Secondary metabolism by industrially improved Penicillium chrysogenum strains

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Propositions with the thesis:

'' Secondary metabolism by industrially improved *Penicillium chrysogenum* strains''

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1. A successful strain improvement programme requires a narrow focus on the desired phenotype. Therefore, not all the features of the evolved mutant are predictable (*Chapter 2*)

2. The improved titer of β-lactam production obtained by the classical strain improvement programme is only a minor reflection of the broad mutational impact on secondary metabolism of *P. chrysogenum* (*Chapter 2*)

3. NRPS related secondary metabolite production is a main beneficiary of the amino acid flux alternations induced by the industrial strain improvement program of *P.chrysogenum* (*Chapter 2*)

4. The single amino acid substitution of Pks13 (*Pc21g05080*) led to the elimination of sorbicillionoids from the secondary metabolism of the *P. chrysogenum* (*Chapter 4*)

5. Histone deacetylase HdaA is a pleiotropic regulator of secondary metabolism in *P.chrysogenum* (*Chapter 3*)

6. Reliable studies on epigenetic regulation of fungal secondary metabolism can be only achieved when using strains with a wild-type background (*Chapter 3*)

7. In *P.chrysogenum*, there are two functional 6-methylsalicylic acid synthases (Pks4 and Pks18) that operate in two putative biosynthetic pathways (Chapter 5)

8. All you have to do is take a close look at yourself and you will understand everyone else. (*Isaak Asimov, Foundation's Edge*)