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Short Communication

Innate IgG Subclasses and Innate Lymphoid B Cells

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GM all types are genetic markers of immunoglobulin heavy constant G chains, IGHG (Fc γ) (GM) genes. The common Mendelian IGHG (Fc γ) (GM) genes have impact on disease and phenotypes of disease, with risk, protection, prognosis and outcome of disease and therapy. The alternative GM allow types of γ3, γ1 and γ2, respectively, from chromosome 14q32.3 (5´μ, δ, γ3, γ1,ψε, α1, γ2, γ4, ε, α23´) are identified with a new competitive ELISA for typing IGHG genes and subsequently assessing protein levels of innate IgG subclasses. The IgG subclasses are expressed the homozygous or heterozygous way IgG3*b/*b, IgG3*g/*g and IgG3*b/*g, IgG1*f/*f, IgG1*a/*a and IgG1*f/*a, IgG2*n/*n, IgG2*-n/*-n and IgG2*n/*-n, respectively. The alternative innate IgG sub classes are unique entities with different structures and functions. The expression from γ3–γ1– γ2 haplotypes IGHG*bfn, IGHG*bf-n, IGHG*gan and IGHG*ga-n, are indirect genetic markers of new innate lymphoid B cells. 10 Mendelian IGHG(Fcγ) (GM) diplo types, are typed in healthy Caucasians. The homozygous genotypes express restrictively of IgG molecules, seen in extreme phenotypes. The alternative GM allows types discriminate allergens, bacterial-, viral- and cancer- antigens. They control IgG subclass levels and amounts of specific IgG antibodies. The IGHG(Fc γ)(GM) genes variation have impact on diseases as infections, primary immune deficiencies, autoimmune disorders, asthma, allergy and malignancy and on active and passive immunotherapy. New innate IgG subclasses and new innate lymphoid B cells, their functional consequences and biological mechanisms, have already yielded important new insight into disease pathogenesis and individual IgG immunity.

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