**Observation**

**Escherichia coli:** Great Diversity around a Common Core

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**Abstract** The 2011 *Escherichia coli* outbreak in Germany, which resulted in more than 4,000 cases, including 908 cases of hemolytic-uremic syndrome (HUS) and at least 50 deaths, highlighted the genome plasticity of *E. coli* and the potential for new virulent strains to emerge. The analysis of 170 *E. coli* genome sequences for the presence of nine previously identified protective extraintestinal pathogenic *E. coli* antigens suggested the feasibility of a combination vaccine as a universal intervention against all pathogenic *E. coli* strains.

**Importance** This article reports on the feasibility of a combination vaccine as a universal intervention against all pathogenic *Escherichia coli* strains.
genic *E. coli* strains is highlighted in Fig. 1, which shows that all *E. coli* strains sequenced to date could be covered by a vaccine that contains at least four antigens: ECOK1_0290, ECOK1_3385, ECOK1_3457, and c0975. The first two of these antigens have been further characterized, and ECOK1_0290 is a broadly conserved adhesin, renamed FdeC (Factor adherence *E. coli*), that elicits protection in mouse sepsis and mouse urinary tract infection models (6, 7). ECOK1_3385, a putative metallopeptase, which is surface exposed and is secreted by a novel type two secretion system (T2SS), is able to confer nearly complete protection from bacteremia and mortality in a murine model of sepsis after either active or passive immunization (6). ECOK1_3457 is in-
olved in iron acquisition (8), and c0975 is annotated as a hypothetical protein. The ability of these antigens to also confer protection against intestinal pathotypes, the route of administration, and the duration of the immune response will need further investigation. In addition, the effect of vaccinating with antigens, which in some cases are also present in *E. coli* commensals, on the composition of the natural intestinal flora requires additional evaluation. However, proteobacteria (including *E. coli*) represent less than 0.1% of the human flora (9).

In conclusion, we propose that *E. coli* should be treated as a single microorganism capable of causing varied diseases in both humans and animals. Despite the alternative mechanisms that have evolved to colonize and adapt to new niches, *E. coli* strains have maintained a core genome sequence and therefore share several components that could be useful targets for a universal vaccine against *E. coli*. From an evolutionary point of view, any commensal or environmental isolate has the potential to acquire novel virulence factors and become a pathogenic strain, and the continuous exchange of genetic material between pathotypes could impact the future coverage and efficacy of a vaccine against *E. coli*. Therefore, we need to consider *E. coli* as a microorganism that is continuously evolving and look for highly represented antigens that, in combination, could provide an effective vaccine that would prevent outbreaks from occurring in the future.

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**REFERENCES**