C-reactive protein (CRP) is an acute-phase protein that is integral to the complement pathway of the innate immune response. CRP concentrations are highly sensitive to low-grade inflammation and have been found to be predictive of cardiovascular disease (CVD). Numerous other predictors of CVD have been found to co-vary with CRP in Western populations and other populations going through nutritional and epidemiological transitions. Less is known, however, about the covariates of CRP in populations that still live in pre-transition contexts. While Tsimane adults have higher mean CRP levels compared to the US, this difference is largely due to many more acute inflammatory cases (CRP > 10 mg/l) in the Tsimane sample, particularly for women. Even among "baseline" levels (<10 mg/l), however, Tsimane maintain higher CRP levels after controlling for their lower BMI. Here, we explore the associations between baseline CRP concentrations and numerous CVD risk and health indicators (such as BMI, blood pressure, leukocyte counts, total cholesterol, etc.), and how these associations differ from those found in Western populations. Results indicate that BMI and sedentary rate are two of the strongest predictors of higher CRP levels among the Tsimane.

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Measuring cumulative health burden as allostatic load in township-dwelling women of Cape Town, South Africa. CM Worthman1, I Le Roux2, MJ Rotheram-Borus3, 1Emory University, Atlanta, Georgia; 2Philani Nutrition and Development Project, Cape Town, South Africa; 3UCLA, Los Angeles, California.

Measurement of allostatic load as an index of cumulative physiologic burden holds promise for advancing health research and intervention, particularly for tracking life course trajectories and disparities in health. However, the construction and interpretation of indices for allostatic load have proven challenging. We report a formative study that applied systems and life history approaches to build a measure tapping key physiologic dimensions (cardiovascular, metabolic, inflammatory, pulmonary, nutritional, anthropometric) based on field-robust biomarkers (respectively, blood pressure, glycosylated hemoglobin, C-reactive protein, peak expiratory flow, hemoglobin, body mass index). Undertaken in a population with high health burden, study methods were selected to maximize on-site information return for participants (33 women ages 26–54 years) for purposes of incentivizing health messages and potentiating behavior change. Agreement for participation was 100%; a subset (n = 12) participated in a test–retest reliability study. Biomarker readings were scored using cut-off values for health risk, and the number of biomarkers exceeding cut-offs was summed to yield a scale for allostatic load. Scale components were substantially independent, meaning that each contributes unique information about allostatic load and underscoring the need for a multisystem approach. Test–retest repeats for biomarkers were strong to excellent (betas ranged 0.80–1) predictably excepting blood pressure (0.46); those for derived risk scores and scale were acceptable to excellent (kappas ranged 0.63–1). These characteristics plus a broad unskewed score distribution suggest the measure of allostatic load provides a useful index for cumulative health risk and permits analysis of health trade-offs.

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The Basques in the genetic landscape of Europe. K Young1, A Apraiz2, EJ Devor3, M Grose2, G Sun3, R Deka4, MH Crawford2. 1Family Medicine Research Division, University of Kansas Medical Center, Kansas City, Kansas; 2Department of Anthropology, University of Kansas, Lawrence, Kansas; 3Integrated DNA Technologies, Coralville, Iowa; 4Department of Environmental Health, University of Cincinnati, Cincinnati, Ohio.

This study examines the position of the Basques in the genetic landscape of Europe. Biparental (autosomal STRs and classical markers) and uniparental (mtDNA haplogroups and HVS-I sequences, and Y-chromosome STR haplotypes) markers are used to address the origin of the Basque population of Spain, as well as their role in the peopling of Europe. Three hypotheses of Basque origins are tested: The Basques (1) share a recent common ancestor with populations of the Caucasus; (2) are descendants of ancient Iberian populations who migrated from North Africa during the Neolithic; and (3) are a remnant population, the descendants of Paleolithic Europeans, who evolved in situ, with little gene flow from Neolithic farmers. Analysis of the molecular systems does not support a recent common ancestor between the Basques and populations either from the Caucasus or North Africa. Distribution of uniparental haplogroups demonstrates varying levels of Neolithic admixture in the Basque population, with both Neolithic maternal lineages (J) and paternal lineages (E1b1b, G2, J2a) present. Although these results do not suggest that the ancient Basque population had direct contact with Neolithic farmers, the presence of these markers cautions against using the Basques as a proxy Paleolithic population in genetic studies. However, the Basques do have high frequencies of other markers considered to be of Paleolithic origin (Y-chromosome: R1b, mtDNA: H, U5), and analysis of HVS-I sequences places the date of population expansion among the Basques squarely in the Paleolithic, arguing against the complete replacement demic diffusion model of the Neolithic transition.