

Cover Page



Universiteit Leiden



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**Title:** On the evolution of genetic diversity in RNA virus species : uncovering barriers to genetic divergence and gene length in picorna- and nidoviruses

**Date:** 2012-10-30

## Propositions

- 1) Virus classification, if built on a genetic foundation, can provide important biological implications beyond a sole taxonomic purpose.  

|                    |               |                                          |
|--------------------|---------------|------------------------------------------|
| <i>this thesis</i> | <i>versus</i> | <i>King et al. (2012) Academic Press</i> |
|--------------------|---------------|------------------------------------------|
- 2) The observed separation of many RNA virus species on a genetic level demands an explanation. Considering these species as being biological entities may open up such an explanation.  

|                                         |               |                               |
|-----------------------------------------|---------------|-------------------------------|
| <i>this thesis</i>                      | <i>versus</i> | <i>van Regenmortel (2007)</i> |
| <i>Dobzhansky (1937) Col.Univ.Press</i> |               | <i>Inf.Genet.Evol.</i>        |
| <i>Lukashev (2010) Rev.Med.Virol.</i>   |               |                               |
- 3) The upper limit of genome size in RNA viruses may be no sole consequence of the high error rate of viral polymerases.  

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|--------------------|---------------|--------------------------------------|
| <i>this thesis</i> | <i>versus</i> | <i>Steinhauer et al. (1992) Gene</i> |
|--------------------|---------------|--------------------------------------|
- 4) A single new virus genome can provide as much critical information as hundreds of known ones do together. Hence, research in virology will benefit from the continuation and broadening of virus discovery efforts.  

*this thesis*
- 5) Comparative genomics strongly suggests that the replicative uridylyate-specific endoribonuclease is not a genetic marker of nidoviruses.  

|                    |               |                                  |
|--------------------|---------------|----------------------------------|
| <i>this thesis</i> | <i>versus</i> | <i>Snijder et al. (2003) JMB</i> |
|                    |               | <i>Ivanov et al. (2004) PNAS</i> |
- 6) Viruses present an exquisite model for studying the principals of evolution and genetic innovation in nature.  

*Moya et al. (2004) Nature Reviews*  
*Holmes et al. (2009) Annu.Rev.Ecol.Evol.Syst.*
- 7) RNA viruses exist as quasispecies, cooperative populations that are targeted as a whole by natural selection, aren't they?  

|                                         |               |                                  |
|-----------------------------------------|---------------|----------------------------------|
| <i>Eigen (1993) Scientific American</i> | <i>versus</i> | <i>Jenkins et al. (2001) MBE</i> |
| <i>Domingo et al. (1985) Gene</i>       |               | <i>Holmes (2010) JMB</i>         |
| <i>Vignuzzi et al. (2006) Nature</i>    |               |                                  |
- 8) The intrinsic difficulty of communicating a proper discrimination of facts and interpretations in bioinformatics studies results in the frequent underestimation of implications brought by bioinformatics findings as well as the effort to obtain them. Closing this cultural gap between computational and experimental research will only bring mutual benefits.  

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|----------------------------------------------|---------------|-------------------------------------|
| <i>Gorbalenya et al. (1989) FEBS Letters</i> | <i>versus</i> | <i>Allaire et al. (1994) Nature</i> |
| <i>Snijder et al. (2003) JMB</i>             |               | <i>Minskaia et al. (2006) PNAS</i>  |
- 9) As large-scale data-driven approaches are becoming common practice in biology the visual communication of results emerges as being equally important as obtaining the results.  

*Eisen et al. (1998) PNAS*  
*The 1000 Genomes Project Consortium (2010) Nature*  
*Nielsen et al. (2010) Nature Methods*
- 10) "What I cannot create, I do not understand."  

*Richard Feynman*
- 11) The number of stars in the universe is finite; otherwise there would be no darkness at night.