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Respiratory disease phenotypes in a general population sample: latent transition analysis

Epidemiology, Asthma, COPD

S. Maio¹, S. Fasola², S. Baldacci¹, L. Carrozzi³, F. Pistelli⁴, M. Simoni¹, S. La Grutta², V. Muggeo⁵, G. Viegi²

¹Pulmonary Environmental Epidemiology Unit, CNR Institute of Clinical Physiology - Pisa (Italy),

²CNR Institute of Biomedicine and Molecular Immunology (IBIM) "A. Monroy" - Palermo (Italy),

³Department of Surgical, Medical, Molecular Pathology and Critical Area, University of Pisa and Pulmonary Unit, University Hospital of Pisa - Pisa (Italy), ⁴Unit of Pulmonology, Cardio-Thoracic and Vascular Department, University Hospital of Pisa - Pisa (Italy), ⁵Dept of Economics, Business and Statistics, Palermo University - Palermo (Italy)

Background: Few data are available on the temporal pattern of respiratory disease phenotypes in general population.

Aim: To detect longitudinal patterns of disease phenotypes related to risk factors and physician visits.

Methods: Pisan general population sample from 2 cross-sectional studies (PI1: 1991-93; PI2: 2009-11; n=1107), questionnaire-based data. Latent transition analysis (LTA) was performed to assess respiratory disease phenotypes at PI1 and PI2, labelled according to disease/symptom occurrence. Possible patterns were persistence, worsening and improvement of the phenotype. Multiple logistic regression models were estimated to assess the association among phenotype patterns, risk factors (smoking habits-SH and occupational exposure-OE) and physician visits, adjusting for age, sex and educational level.

Results: 4 cross-sectional phenotypes were ranked by severity in PI1 and in PI2: healthy (H) (59 and 55%), allergic rhinitis (AR) (28 and 27%), cough/phlegm (CP) (11 and 15%), asthma (A) (3 and 4%). The longitudinal patterns were: persistent H (53%), persistent AR (27%), persistent CP (9%), improvement (2%), worsening (10%).

Significant associations: persistent CP with persistent SH (OR 5.9), persistent OE (OR 2.9) and incident OE (OR 2.2); persistent CP and worsening of phenotype with current visits of family physician (OR 5.4 and OR 4.7, respectively) and of specialist (OR 2.7 and OR 3.9, respectively).

Conclusions: LTA allowed to identify four different phenotypes based on respiratory symptoms/diseases and their longitudinal patterns over 18 years. Such analysis brings new perspectives in the analyses of population-based data.

