FDA U.S. FOOD & DRUG
ADMINISTRATION

Cross-Protective Norovirus Epitope and Monoclonal Antibodies

Technology Summary

Norovirus accounts for the majority of the acute gastroenteritis worldwide. The dominance and persistence of norovirus is partially explained by the continuous emergence of antigenically distinct variants which escape immunity developed against previously-circulating variants. Using large-scale genomics, inventors at the FDA identified a cluster of amino acids that mapped to the surface of the major capsid protein (VP1) of GII.4 noroviruses, the predominant genotype that appears to be involved in the emergence and antigenic topology of GII.4 variants. Analyzing the sequence and epidemiological data, the cluster of amino acids represent an undescribed (potentially protective) epitope that is conserved among emerging variants.

A panel of monoclonal antibodies (mAbs) against the VP1 of the norovirus GII.4 Sydney (the current pandemic strain) and a panel of mutant virus-like particles (VLPs) has been developed and is available for licensing. Two of the mAbs showed cross-reactivity against different norovirus genotypes, by means of immunoassays using VLPs as antigens. One mAb is cross-reactive with viruses from three different genogroups (GI, GII, and GIV) infecting humans and could be used to develop different diagnostic tests.

Potential Commercial Applications

- Development of diagnostic tests or as laboratory reagents for different studies of noroviruses.
- Development of a cross-reactive vaccine

Competitive Advantages

Antibodies target a novel epitope that is:

- Immunodominant and potentially protective
- variable, but conserved among the emerging strains

Development Stage:

- Testing of extent of the cross-reactivity with VLPs representing additional genotypes.
- Testing of reactivity of the two mAbs with native viruses detected in stool samples.

Inventors: Gabriel Parra, Lauren Siltz, Kentaro Tohma

Publications:

- Ford-Siltz, L. A., et. al. Genotype-Specific Neutralization of Norovirus Is Mediated by Antibodies Against the Protruding Domain of the Major Capsid Protein. J Infect Dis. 2020 Mar 17;jiaa116. PMID: 32179892
- Parra, G. Emergence of norovirus strains: A tale of two genes. Virus Evolution. 2019, 5(2): vez048. PMID: 32161666
- Tohma, K., et. al. Population Genomics of GII.4 Norovirus Reveal Complex Diversification and New Antigen Sites Involved in the Emergence of Pandemic Strains. mBio. 2019 Sep 24;10(5):e02202-19. PMID: 31551337
- Tohma, K., et. al. Evolutionary Dynamics of non-GII Genotype 4 (GII.4) Noroviruses Reveal Limited and Independent Diversification of Variants. J Gen Virol. 2018 Aug; 99(8):1027-1035. PMID: 29916802

Intellectual Property:

Product Area: antigenic variation, caliciviruses, evolution, gastrointestinal, infection, norovirus, phylogenetic, virus, antibodies, neutralizing, epitope, method, peptide, monotypic, interfere, sequence, amino acid, binding, inhibiting, gene, genomics

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