

between-host pathogenic spread (in form of a stochastic transmission model). The model allows analyzing how the combined effects of different life history properties of a pathogen affect the evolution of novel resistant variants.

**Results:**

Vaccine resistance in highly infectious pathogens was prevented by the full-vaccine, one targeting all available epitopes, but only when the rate of pathogen evolution was low. Strikingly, a bet-hedging strategy of random administration of vaccines targeting different epitopes was the most effective in preventing vaccine resistance in pathogens with low rate of infection and high rate of evolution.

**Conclusions:**

Complex vaccination strategies utilizing a diversified vaccine portfolio may be preferable to the currently used single-vaccine approaches for long-term control of disease outbreaks. Depending on the rate of evolution and the transmissibility of a pathogen, an optimal vaccine portfolio may greatly reduce the risk of newly evolving variants. Given the biological feasibility and our knowledge about the life history of a pathogen, we recommend stronger consideration of diversification in vaccine design.

**Key messages:**

- Diversification of vaccine targets reduces the pathogens propensity to evolve vaccine resistance.
- Fast evolving pathogens are best contained by random administration of diverse multi-epitope vaccines.

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**Complex vaccination strategies prevent the emergence of vaccine resistance**

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**Background:**

Vaccination is among the most effective tools to control infectious diseases. However, the evolution of vaccine resistance, exemplified by vaccine-resistance in SARS-CoV-2, Influenza or Hepatitis B, remains a concern. As an attempt at containing antigenic evolution, multi-epitope vaccines were proposed, but displayed varying success. Rapidly evolving pathogens call for alternative vaccination procedures.

**Methods:**

We model complex vaccination strategies against a pathogen with multiple epitopes, by diversification of available vaccine targets across the vaccinated population. Our analytical model incorporates within-host evolution in response to vaccination (in form of an evolutionary Wright Fisher model) as well as