented by segments of a path still parallel to the major axis of tolerance ellipses. Small, hatched ellipses represent the 95% confidence of the mean, pre (lower ellipse) to post (higher ellipse) dialysis vector displacement in a large Italian population [3].

progressively shortened along a linear trajectory made by measures after 24, 48, and 68 hours. Interestingly, the vector at 48 hours (label e) reached the baseline vector position at the start of the previous session (dot at the foot of the arrow), indicating a same fluid overload, while the vector at 68 hours shortened further, indicating a greater fluid overload (longer interdialysis period).

These findings complete the pre-post pattern we previously described in 1116 hemodialysis patients (small hatched ellipses), where the wet-dry weight cycling was associated with a cyclical, backward-forward displacement of the impedance vector [3], which can be observed

at any current frequency [4]. Linearity supports validity of monitoring with only pre- and postdialysis measurements.

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## Reply from the Authors

We appreciate Piccoli's interest in our article [1], and thank him for further analysis of the data we presented. We fully agree that a cyclical variation in BIA variables was apparent in hemodialysis patients during both dialysis and interdialysis periods according to the concept that dialysis causes a reduction of total body water, and especially (or only) of extracellular body water, and that total body water progressively increases between dialysis sessions due to water retention.

Indeed, change in resistance, reactance, and phase angle during a hemodialysis session can be affected by other factors, such as an increase in hematocrit, variations in electrolytes concentration, a rapid shift from intracellular to extracellular water, and others [2]. As a matter of fact, acute changes in body water induced by dialysis are not predicted well by data derived from BIA [3], and when BIA was applied to estimate the fluid loss during hemodialysis, overestimation usually occurred. As a consequence, changes in BIA variables during either dialysis or interdialysis periods are expected to reflect variation in total body water and its extracellular/intracellular distribution, but also to be affected by other factors. Further studies seem necessary to us to understand to which extent these data can be compared with those obtained in a healthy population or in predialysis patients. In addition, our results indicate that the measurement timing with respect to dialysis session is a crucial aspect in assessing BIA in such patients. Furthermore, since phase angle is considered an independent marker of survival [4–6], the

point of time for performing the analysis may influence the prognostic significance of such a parameter.

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## End-stage renal disease increases plasma transcobalamin and neutralizes influence of TCN 776C>G polymorphism

**To the Editor:** A lack of influence of *TCN 776C>G* has been recently reported on transcobalamin and homocysteine plasma levels in two series of patients with kidney transplant and end-stage renal disease (ESRD), contrary to what was previously observed in a healthy population [1–3]. In the ESRD series, which included 66 hemodialysis patients, influences of *MTHFR 677TT* ( $P = 0.024$ ) and *TCN 776CC* ( $P = 0.036$ ) on homocysteine disappeared in a multivariate model that included a combination of *677TTx776CC* genotypes, a confounder of each polymorphism [2]. The lack of influence of *MTHFR* agreed with some of the previous data [4]. We performed a similar study in 55 nonsupplemented hemodialysis patients. We confirmed the lack of influence of either *TCN*