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I patronimici in -ιδής del greco antico tra conservazione e innovazione¹

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Cet essai analyse les dérivés en -ιδής en grec ancien, présence bien attestée – avec la valeur de patronymique – dans la langue homérique. Après avoir écarté la validité des interprétations de la racine en -ιδ- de son origine de ce suffixe, qui est maintenant considéré pour le suffixe -ιδής dans sa globalité. Il s'agit, en effet, de suffixe indo-européen *-iyo- (cf. affixe bien attesté pour les adjectifs de relation), qui serait mêlé du hylem, vu qu'il présente l'évolution phonétique *y > i en position intervocalique, phénomène qui apparaît fréquemment dans la langue lydienne.

1. In greco antico vari tipi di costrutti, sia simitici che analitici, esprimono il patronimico: la perifrasi con il genitivo del nome del padre, accompagnato o meno da $\iota\delta\eta\varsigma$ o $\sigma\tau\iota\upsilon\varsigma$; un derivato con il suffisso degli aggettivi relazionati -ιδής; un derivato in -ιδής; un derivato in -ιδω-. I patronimici in -ιδής / -ιδω- sono ampiamente documentati nei poemi omerici e la loro diffusione nella tradizione successiva è stata studiata e contestata diligentemente da chi ha che chiare: certo è che, nel corso del tempo, hanno progressivamente perso il valore di patronimici e sono diventati semplici antroponimi. In un saggio del 1965 O. Masson ha negato l'esistenza, nei testi epigrafici, di autentici patronimici in -ιδής; queste forme sarebbero ormai solo antroponimi². Sarebbe

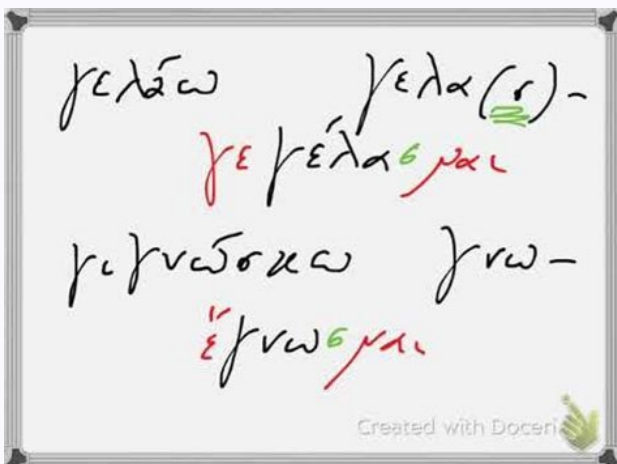
1. I temi affrontati in questo contributo rientrano nel progetto di ricerca PRIN 2008 « Mutamento e contatto tra varietà nella dialettologia linguistica del Mediterraneo » (2008-2010), coordinato da Paola Dardano, Università per Stranieri di Siena, in Göttingen 43, 1966, p. 217-234. Per un'analisi di dettaglio del fenomeno di derivazione di patronimici in -ιδής / -ιδω- cfr. p. 222-227. La spiegazione è abbastanza evidente: nel corso del tempo i patronimici hanno perso il valore originario e la documentazione epigrafica ne attesta solo l'uso come antroponimi. Non si tratta di un fenomeno sorprendente, anzi il passaggio dal patronimico all'antroponimo è frequente: basti pensare a nomi come Johnson oppure Ferrarini, che sono più o meno come « figlio di John » o « figlio di Lar ». L'ipotesi alternativa che prevede un'origine in greco antico è a ben guardare, poco convincente.



Maria-Cristina Riffero



Il mosaico drammaturgico perfetto: Arrigo Boito e la nascita di Falstaff tra Shakespeare e la Commedia dell'Arte



Perfetto vietnam.

Feuermann, P. [PMC free article] [PubMed] [Google Scholar]27. Another observation that emerged is that older annotations from isolated phenotypic observations, taken outside of other contextual data, often do not provide evidence of direct involvement of a gene in a biological process. Hinz, C. Refinements to the MAPK cascade included defining the molecular functions that are parts of the process: 'GO:0004707 MAP kinase activity', 'GO:0004708 MAP kinase kinase activity', 'GO:0004709 MAP kinase kinase kinase activity' and 'GO:0008349 MAP kinase kinase kinase activity'. Courtot, D. Mushayahama, EcolliWiki, Departments of Biology and Biochemistry and Biophysics, Texas A&M University (College Station, TX, USA); J.C. Hu, S.A. LaBonte, D.A. Siegel; FlyBase, Department of Physiology, Development and Neuroscience, University of Cambridge (Cambridge, UK); G. [PMC free article] [PubMed] [Google Scholar]3. AI Matters, Howe, S. We provide GO annotations in multiple formats: as standard GAF (Gene Association Format) and GPAD (Gene Product Association Data) annotation files, in Turtle (OWL serialization format) [], and a Blazegraph [journal, replacing the legacy MySQL output.GO is an open project, and we encourage community contributions to the knowledgebase and software. Kuiper, A. The GO ribbon visualization metaphor borrows from a viewer originally developed by the Mouse Genome Database team (28), but in contrast, the GO ribbon was developed as a lightweight, reusable widget that can be embedded in any website, and retrieves data directly from the GO resource via API.To generate a GO ribbon, all the functions (GO terms) associated with a gene of interest are mapped onto a specified GO subset using the ontology structure. Authors can contact the helpdesk at the GO website to suggest new annotations or changes to existing annotations. Pedruzzi, K. We will continue to work on improving the quality of the annotations and reviewing legacy data when appropriate. Berriman, L. GO also hosts subsets useful to groups using GO; we currently have 11 such subsets (Table 2). The GO is currently rapidly increasing the curation of GO-CAM models, and the model repository is growing. Shyptsyna, A. [PMC free article] [PubMed] [Google Scholar]4. et al.. Raciti, K. Sangrador-Vegas; Mouse Genome Informatics, The Jackson Laboratory (Bar Harbor, ME, USA); J.A. Blake, K.R. Christie, M.E. Dolan, H.J. Drabkin, D.P. Hill¹, L. Caspi R., Billington R., Fülcher C.A., Keseler I.M., Kothari A., Krummenacker M., Latendresse M., Midford P.E., Ong Q., Ong W.K. et al.. The new top level term 'GO:0140110 transcription regulator activity' has three main children - 'GO:0003700 DNA-binding transcription factor activity' (formerly labeled 'transcription factor activity, sequence-specific DNA binding'), 'GO:0140223 general transcription initiation factor activity' and 'GO:0003712 transcription coregulator activity'.The transcription factor areas of GO had previously been refactored between 2010 and 2012 (26,27) with the aim of more finely capturing all combinations of different types of protein and DNA binding activities (e.g. binding to different types of regulatory regions such as promoters and enhancers) and transcription regulation processes (positive and negative regulation). 1994; 54:5539-5542. Nucleic Acids Res. [PMC free article] [PubMed] [Google Scholar]9. The GO knowledgebase is structured using a formal ontology, by defining classes of gene functions (GO terms) that have specified relations to each other (Figure 1A). In addition, high-throughput experiments can be subject to relatively high false positive rates. Before sharing sensitive information, make sure you're on a federal government site. The ontology is versioned and tracked using a GitHub repository (. Grove, M.C. Harrison, K. Roncaglia; Gene Regulation Consortium (GRECO), Norwegian University of Science and Technology (Trondheim, Norway); M.L. Acencio, M. Tauber; IntAct/Complex Portal, EMBL-EBI (Hinxton, UK); M.J. Duesbury, N Del-Toro, B.H.M. Meldal, L. Denny P., Feuermann M., Hill D.P., Lovering R.C., Plun-Favreau H., Roncaglia P., Binkley, B.L. Dunn, J.M. Cherry, S.R. Engel, F. Diehl; WormBase California Institute of Technology (Pasadena, CA, USA), Wellcome Trust Sanger Institute (Hinxton, UK), EBI (Hinxton, UK), and Ontario Institute for Cancer Research (Toronto, Canada); J. Tripathi S., Christie K.R., Balakrishnan R., Huntley R., Hill D.P., Thommesen L., Blake J.A., Kuiper M., Lægreid A., Huala; UniProt: EMBL-EBI (Hinxton, UK), SIB Swiss Institute of Bioinformatics (SIB) (Geneva, Switzerland), and Protein Information Resource (PIR) (Washington, DC, USA and Newark, DE, USA): C. Roncaglia P., van Dam T.J.P., Christie K.R., Nacheva L., Toedt G., Huynen M.A., Huntley R.P., Gibson T.J., Lomax J.. 2017; 45:4279. 2018; 14:419-436. Douglas, N. Cilia. Zaru, C. [PMC free article] [PubMed] [Google Scholar]19. Terms moved (assigned to a new parent) are indicated by arrows. 2017; 45:D331-D338. Methods Mol. The NCBI Taxonomy database. Each triple is supported by one or more pieces of evidence, consisting of a class from ECO and a citable source, usually a scientific publication. Griffin P.C., Khadake J., LeMay K.S., Lewis S.E., Orchard S., Pask A., Pope B., Roessner U., Russell K., Seemann T., Bely, M.-C. The reactome pathway knowledgebase. GO terms are often given logical definitions, or equivalence axioms, that define the term relative to other terms in the GO or other ontologies, so that their relationships can be computationally inferred using logical reasoning (Figure 1B). If no GO LinkOut is present, that may indicate that the publication has not been used for GO annotation. Shrivastava, Z. Logie; Institute of Cardiovascular Science, University College London (London, UK); R.C. Lovering, R.P. Huntley, P. The subset can be developed for high coverage of specific species, or to represent only certain areas of the ontology, and in most cases, contain only high-level GO terms to provide a broad biological overview. If inconsistencies are noticed, they are reported to the contributing group for verification and correction as appropriate.In a pilot quality assurance effort, we have requested the review (by GO Consortium biocurators) of ~2500 manual annotations (

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