Significant protein sequence alignment between vaccine antigens and Alopecia Areata associated autoantigen

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Background

Leung et al.[1,2] identified trichohyalin as an autoantigen involved in alopecia areata. We know from Pandemrix induced narcolepsy[3] that vaccine antigens can induce autoimmunity due to molecular mimicry. Protein sequence alignment between trichohyalin and vaccine antigens or vaccine contaminants was examined to check if the autoantibodies could have been induced by vaccines.

Method

Protein sequence for trichohyalin was obtained from Uniprot.[4]

As previously described[5], a BLASTP sequence alignment score of 19.3 was obtained comparing human hypocretin receptor and H1N1 nucleoprotein. This level of sequence alignment was sufficient to cause autoimmunity that resulted in hypocretin dysregulation and narcolepsy.[3] Therefore any score equal to or higher than 19.3 suggests high probability of autoimmunity.

While vaccines target one or a few particular viral/bacterial proteins, most vaccines are contaminated with all proteins from the virus or bacteria. Example: the Pandemrix vaccine contained both H1N1 hemagglutinin (target) and H1N1 nucleoproteins (contaminant). The exceptions are recombinant vaccines. In recombinant vaccines, the vaccine contains only the target protein from the target organism. The target protein is produced usually by genetically modifying yeast (*Saccharomyces cerevisiae*). Hepatitis B[6,7] and HPV vaccines[8] are produced using this technique. Such vaccines are however, contaminated with all Saccharomyces cerevisiae proteins.

Results

class I outer membrane porin, partial [Neisseria meningitidis]
ABB46225.1 249 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
26.2 bits(56)	3.5	Compositional matrix adjust.	10/21(48%)	11/21(52%)	0/21(0%)

```
Query  690  QEQARERIKSRIPKWQWQLES  710
            Q  AR    +R P W WQL S
Sbjct  16   QAGARTSGATRNPYWAWQLNS  36
```

bifunctional tRNA (5-methylaminomethyl-2-thiouridine)(34)-methyltransferase MnmD/FAD-dependent 5-carboxymethylaminomethyl-2-thiouridine(34) oxidoreductase MnmC [Haemophilus influenzae]
WP_065245294.1 670 1

See 1 more title(s)

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
26.2 bits(56)	4.9	Compositional matrix adjust.	13/34(38%)	15/34(44%)	9/34(26%)

```
Query  1268  QHLLGEQQERDREQERRRWQQRDRHFPEEEQLER  1301
              H +G    RD           DRHF E+EQLE
Sbjct  516   SHCIGASHIRDN---------VDRHFSEQEQLEN  540
```

excalibur domain-containing protein [Streptococcus pneumoniae]
COE78740.1 303 8

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
25.4 bits(54)	6.7	Compositional matrix adjust.	28/76(37%)	62/76(81%)	9/76(11%)

```
Query  307  RRKQEEERREQQEERR--EQQERREQQEERR--EQQLRREQEERR---EQQLRREQEEER  359
                +R+ +E+ R+Q++E+R  ++Q R++Q+E++R  ++Q+R++QEE++  ++Q R++QEE++
Sbjct  159  KRQADEQARKQEDEKRLADEQARKQQEEQKRLADEQVRKQQEEQKRLADEQTRKQQEEQK  218

Query  360  R--EQQLRREQEEERR  373
             R  ++Q R++QEE++R
Sbjct  219  RLADEQARKQQEEQKR  234
```

DEAD/DEAH box helicase [Corynebacterium diphtheriae]
WP_082261646.1 778 1

See 2 more title(s)

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
23.1 bits(48)	40	Compositional matrix adjust.	11/32(34%)	15/32(46%)	4/32(12%)

```
Query  1204  ELQRQKRKQRYRDEDQRSDLKWQWEPEKENAV  1235
              EL+R+   Q Y  + Q +DL W       N V
Sbjct  56    ELERRGIAQLYSHQAQAADLAWT----GTNVV  83
```

polymerase I [Saccharomyces cerevisiae]
AAA34888.1 1468 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
22.3 bits(46)	88	Compositional matrix adjust.	8/15(53%)	12/15(80%)	0/15(0%)

```
Query  235  DRVFQEEEEKEWRKR  249
            DR++ E +EKE+R R
Sbjct  34   DRIYDEIDEKEYRAR  48
```

protein TolA [Bordetella pertussis]
WP_065507223.1 326 1

See 1 more title(s)

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
17.7 bits(34)	1933	Compositional matrix adjust.	20/44(45%)	32/44(72%)	2/44(4%)

```
Query  520  KRQEEEERLQQRLRSEQQLRREQEERREQLLKREEEKRLEQERR  563
            K++E+EE+ +Q   + ++  R +EERR+  LK  E++RLEQERR
Sbjct  131  KKREQEEKARQAAEAAKEKARLEEERRQAELK--EKQRLEQERR  172
```

No matches were detected to measles, mumps, rubella, Hepatitis B, *C. tetani* or polio virus.

Discussion

The results above show significant sequence alignment between alopecia areata associated autoantigens and vaccine antigens. Therefore there is a high probability that these autoantibodies were induced as a result of vaccination.

Most vaccines involve injecting viral or bacterial proteins as an intramuscular injection. The route of exposure during natural infection by these viruses and bacteria is usually through the eyes, nose or mouth and not intramuscular injection. We have evolved immune mechanisms specific to routes of exposure and specific to pathogens. Examples include skin-homing versus gut-homing immune cells produced by different lymph nodes.[9] Pathogen Associated Molecular Patterns (PAMP) or Danger Associated Molecular Patterns (DAMP) recognized by pattern recognition receptors (PRR) expressed on dendritic cells (DC). Aluminum adjuvanted vaccines artificially boost and induce immune responses to viral/bacterial antigens introduced through an artificial route of exposure. This completely disrupts the natural immune response to the vaccine antigens by activating immune pathways quite different

from the pathways involved during natural infection. Therefore, protections against autoimmunity during natural infection which have evolved over millions of years, are bypassed in the case of vaccine induced immune responses.

One can therefore logically expect a skewed immune response which could include autoimmunity as was demonstrated in the case of Pandemrix induced narcolepsy. Pandemrix vaccine contained H1N1 viral proteins along with squalene as an adjuvant.

Similarly, with aluminum adjuvanted vaccines that artificially boost immune response to weakly immunogenic vaccine antigens, the natural protection against autoimmunity can be disrupted.[10]

Genetic susceptibility

The efficiency of producing autoimmunity in the presence of molecular mimicry could of course be influenced by genetic variations. So it may be possible to identify genetic markers for such susceptibility. While such identification would be interesting, the root cause, vaccines, need to be fixed.

Action

All contaminating proteins in vaccines must be removed immediately.[11] All proteins in vaccines needed for disease protection must also be thoroughly scrutinized for molecular mimicry that can result in allergic or autoimmune diseases.

References

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